

**Yaen, Christopher**

---

**From:** Yaen, Christopher  
**Sent:** Tuesday, April 23, 2002 5:07 PM  
**To:** STIC-Biotech/ChemLib  
**Subject:** 09689469

could you please do a seq search on seq id no: 3-6 regular search (containing language) and oligo search (comprising language)

claims priority to 09/062,365 4/17/1998

thanks

Christopher Yaen  
Patent Examiner  
Art Unit 1642  
CM1-Rm 8E18  
Mail Box 8E12  
703-305-3586

**THIS PAGE BLANK (USPTO)**



From: Yaen, Christopher  
Sent: Tuesday, April 23, 2002 5:07 PM  
To: STIC-Biotech/ChemLib  
Subject: 09689469

could you please do a seq search on seq id no: 3-6 regular search (containing language) and oligo search (comprising language)

claims priority to 09/062,365 4/17/1998

thanks

Christopher Yaen  
Patent Examiner  
Art Unit 1642  
CM1-Rm 8E18  
Mail Box 8E12  
703-305-3586

Point of Contact:  
Toby Port  
Technical Info. Specialist  
CM1 6A04  
703-308-3634

RECEIVED  
APR 24 2002  
STIC

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 4/24  
Date Completed: 4/24  
Searcher Prep/Review: 10  
Clerical: \_\_\_\_\_  
Online time: 10

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: 8  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST(where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: es  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:17:41 ; Search time 66.52 Seconds  
(without alignments)  
44.542 Million cell updates/sec

Title: US-09-689-469-3  
Perfect score: 40  
Sequence: 1 DAERHDSGYEVHHQKLVFAEDVGNKGAIIIGMGV 40

Scoring table:  
Gapop 60.0 , Gapext 60.0

Searched: 522463 seqs, 74073290 residues

Word size : 0

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database :

A.Geneseq\_1101:\*

1: /SID8/gcgdata/geneseq/geneseq/AA1980.DAT:\*

2: /SID8/gcgdata/geneseq/geneseq/AA1981.DAT:\*

3: /SID8/gcgdata/geneseq/geneseq/AA1982.DAT:\*

4: /SID8/gcgdata/geneseq/geneseq/AA1983.DAT:\*

5: /SID8/gcgdata/geneseq/geneseq/AA1984.DAT:\*

6: /SID8/gcgdata/geneseq/geneseq/AA1985.DAT:\*

7: /SID8/gcgdata/geneseq/geneseq/AA1986.DAT:\*

8: /SID8/gcgdata/geneseq/geneseq/AA1987.DAT:\*

9: /SID8/gcgdata/geneseq/geneseq/AA1988.DAT:\*

10: /SID8/gcgdata/geneseq/geneseq/AA1989.DAT:\*

11: /SID8/gcgdata/geneseq/geneseq/AA1990.DAT:\*

12: /SID8/gcgdata/geneseq/geneseq/AA1991.DAT:\*

13: /SID8/gcgdata/geneseq/geneseq/AA1992.DAT:\*

14: /SID8/gcgdata/geneseq/geneseq/AA1993.DAT:\*

15: /SID8/gcgdata/geneseq/geneseq/AA1994.DAT:\*

16: /SID8/gcgdata/geneseq/geneseq/AA1995.DAT:\*

17: /SID8/gcgdata/geneseq/geneseq/AA1996.DAT:\*

18: /SID8/gcgdata/geneseq/geneseq/AA1997.DAT:\*

19: /SID8/gcgdata/geneseq/geneseq/AA1998.DAT:\*

20: /SID8/gcgdata/geneseq/geneseq/AA1999.DAT:\*

21: /SID8/gcgdata/geneseq/geneseq/AA2000.DAT:\*

22: /SID8/gcgdata/geneseq/geneseq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID       | Description          |
|------------|-------|-------------|--------|-------------|----------------------|
| 1          | 40    | 100.0       | 40     | 14 AAR33191 | Beta-amyloid pepti   |
| 2          | 40    | 100.0       | 40     | 15 AAR60364 | Beta-amyloid (1-40   |
| 3          | 40    | 100.0       | 40     | 18 AAW37507 | Amyloid beta prote   |
| 4          | 40    | 100.0       | 40     | 18 AAW23335 | Amyloid beta prote   |
| 5          | 40    | 100.0       | 40     | 19 AAW47226 | Beta-amyloid pepti   |
| 6          | 40    | 100.0       | 40     | 20 AAY39339 | Beta-amyloid prote   |
| 7          | 40    | 100.0       | 40     | 20 AAY39804 | Beta-amyloid prote   |
| 8          | 40    | 100.0       | 40     | 20 AAY25135 | Human amyloid beta   |
| 9          | 40    | 100.0       | 40     | 20 AAY14099 | Human amyloid beta   |
| 10         | 40    | 100.0       | 40     | 20 AAW9584  | Wild type aggregated |
| 11         | 40    | 100.0       | 40     | 20 AAW92723 | Human tachykinin a   |

|    |    |       |    |             |                    |
|----|----|-------|----|-------------|--------------------|
| 12 | 40 | 100.0 | 40 | 20 AAW81473 | Synthetic amyloid  |
| 13 | 40 | 100.0 | 40 | 22 AAE05483 | Human peptide anti |
| 14 | 40 | 100.0 | 40 | 22 AAB84426 | Partial sequence o |
| 15 | 40 | 100.0 | 40 | 22 AAB91780 | Amyloid beta-prote |
| 16 | 40 | 100.0 | 40 | 22 AAB91802 | Amyloid beta-prote |
| 17 | 40 | 100.0 | 40 | 22 AAB91813 | Amyloid beta-prote |
| 18 | 40 | 100.0 | 40 | 22 AAB91829 | Amyloid beta-prote |
| 19 | 40 | 100.0 | 41 | 15 AAB60365 | Beta-amyloid (1-41 |
| 20 | 40 | 100.0 | 41 | 20 AAY25136 | Human amyloid beta |
| 21 | 40 | 100.0 | 41 | 21 AAB11497 | Human amyloid beta |
| 22 | 40 | 100.0 | 42 | 13 AAR20330 | Sequence of A99 (b |
| 23 | 40 | 100.0 | 42 | 15 AAB60366 | Beta-amyloid (1-42 |
| 24 | 40 | 100.0 | 42 | 17 AAR95248 | Beta/A4-amyloid pe |
| 25 | 40 | 100.0 | 42 | 17 AAR94591 | Alzheimer amyloid  |
| 26 | 40 | 100.0 | 42 | 18 AAW12828 | Beta A4 peptide.   |
| 27 | 40 | 100.0 | 42 | 19 AAW64507 | Neurotoxic beta-am |
| 28 | 40 | 100.0 | 42 | 19 AAW47230 | Beta-amyloid pepti |
| 29 | 40 | 100.0 | 42 | 19 AAW42389 | Full length beta-a |
| 30 | 40 | 100.0 | 42 | 20 AAY49691 | Human beta amyloid |
| 31 | 40 | 100.0 | 42 | 20 AAY33407 | Human amyloidogeni |
| 32 | 40 | 100.0 | 42 | 20 AAY25137 | Human amyloid beta |
| 33 | 40 | 100.0 | 42 | 20 AAY08607 | Human beta-amyloid |
| 34 | 40 | 100.0 | 42 | 20 AAW29093 | A-beta-binding pep |
| 35 | 40 | 100.0 | 42 | 20 AAW9585  | Mutant aggregating |
| 36 | 40 | 100.0 | 42 | 20 AAW92726 | Human tachykinin a |
| 37 | 40 | 100.0 | 42 | 20 AAW81474 | Synthetic amyloid  |
| 38 | 40 | 100.0 | 42 | 21 AAY6956  | Beta-amyloid 1-42  |
| 39 | 40 | 100.0 | 42 | 22 AAB82622 | Amyloid-beta pepti |
| 40 | 40 | 100.0 | 42 | 22 AAE05484 | Human peptide anti |
| 41 | 40 | 100.0 | 42 | 22 AAB86134 | Human Alzheimer-be |
| 42 | 40 | 100.0 | 42 | 22 AAB91779 | Amyloid beta-prote |
| 43 | 40 | 100.0 | 42 | 22 AAB91812 | Amyloid beta-prote |
| 44 | 40 | 100.0 | 42 | 22 AAB49098 | Human amyloid beta |
| 45 | 40 | 100.0 | 42 | 22 AAB48497 | Human amyloid prot |

#### ALIGNMENTS

| RESULT | ID  | AA                        | Description |
|--------|---|---------------------------|-------------|
| 1      | AAR33191  | standard; peptide; 40 AA. |             |
| XX     | XX  |                           |             |
| AC     | AAR33191;   |                           |             |
| XX     | XX  |                           |             |
| DT     | 01-JUL-1993   | (first entry)             |             |
| XX     | XX  |                           |             |
| DE     | Beta-amyloid peptide.   |                           |             |
| XX     | XX  |                           |             |
| KM     | Alzheimer's disease; amyloid deposition; diagnosis; therapy.      |                           |             |
| XX     | XX  |                           |             |
| OS     | Synthetic.  |                           |             |
| XX     | XX  |                           |             |
| PN     | WO9304194-A.  |                           |             |
| XX     | XX  |                           |             |
| PD     | 04-MAR-1993.  |                           |             |
| XX     | XX  |                           |             |
| PF     | 10-AUG-1992;  | 92WO-US06700.             |             |
| XX     | XX  |                           |             |
| PR     | 13-AUG-1991;  | 91US-0744767.             |             |
| XX     | XX  |                           |             |
| PA     | (HARD ) HARVARD COLLEGE.  |                           |             |
| PA     | (MINU ) UNIV MINNESOTA.   |                           |             |
| XX     | XX  |                           |             |
| PI     | Maggio JE, Mantyh PW;   |                           |             |
| XX     | XX  |                           |             |
| DR     | WPI; 1993-094020/11.  |                           |             |
| XX     | XX  |                           |             |
| PT     | Detecting Alzheimer's disease using beta-amyloid peptide -        |                           |             |
| PT     | includes quantitating amyloid deposition onto tissue samples, and |                           |             |
| XX     | using screen agents as therapeutic agents                         |                           |             |
| PS     | Disclosure; Page 34; 51pp; English.                               |                           |             |

XX The peptide is an internal fragment of the beta amyloid peptide (BAP)  
 CC precursor, which was produced synthetically. The peptide, when  
 CC labelled, may be used in in vitro methods for the detection of  
 CC Alzheimer's disease.  
 CC See also AAR33192.  
 CC  
 XX

SO Sequence 40 AA;

Query Match 100.0%; Score 40; DB 14; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-36;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAERHDSGYEVHOKLVFAEDVGSNKGAIIIGLMGVV 40  
 Db 1 daerhdsgyevhoklvfaedvgsnkgaiiglmvgvv 40

# RESULT 2

ID AAR60364 standard; peptide; 40 AA.

AC AAR60364;

DT 15-MAR-1995 (first entry)

DE Beta-amyloid (1-40).

XX Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;  
 KW anti-beta-amyloid antibody; diagnosis.  
 XX

OS Homo sapiens.

PN WO9417197-A.

PD 04-AUG-1994.

PF 24-JAN-1994; 94MO-JP00089.

PR 25-JAN-1993; 93JP-0010132.

PR 05-FEB-1993; 93JP-0019035.

PR 16-NOV-1993; 93JP-0286985.

PR 28-DEC-1993; 93JP-0334773.

XX (TAKE ) TAKEDA CHEM IND LTD.

PI Kitada C, Odaka A, Suzuki N;

XX WPI; 1994-264110/32.

PT Antihodies recognising specific parts of beta-amyloid - can be

PT used for diagnosis of diseases implicating beta-amyloid, such as

PT Alzheimer's disease

XX Disclosure: Page 82; 116pp; Japanese.

PS Antihodies which recognise specific subfragments of the beta-amyloid

CC protein are claimed. Specifically, the antibodies (which are pref.

CC monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal

CC portion of beta-amyloid or they recognise residues 25-35 or 35-43

CC from the C-terminal portion. The antibodies are useful for assaying

CC beta-amyloid and its derivatives for diagnosis of Alzheimer's

CC disease.  
 CC  
 XX  
 SO Sequence 40 AA;

Db 1 daerhdsgyevhoklvfaedvgsnkgaiiglmvgvv 40

# RESULT 3

ID AAW37507 standard; peptide; 40 AA.

AC AAW37507;

DT 20-APR-1998 (first entry)

DE Amyloid beta protein fragment (1-40) immunogen.

XX Amyloid beta protein; A beta; immunogen; human; Alzheimer's disease;

KW amyloid precursor protein; soluble; APP; monoclonal antibody; diagnosis.

OS Synthetic.

PN Homo sapiens.

FT Key Location/Qualifiers

FT Cleavage-site 16..17

PN EP783104-A1.

PD 09-JUL-1997.

PE 17-DEC-1996; 96EP-0120269.

PR 27-DEC-1995; 95JP-0351296.

XX (ORIT ) ORIENTAL YEAST CO LTD.

PI Fujita T, Matuo Y, Taniguchi Y;

XX WPI; 1997-343989/32.

PT Assay for soluble amyloid precursor protein useful to diagnose

PT Alzheimer's disease - uses antibodies against amyloid beta-protein,

PT also new hybridoma producing antibodies

XX Example 1; Fig 2; 10pp; English.

XX A novel method has been developed of assaying for soluble amyloid

CC precursor protein (SAPP). The method uses an antibody against amyloid

CC beta-protein (A beta; produced from SAPP) or SAPP. The present sequence

CC represents amino acids 1 to 40 of amyloid beta-protein. SAPP can be

CC assayed accurately, and when including a monoclonal antibody recognising

CC the N-terminus of A beta and a monoclonal antibody recognising SAPP, the

CC assay can be used to diagnose Alzheimer's disease. Senior plaque

CC observed in the brain of Alzheimer's patients is primarily composed of

CC A beta, which is generated from SAPP. Simple and accurate assay of SAPP

CC is possible. The antibody (preferably monoclonal) preferably has an

CC antigen recognition site which is an amino acid sequence common to

CC A beta and SAPP, or specific to SAPP. The SAPP assayed for preferably

CC has part of the A beta sequence at its amino terminus and is preferably

CC solubilised through cleavage of the A beta between positions 16 (lysine)

CC and 17 (leucine) from the amino acid terminus. The preferred method

CC comprises immobilising one antibody (especially generated by (2)) on to

CC an insoluble carrier, capturing a substance to be assayed on to this

CC antibody, reacting another, labelling, antibody with the assay substance

CC and detecting the activity of the labelling substance bound to the

CC carrier.  
 CC  
 XX  
 SO Sequence 40 AA;

Query Match 100.0%; Score 40; DB 18; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-36;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAERHDSGYEVHOKLVFAEDVGSNKGAIIIGLMGVV 40  
 ||||||||||||||||||||||||||||||||||||||||

Db 1 daefrhdsygevhhqklvffaedvgsnkgaliglmvgvv 40

## RESULT 4

AAW23335  
ID AAW23335 standard; peptide; 40 AA.

XX  
AC AAW23335;

XX  
DT 12-MAR-1998 (first entry)

XX  
DE Amyloid beta peptide 1 used to inhibit damage to cells in Alzheimer's.

XX  
KM Amyloid beta peptide; extracellular deposit; Alzheimer's disease;

KW neurite outgrowth; microglial activation; neuronal cell degeneration;

KM receptor for advanced glycosylation end product;

KW amyloid beta peptide fibril.

XX  
OS Homo sapiens.

XX  
PN W09726913-A1.

XX  
PD 31-JUL-1997.

XX  
PF 21-JAN-1997; 97WO-US00857.

XX  
PR 26-JAN-1996; 96US-0592070.

XX  
PA (UYCO ) UNIV COLUMBIA NEW YORK.

XX  
PI Schmidt AM, Stern D, Yan SD;

XX  
DR WPI, 1997-393374/36.

XX  
PT Inhibiting damage to cells in e.g. Alzheimer's disease - using an

XX  
PT agent which inhibits interaction of an amyloid-beta peptide with a

XX  
PT receptor for advanced glycosylation end product

XX  
PS Claim 4; Page 10; 91pp; English.

XX  
CC Peptides AAW23335-36 are portions of the the amyloid beta peptide, which

XX  
CC is the principal component of extracellular deposits in Alzheimer's

XX  
CC disease. It has been shown to promote neurite outgrowth, generate

XX  
CC reactive oxygen intermediates, induce cellular oxidant stress, lead to

XX  
CC neuronal cytotoxicity, and promote microglial activation. The present

XX  
CC peptide, which comprises amino acids 1-40 of the amyloid beta peptide,

XX  
CC is used in a pharmaceutical composition. This composition comprises an

XX  
CC agent capable of inhibiting interaction of an amyloid-beta peptide with

XX  
CC a receptor for advanced glycosylation and product and a carrier. A

XX  
CC method for inhibiting interaction of amyloid beta peptide with a receptor

XX  
CC for advanced glycosylation on the surface of a cell comprises contacting

XX  
CC the cell with e.g. present peptide. Depending on the type of cell,

XX  
CC inhibiting the interaction between the amyloid beta peptide and the

XX  
CC receptor for advanced glycosylation can be used for inhibiting

XX  
CC degeneration of a neuronal cell, inhibiting formation of an amyloid beta

XX  
CC peptide fibril on a cell, inhibiting extracellular assembly of amyloid

XX  
CC beta peptide into a fibril, inhibiting aggregation of amyloid beta

XX  
CC peptide on the surface of a cell, inhibiting infiltration of a microglial

XX  
CC cell into senile plaques, and inhibiting activation of microglial cells

XX  
CC by amyloid beta peptide. The methods can be used for treating e.g.

XX  
CC diabetes, Alzheimer's Disease, senility, renal failure, hyperlipidemic

XX  
CC atherosclerosis, neuronal cytotoxicity, Down's syndrome, dementia

XX  
CC associated with head trauma, amyotrophic lateral sclerosis, multiple

XX  
CC sclerosis or neuronal degeneration.

XX  
SQ Sequence 40 AA;

XX  
Query Match 100.0%; Score 40; DB 18; Length 40;

XX  
Best Local Similarity 100.0%; Pred. No. 5.8e-36;

XX  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX  
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGALIGLMVGCV 40

Db 1 daefrhdsygevhhqklvffaedvgsnkgaliglmvgvv 40

## RESULT 5

AAW47226  
ID AAW47226 standard; peptide; 40 AA.

XX  
AC AAW47226;

XX  
DT 22-MAY-1998 (first entry)

XX  
DE Beta-amyloid peptide residues 1-40.

XX  
KM Screening assay: beta-amyloid peptide; treatment;

KW amyloidosis disease; Alzheimer's disease.

XX  
OS Homo sapiens.

XX  
PN US5721106-A.

XX  
PD 24-FEB-1998.

XX  
PF 12-SEP-1994; 94US-0304585.

XX  
PR 12-SEP-1994; 94US-0304585.

XX  
PR 13-AUG-1991; 91US-0744767.

XX  
PA (HARD ) HARVARD COLLEGE.

XX  
PI (MINU ) UNIV MINNESOTA.

XX  
PI Maglio JE, Mantyh PW;

XX  
DR WPI, 1998-168404/15.

XX  
PT New in vitro screening assay for Alzheimer's disease drugs -

XX  
PT comprises assessing binding of labelled beta-amyloid peptide to silk

XX  
PT sample

XX  
PS Claim 8; Columns 29-30; 36pp; English.

XX  
CC The present sequence was used in the development of a novel in

XX  
CC vitro screening assay for agents capable of affecting the

XX  
CC deposition of beta-amyloid peptide (BAP) on tissue. The method

XX  
CC comprises contacting a silk sample with labelled BAP, optionally

XX  
CC in the presence of a test agent, detecting the amount of label

XX  
CC bound to the silk and assessing the effect of the agent on the

XX  
CC deposition of BAP. Agents that inhibit binding of BAP to silk are

XX  
CC potentially useful for treating amyloidosis diseases, especially

XX  
CC Alzheimer's disease.

XX  
SQ Sequence 40 AA;

XX  
Query Match 100.0%; Score 40; DB 19; Length 40;

XX  
Best Local Similarity 100.0%; Pred. No. 5.8e-36;

XX  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX  
QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGALIGLMVGCV 40

XX  
RESULT 6

XX  
ID AAY39339 standard; protein; 40 AA.

XX  
AC AAY39339;

XX  
DT 01-DEC-1999 (first entry)

XX  
DE Beta-amyloid protein.

KW Beta-amyloid protein; Alzheimer's disease; extracellular amyloid plaque;  
 KM cerebral blood vessel; sulphated macromolecule; Kuru;  
 KM conophilic maltase-cross spherical amyloid plaque;  
 KM Creutzfeldt-Jacob disease; Gertsman-Straussler syndrome.  
 XX  
 OS Homo sapiens.  
 PN WO9945947-A1.  
 XX  
 XX 16-SEP-1999.  
 PD  
 XX 12-MAR-1999; 99WO-US05438.  
 PF  
 XX 13-MAR-1998; 98US-0077924.  
 PR  
 XX (UNITV ) UNIV WASHINGTON.  
 PA  
 XX Castillo G, Snow AD;  
 PI  
 DR WPI; 1999-571686/48.  
 XX  
 XX Formation of amyloid plaques using amyloid protein and sulphated  
 PT macromolecules; for, e.g. identification of agents for treating  
 PT Alzheimer's disease -  
 PS  
 XX Claim 3; Page 87; 89pp; English.  
 CC This sequence is 40 amino acids of the beta-amyloid protein. Alzheimer's  
 CC disease is characterised by the accumulation of a 39-43 amino acid  
 CC peptide termed the beta-amyloid peptide in the form of extracellular  
 CC amyloid plaques and as amyloid in the walls of cerebral blood vessels.  
 CC The invention relates to methods for the formation of conophilic  
 CC maltase-cross spherical amyloid plaques, which are characteristic of  
 CC Alzheimer's disease. The amyloid plaques are formed by co-incubation of  
 CC this beta-amyloid protein with sulphated macromolecules. The methods can  
 CC be used to study the formation of amyloid plaques and to identify  
 CC anti-plaque therapeutics. They can be used for diseases such as  
 CC Alzheimer's disease, Creutzfeldt-Jacob disease, Gertsman-Straussler  
 CC syndrome and Kuru.  
 CC  
 XX Sequence 40 AA:  
 SQ  
 Query Match 100.0%; Score 40; DB 20; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-36;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40  
 DB 1 daefrhdsgyevhhqklvffaedvgsnkgaiiglmvgvv 40  
 RESULT 7  
 AAY39804  
 ID AAY39804 standard; peptide; 40 AA.  
 XX  
 AC AAY39804;  
 XX  
 XX 29-NOV-1999 (first entry)  
 DT  
 XX  
 XX Beta-amyloid protein, Beta/A4 amyloid (1-40).  
 DE  
 XX  
 KM Beta-amyloid protein; Alzheimer's disease; amyloidosis; joint swelling;  
 KM long-standing inflammation; malignancy; Familial Mediterranean Fever;  
 KM multiple myeloma; plasma cell dyscrasia; long-term haemodialysis; Kuru;  
 KM carpal tunnel syndrome; multiple spontaneous fracture; radiolucency;  
 KM endocrine tumour; medullary carcinoma; Down's syndrome; scrapie;  
 KM Creutzfeldt-Jacob disease; Gertsman-Straussler Syndrome;  
 KM subacute spongiform encephalopathy; therapy.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 PN US5958883-A.

XX  
 PD 28-SEP-1999.  
 XX  
 PF 05-JUN-1995; 95US-0461216.  
 XX  
 PR 23-OCT-1992; 92US-0969734.  
 PR 23-SEP-1992; 92US-0950417.  
 XX  
 PA (UNITV ) UNIV WASHINGTON.  
 XX  
 XX Snow AD;  
 PI  
 DR WPI; 1999-561062/47.  
 XX  
 XX Peptides of 6-8 amino acids useful for treating or preventing  
 PT amyloidosis -  
 PS Disclosure; Column 67-68; 83pp; English.  
 CC This sequence represents a fragment of the beta-amyloid protein. The  
 CC invention relates to a method for treating or preventing a form of  
 CC amyloidosis, including Alzheimer's disease using this sequence. The  
 CC compositions may be useful for treating or preventing the amyloidosis  
 CC associated with long-standing inflammation, various forms of malignancy  
 CC (including B-cell type malignancies), Familial Mediterranean Fever,  
 CC multiple myeloma, plasma cell dyscrasias, long-term haemodialysis, carpal  
 CC tunnel syndrome, joint swelling, multiple spontaneous fractures,  
 CC radiolucency in the wrist and hip, endocrine tumours, medullary carcinoma  
 CC of the thyroid, diabetes, Alzheimer's disease, Down's syndrome,  
 CC Creutzfeldt-Jacob disease, Gertsman-Straussler Syndrome, Kuru, scrapie  
 CC and other subacute spongiform encephalopathies.  
 CC  
 XX Sequence 40 AA:  
 SQ  
 Query Match 100.0%; Score 40; DB 20; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-36;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40  
 DB 1 daefrhdsgyevhhqklvffaedvgsnkgaiiglmvgvv 40  
 RESULT 8  
 AAY25135  
 ID AAY25135 standard; peptide; 40 AA.  
 XX  
 AC AAY25135;  
 XX  
 XX 26-AUG-1999 (first entry)  
 DT  
 XX  
 XX Human amyloid beta-A4 peptide 2.  
 DE  
 XX  
 KM Amyloid protein; beta-A4 peptide; aggregation; screening; inhibition;  
 KM therapeutic drug; brain; Alzheimer's disease.  
 KM  
 XX Homo sapiens.  
 OS  
 XX  
 PN US5919631-A.  
 PD  
 XX 06-JUL-1999.  
 PF  
 XX 17-JUL-1996; 96US-0682245.  
 PR  
 XX 17-JUL-1996; 96US-0682245.  
 XX  
 PA (HMRI ) HOECHST MARION ROUSSEL INC.  
 XX  
 XX Goyal S, Paul JW, Riedel NG, Sahasrabudhe SR;  
 PI  
 DR WPI; 1999-403957/34.

PT Determination of degree of aggregation of a peptide, useful for  
PR identifying therapeutic drugs for treating Alzheimer's disease  
PS Disclosure; Column 5-6; 8pp; English.  
XX  
CC This invention describes a novel method for the determination of the  
CC degree of aggregation of an amyloid beta A4 peptide (I) in solution.  
CC Determination comprises: (a) incubating a sample of unaggregated  
CC (I) with Coomassie Brilliant Blue G 250 dye (II) which only binds to  
CC unaggregated (I); (b) measuring the amount of (II) bound to (I) to  
CC obtain a value (I); (c) repeating steps (a) and (b) with a second  
CC sample at a different time to obtain a second value (II); and (d)  
CC determining the difference between (I) and (II) which is inversely  
CC related to the degree of aggregation of (I). This method may be  
CC applied to a screen for compounds that inhibit aggregation of (I).  
CC These inhibitors may be used as therapeutic drugs to inhibit the  
CC formation of these aggregates in the brains of patients suffering  
CC from Alzheimer's disease.  
XX  
SQ Sequence 40 AA:  
  
Query Match 100.0%; Score 40; DB 20; Length 40;  
Best Local Similarity 100.0%; Pred. No. 5.8e-36;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DAEFRHDSGYEVHOKLVFEADVGSNKGAIIGLMVGVV 40  
DB 1 daefrhdsgyevhoklvfeadvgvsnkgaiiglmvgvv 40  
  
RESULT 9  
AAV14099  
ID AAV14099 standard; peptide; 40 AA.  
XX  
AC AAV14099;  
XX  
DT 21-JUL-1999 (first entry)  
XX  
DE Human beta-amyloid protein fragment.  
XX  
KW Beta-amyloid; human; amyloid plaque deposition; Alzheimer's disease;  
KM induction; AD; sleep; circadian activity; circadian rhythm disturbance.  
XX  
OS Homo sapiens.  
XX  
PN W09921978-A1.  
XX  
PD 06-MAY-1999.  
XX  
PF 27-OCT-1998; 98WO-US22731.  
XX  
PR 28-OCT-1997; 97US-0959148.  
XX  
PA (MIRI-) MIRIAM HOSPITAL LIFESPAN PARTNER.  
XX  
PI Majocha R, Newton JL, Tate BA;  
XX  
DR WPI; 1999-326700/27.  
XX  
PT Inducing amyloid plaque deposition in a mammal, used to screen for  
PT agents against Alzheimer's disease  
XX  
PS Claim 2; Page 30; 43pp; English.  
XX  
CC This sequence represents a fragment of the human beta-amyloid protein,  
CC and can be used in the method of the invention. The method is for  
CC inducing amyloid plaque deposition in a mammal by infusing into the brain  
CC an amyloid peptide (I) at a basic pH. Animals in which amyloid plaque  
CC deposition has been induced are models of human Alzheimer's disease (AD)  
CC and are used to screen for agents (A) that inhibit: (a) deposition of  
CC amyloid plaque; and (b) AD-associated disruptions to sleep and circadian  
CC activity. They may also be used to study the etiology of AD. Compared

CC with known methods for inducing plaque deposition, this process causes  
CC less mechanical damage; the vehicle used is less neurotoxic and at basic  
CC pH (I) is soluble enough for delivery by continuous infusion with  
CC effective delivery to brain tissue. The control peptide causes few, if  
CC any, plaques and does not stimulate an immune response. Most (I)-treated  
CC animals develop AD-type pathology (contrast transgenic models of the  
CC disease), including sleep and circadian rhythm disturbances.  
XX  
SQ Sequence 40 AA:  
  
Query Match 100.0%; Score 40; DB 20; Length 40;  
Best Local Similarity 100.0%; Pred. No. 5.8e-36;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DAEFRHDSGYEVHOKLVFEADVGSNKGAIIGLMVGVV 40  
DB 1 daefrhdsgyevhoklvfeadvgvsnkgaiiglmvgvv 40  
  
RESULT 10  
AAW99584  
ID AAW99584 standard; peptide; 40 AA.  
XX  
AC AAW99584;  
XX  
DT 22-JUN-1999 (first entry)  
XX  
DE Wild type aggregating amyloid-beta peptide.  
XX  
KW Aggregation; amyloid-beta peptide; fluorescent group; detection;  
KM diagnosis; Alzheimer's disease.  
XX  
OS Synthetic.  
XX  
PN Homo sapiens.  
XX  
PN W09908695-A1.  
XX  
PD 25-FEB-1999.  
XX  
PF 13-AUG-1998; 98WO-US16809.  
XX  
PR 14-AUG-1997; 97US-0055660.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Garzon-Rodriguez W, Glabe C;  
XX  
DR WPI; 1999-190112/16.  
XX  
PT New fluorescent labeled amyloid A-beta peptides  
XX  
PS Example 1; Page 21; 50pp; English.  
XX  
CC This sequence corresponds to an aggregating amyloid-beta peptide which  
CC can be covalently labeled with a fluorescent group. The detection or  
CC monitoring of an amyloid aggregate in a sample can be used to diagnose  
CC or detect a predisposition to Alzheimer's disease. The screening assays  
CC can be used to identify compounds for the treatment or amelioration of  
CC Alzheimer's disease or its symptoms. The fluorescent derivatives of the  
CC amyloid-beta peptide are also useful for exploring other aspects of  
CC amyloid structure.  
XX  
SQ Sequence 40 AA:  
  
Query Match 100.0%; Score 40; DB 20; Length 40;  
Best Local Similarity 100.0%; Pred. No. 5.8e-36;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DAEFRHDSGYEVHOKLVFEADVGSNKGAIIGLMVGVV 40  
DB 1 daefrhdsgyevhoklvfeadvgvsnkgaiiglmvgvv 40

```

RESULT 11
AAW92723
ID AAW92723 standard; peptide; 40 AA.
XX
XX
AC AAW92723;
XX
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #69.
XX
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX hereditary cerebral haemorrhage; non-inherited congenital angiodysplasia.
OS Homo sapiens.
XX
XX US5876948-A.
XX
XX 02-MAR-1999.
XX
XX 27-JUL-1991; 91US-0737371.
XX
XX 29-JUL-1991; 91US-0737371.
XX
XX 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX Yankner BA;
XX
XX WPI; 1999-189630/16.
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX Claim 1b; Column 41-42; 28pp; English.
XX
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodysplasia with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
XX Sequence 40 AA;
XX
Query Match 100.0%; Score 40; DB 20; Length 40;
Best Local Similarity 100.0%; Pred. No. 5.8e-36;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVV 40
DB 1 daefrhdsgyevhhqklvfaedvgsnkgaiiglmvgvv 40
RESULT 12
AAW81473
ID AAW81473 standard; peptide; 40 AA.
XX
XX
AC AAW81473;
XX
XX 28-JAN-1999 (first entry)
XX
XX Synthetic amyloid beta (Abeta) peptide 8 (residues 1-40).
DE Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
KW research; neurotoxicity; free-radical; glutamine synthetase.
XX
XX

```

```

OS Synthetic.
XX
XX US5840838-A.
XX
XX 24-NOV-1998.
XX
XX 29-FEB-1996; 96US-0609090.
XX
XX 29-FEB-1996; 96US-0609090.
XX
XX (KENT) UNIV KENTUCKY RES FOUND.
XX
XX Aksekov M, Butterfield DA, Carney JM, Hensley K;
XX WPI; 1999-034120/03.
XX
XX Process for treating synthetic amyloid beta peptides - by organic
XX solvent treatment, useful for studying neurotoxicity
XX
XX Claim 5; Columns 11-12; 14pp; English.
XX
XX Sequences AAW81466 to AAW81476 represent synthetic amyloid beta (Abeta)
CC peptides. The invention provides a process for treating a synthetic
CC Abeta peptide that comprises dissolving the peptide in a deoxygenated
CC solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl
CC sulfoxide, morpholinopropanesulphonic acid, dimethylformamide and
CC acetonitrile to a concentration of 0.01-10 mg/mL. Incubating the
CC solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by
CC 'evaporative deposition' in 5-10 minutes. Synthetic amyloid beta
CC peptides are useful as research tools for studying neurotoxicity
CC resulting from Abeta peptide -enhanced free-radical production. The
CC treatment increases the activity of the synthetic Abeta peptides in tests
CC to determine free-radical generating capacity and glutamine synthetase
CC inactivation.
XX
XX Sequence 40 AA;
XX
Query Match 100.0%; Score 40; DB 20; Length 40;
Best Local Similarity 100.0%; Pred. No. 5.8e-36;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVV 40
DB 1 daefrhdsgyevhhqklvfaedvgsnkgaiiglmvgvv 40
RESULT 13
AAE05483
ID AAE05483 standard; peptide; 40 AA.
XX
XX
AC AAE05483;
XX
XX 24-SEP-2001 (first entry)
XX
XX Human peptide antigen comprising beta amyloid (Abeta) 40.
DE Human; heat shock protein; hsp; A beta 40; beta amyloid; hypotensive;
XX neurodegenerative disorder; vaccine; Alzheimer's disease; hypertension;
XX age-related cognitive function loss; senile dementia; Wilson's disease;
XX Parkinson's disease; amyotrophic lateral sclerosis; cerebroprotective;
XX cerebral palsy; progressive supranuclear palsy; Guam disease; ataxia;
XX Lewy body dementia; prion disease; spongiform encephalopathy; glaucoma;
XX Creutzfeldt-Jakob disease polyglutamine disease; Huntington's disease;
XX myotonic dystrophy; neuropsychiatric disorder; seizure disorder; stroke;
XX Gilles de la Tourette's syndrome; nocturnal; chronic seizure disorder;
XX brain trauma; spinal cord trauma; acquired immunodeficiency syndrome;
XX AIDS; dementia; alcoholism; autism; retinal ischemia; ophthalmological;
XX autonomic function disorder; Friedreich's ataxia; schizophrenia; therapy;
XX vasotropic; neuroprotective; anti-HIV; human immunodeficiency virus;
XX anticonvulsant; epilepsy; neuroleptic; immunostimulant.
XX
XX Homo sapiens.
XX

```



[illegible]

|           |   |   |
|-----------|---|---|
| PR        | 08-DEC-1999;  | 99US-0169687.   |
| XX        |   |   |
| PA        | (MIND-) MINDSET BIOPHARMACEUTICALS USA INC.   |   |
| XX        |   |   |
| PI        | Chain B;  |   |
| XX        |   |   |
| DR        | WPI: 2001-381648/40.  |   |
| XX        |   |   |
| PT        | Novel chimeric peptide containing N- or C-terminal end-specific B cell epitope from naturally occurring internal peptide cleavage product (such as beta amyloid peptide) of a precursor protein, joined to T cell epitope -   |   |
| PS        | Claim 3; Page 41; 47pp; English.  |   |
| XX        |   |   |
| CC        | The present sequence represents a partial sequence of a human beta-amyloid precursor protein (APP). The peptide is used to create chimeric peptides of the invention. The chimeric peptides contain a N- or C-terminal end-specific B cell epitope from a naturally occurring internal peptide cleavage product of a precursor or mature protein, as a free N- or C-terminus, joined to a T cell epitope, with or without a spacer amino acid residue. Chimeric peptides comprising betaAP peptides slow down, reduce or prevent the accumulation of amyloid beta peptide in the extracellular space, interstitial fluid and cerebrospinal fluid of the brain, and aggregation into senile amyloid deposits or plaques. They also block the interaction of amyloid beta peptides with other molecules that contribute the neurotoxicity of amyloid beta. The chimeric peptides are useful for immunizing humans against the free N- or C-terminus of an internal self peptide cleavage product (e.g. APP peptide) derived from a precursor protein or a mature protein. The internal peptide cleavage product is the self molecule of the mammal. |   |
| SC        | Sequence  | 40 AA;  |
| XX        |   |   |
| OY        | Query Match   | 100.0%; Score 40; DB 22; Length 40;<br>Best Local Similarity 100.0%; Pred. No. 5.8e-36;<br>Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0 |
| Dd        | 1 DAEFRHDGSEVHHOKLVEFAEDVGSNKGATIGLMGVVV 40<br>1 daefrhdsgyevhhqklvfaedvgnskgaiglmvgvv 40   |   |
| RESULT 15 |   |   |
| ID        | AAB91780 standard; Peptide; 40 AA.  |   |
| AC        | AAB91780;   |   |
| XX        |   |   |
| DT        | 22-JUN-2001 (first entry)   |   |
| XX        |   |   |
| DE        | Amyloid beta-protein fragment peptide SEQ ID NO:956.  |   |
| XX        |   |   |
| KW        | Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyI; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.   |   |
| XX        |   |   |
| OS        | Homo sapiens.   |   |
| OS        | Synthetic.  |   |
| XX        |   |   |
| PX        | WO200069900-A2.   |   |
| PD        | 23-NOV-2000.  |   |
| XX        |   |   |
| PF        | 17-MAY-2000; 2000WO-US13576.  |   |
| XX        |   |   |
| PR        | 17-MAY-1999; 99US-0134406.  |   |
| PR        | 10-SEP-1999; 99US-0153406.  |   |
| PR        | 15-OCT-1999; 99US-0159783.  |   |
| XX        |   |   |
| PA        | (CONJ-) CONJUCHEM INC.  |   |
| XX        |   |   |

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;  
 XX  
 DR WPI; 2001-112059/12.

XX  
 PT Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure; Page 506; 733pp; English.

XX  
 CC The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutically active amino acid region (III) and a  
 CC reactive group (II) (e.g. succinimido and maleimido groups) attached to  
 CC a less therapeutically active amino acid region (IV), which covalently  
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity  
 CC in vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention.

XX  
 SQ Sequence 40 AA;

Query Match 100.0%; Score 40; DB 22; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-36;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHQKLVFPAEDVGSNKGAIIGLMVGVV 40  
 ||||||||||||||||||||||||||||||||||||||||  
 Db 1 daefrdsygevhhqklvfpaedvgsnkgailglmvgvv 40

Search completed: April 24, 2002, 09:21:50  
 Job time: 249 sec

## RESULT 3

F60045

Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999  
C:Accession: F60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; MUID:92017079

A:Accession: F60045

A:Molecule type: mRNA

A:Residues: 1-57 &lt;JOH&gt;

A:Cross-references: EMBL:X56127; NID:q1895; PIDN:CA39593.1; PID:q1896

C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 40; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.1e-35;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVV 40  
DB 6 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVV 45

## RESULT 4

G60045

Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)  
C:Species: Cavia porcellus (guinea pig)C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: G60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; MUID:92017079

A:Accession: G60045

A:Molecule type: mRNA

A:Residues: 1-57 &lt;JOH&gt;

A:Cross-references: EMBL:X56126

C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 40; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.1e-35;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVV 40  
DB 6 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVV 45

## RESULT 5

D60045

Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: D60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; MUID:92017079

A:Accession: D60045

A:Molecule type: mRNA

A:Residues: 1-57 &lt;JOH&gt;

A:Cross-references: EMBL:X56124

C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 40; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 2.1e-35;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVV 40  
DB 6 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVV 45

## RESULT 6

A60045

Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)  
C:Species: Canis lupus familiaris (dog)C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: A60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045; MUID:92017079

A:Accession: A60045

A:Molecule type: mRNA

A:Residues: 1-57 &lt;JOH&gt;

A:Cross-references: EMBL:X56125

C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 40; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.1e-35;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVV 40  
DB 6 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVV 45

## RESULT 7

B60045

Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)  
C:Species: Ursus maritimus (polar bear)C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999  
C:Accession: B60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045; MUID:92017079

A:Accession: B60045

A:Molecule type: mRNA

A:Residues: 1-57 &lt;JOH&gt;

A:Cross-references: EMBL:X56128; NID:q2165; PIDN:CA39593.1; PID:q2166

C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 40; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.1e-35;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVV 40  
DB 6 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVV 45

## RESULT 8

PQ0438

Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)C>Date: 30-Sep-1993 #sequence\_revision 19-Oct-1995 #text\_change 19-Oct-1995  
C:Accession: PQ0438; C60045

R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.

Biochem. Biophys. Res. Commun. 188, 905-911, 1992

A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs  
A:Reference number: PQ0438; MUID:93075180

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:19:11 ; Search time 38.65 seconds  
(without alignments)  
78.835 Million cell updates/sec

Title: US-09-689-469-3  
Perfect score: 40  
Sequence: 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLWGVV 40

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size: 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Préd. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB     | ID                  | Description           |
|------------|-------|-------------|--------|--------|---------------------|-----------------------|
| 1          | 40    | 100.0       | 42     | 2      | PN0512              | beta-amyloid protease |
| 2          | 40    | 100.0       | 57     | 2      | E60045              | Alzheimer's disease   |
| 3          | 40    | 100.0       | 57     | 2      | F60045              | Alzheimer's disease   |
| 4          | 40    | 100.0       | 57     | 2      | G60045              | Alzheimer's disease   |
| 5          | 40    | 100.0       | 57     | 2      | D60045              | Alzheimer's disease   |
| 6          | 40    | 100.0       | 57     | 2      | A60045              | Alzheimer's disease   |
| 7          | 40    | 100.0       | 57     | 2      | B60045              | Alzheimer's disease   |
| 8          | 40    | 100.0       | 82     | 2      | P00438              | Alzheimer's disease   |
| 9          | 40    | 100.0       | 695    | 1      | A47975              | Alzheimer's disease   |
| 10         | 40    | 100.0       | 770    | 1      | ORH0A4              | Alzheimer's disease   |
| 11         | 27    | 67.5        | 695    | 2      | A27485              | Alzheimer's disease   |
| 12         | 27    | 67.5        | 695    | 2      | S00550              | Alzheimer's disease   |
| 13         | 17    | 42.5        | 747    | 2      | JH0773              | Alzheimer's disease   |
| 14         | 15    | 37.5        | 33     | 2      | S23094              | beta-amyloid protease |
| 15         | 15    | 247         | 2      | B83880 | 3-oxoacyl-(acyl)-ca |                       |
| 16         | 7     | 17.5        | 416    | 2      | S16306              | membrane protein P    |
| 17         | 7     | 17.5        | 416    | 2      | B85558              | probable transport    |
| 18         | 6     | 15.0        | 64     | 2      | S10640              | epua protein - Stri   |
| 19         | 6     | 15.0        | 122    | 2      | S54715              | probable aspartate    |
| 20         | 6     | 15.0        | 130    | 2      | S63533              | profilin basic iso    |
| 21         | 6     | 15.0        | 152    | 2      | T06645              | hypothetical prote    |
| 22         | 6     | 15.0        | 173    | 2      | S44399              | NADH dehydrogenase    |
| 23         | 6     | 15.0        | 176    | 2      | B83837              | hypothetical prote    |
| 24         | 6     | 15.0        | 182    | 2      | T35807              | hypothetical prote    |
| 25         | 6     | 15.0        | 184    | 1      | A30128              | synchronous muscul    |
| 26         | 6     | 15.0        | 189    | 2      | H83281              | conserved hypothet    |
| 27         | 6     | 15.0        | 190    | 2      | G84182              | hypothetical protea   |
| 28         | 6     | 15.0        | 192    | 2      | T22142              | hypothetical protea   |
| 29         | 6     | 15.0        | 205    | 2      | F72422              | KHG-KDPC b1func1io    |

|    |   |      |     |   |        |                    |
|----|---|------|-----|---|--------|--------------------|
| 30 | 6 | 15.0 | 205 | 2 | G82358 | conserved hypothet |
| 31 | 6 | 15.0 | 213 | 2 | D86170 | hypothetical prote |
| 32 | 6 | 15.0 | 214 | 2 | S39644 | acetoin utilizatio |
| 33 | 6 | 15.0 | 219 | 2 | I52644 | neuronal protein - |
| 34 | 6 | 15.0 | 231 | 2 | B82456 | probable acetyltra |
| 35 | 6 | 15.0 | 230 | 2 | H85138 | hypothetical prote |
| 36 | 6 | 15.0 | 234 | 2 | E70982 | probable magnesium |
| 37 | 6 | 15.0 | 266 | 2 | T10609 | hypothetical prote |
| 38 | 6 | 15.0 | 273 | 2 | T06661 | hypothetical prote |
| 39 | 6 | 15.0 | 284 | 2 | S04723 | genome polypeptid  |
| 40 | 6 | 15.0 | 289 | 2 | E64330 | dihydrodipicolinat |
| 41 | 6 | 15.0 | 290 | 2 | E86284 | hypothetical prote |
| 42 | 6 | 15.0 | 291 | 2 | H81132 | hypothetical prote |
| 43 | 6 | 15.0 | 291 | 2 | E81890 | hypothetical prote |
| 44 | 6 | 15.0 | 292 | 1 | A39871 | calponin alpha, sm |
| 45 | 6 | 15.0 | 297 | 1 | S31484 | calponin H1 - pig  |

## ALIGNMENTS

## RESULT 1

PN0512  
beta-amyloid protein - guinea pig (fragment)

C:Species: Cavia porcellus (guinea pig)

C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999

C:Accession: PN0512

R:Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamlya, H.; Ohno

Biochem. Biophys. Res. Commun. 193, 624-630, 1993

A>Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra

A:Reference number: PN0512; MUID:93290653

A:Accession: PN0512

A:Molecule type: protein

A:Residues: 1-42 <SHIT>

C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type protein

C:Keywords: alternative splicing; amyloid

Query Match 100.0%; Score 40; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 1.6e-35;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLWGVV 40  
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLWGVV 40

## RESULT 2

E60045  
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)

C:Species: Ovis sp. (sheep)

C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995

C:Accession: E60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; MUID:92017079

A:Accession: E60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56130

C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type protein

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 40; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.1e-35;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLWGVV 40  
DB 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGATIGLWGVV 45

A:Accession: P00438  
 A:Molecule type: DNA  
 A:Residues: 1-82 <DAY>  
 A:Cross-references: GB:M83556; GB:M83657  
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
 Brain Res. Mol. Brain Res. 10, 299-305, 1991  
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
 A:Reference number: A60045; MUID:92017079  
 A:Accession: C60045  
 A:Molecule type: mRNA  
 A:Residues: 12-68 <JOH>  
 A:Cross-references: EMBL:X56129  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Knitz-type proteinase  
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 40; DB 2; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-35;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DA6FRHDSGEVHOKLVFAEDVGSNKGAITGLMVGIV 40  
 ||||||||||||||||||||||||||||||||||||||||  
 Db 17 DA6FRHDSGEVHOKLVFAEDVGSNKGAITGLMVGIV 56

RESULT 9  
 A:Accession: A49795  
 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque  
 C:Species: Macaca fascicularis (crab-eating macaque)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: A49795  
 R:Podlasky, M.B.; Tolan, D.R.; Selkoe, D.J.  
 Am. J. Pathol. 138, 1423-1435, 1991  
 A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a  
 A:Reference number: A49795; MUID:91273117  
 A:Accession: A49795  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-695 <POD>  
 A:Cross-references: GB:M58727; NID:9342062; PIDN:AAA36829.1; PID:9342063  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Knitz-type proteinase  
 C:Keywords: alternative splicing

Query Match 100.0%; Score 40; DB 1; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DA6FRHDSGEVHOKLVFAEDVGSNKGAITGLMVGIV 40  
 ||||||||||||||||||||||||||||||||||||||||  
 Db 597 DA6FRHDSGEVHOKLVFAEDVGSNKGAITGLMVGIV 636

RESULT 10  
 ORHUA  
 Alzheimer's disease amyloid beta protein precursor [validated] - human  
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inhibi  
 N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular  
 protein precursor splice form APP(770)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Jun-1987 #sequence\_revision 28-Jul-1995 #text\_change 15-Sep-2000  
 C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44  
 4668; A28583; A29302; A60805; J10038; S06121; A60355; A59011; A38384; S29076; S38252; S3  
 R:LeMay, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey  
 Nucleic Acids Res. 17, 517-522, 1989  
 A:Title: The Prec4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b  
 A:Reference number: S02260; MUID:89128427  
 A:Accession: S02260  
 A:Molecule type: DNA  
 A:Residues: 1-288, 'V', 365-770 <LEM1>  
 A:Cross-references: EMBL:X13466  
 A:Note: alternative splice form APP(695)  
 R:LeMay, H.G.

submitted to the EMBL Data Library, November 1988  
 A:Reference number: S05194  
 A:Accession: S05194  
 A:Molecule type: DNA  
 A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>  
 A:Cross-references: EMBL:X13466; NID:935598; PIDN:CAA31830.1; PID:9871360  
 A:Note: alternative splice form APP(695)  
 R:LaFaut, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.  
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989  
 A:Title: Characterization of the 5'-end region and the first two exons of the beta-pr  
 A:Reference number: A32277; MUID:89165870  
 A:Accession: A32277  
 A:Molecule type: DNA  
 A:Residues: 1-75 <LAF>  
 A:Cross-references: GB:M24546; GB:M24547; NID:9341202; PIDN:AA13654.1; PID:9516074  
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.  
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989  
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simila  
 A:Reference number: A33260; MUID:89392030  
 A:Accession: A33260  
 A:Molecule type: DNA  
 A:Residues: 656-737 <JOH>  
 A:Cross-references: GB:M29270; NID:9178863; PIDN:AAA51768.1; PID:9178865  
 R:Prelli, F.; Levy, E.; Van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B  
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990  
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid  
 A:Reference number: A35486; MUID:90321244  
 A:Accession: A35486  
 A:Molecule type: DNA  
 A:Residues: 672-710 <PRE1>  
 A:Note: 693-Gln was found in DNA isolated from HCHWA-D patients  
 R:Yoshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.  
 Gene 87, 257-263, 1990  
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.  
 A:Reference number: I39451; MUID:90236318  
 A:Accession: I39452  
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
 A:Molecule type: DNA  
 A:Residues: 1-770 <YOS1>  
 A:Cross-references: GB:M3112; NID:9178613; PIDN:AA859502.1; PID:9178616  
 A:Accession: I39451  
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
 A:Molecule type: DNA  
 A:Residues: 1-530, 'QMLMPVPAPEWAVGR' <YOS2>  
 A:Cross-references: GB:M34875; NID:9178608; PIDN:AA859501.1; PID:9178615  
 R:Yoshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.  
 Gene 102, 291-292, 1991  
 A:Reference number: A59020; MUID:91340168  
 A:Accession: I39453  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 656-737 <LEW>  
 A:Cross-references: GB:M37896; NID:9178618; PIDN:AAA51727.1; PID:9178620  
 A:Note: a mutation with 693-Gln is presented  
 R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.  
 Science 254, 97-99, 1991  
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe  
 A:Reference number: I59562; MUID:92022553  
 A:Accession: I59562  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 689-716, 'F', 718-737 <MUR>  
 A:Cross-references: GB:S57665; NID:9236720; PIDN:AA19991.1; PID:9236721  
 R:Kamino, K.; Orr, H.T.; Paymal, H.; Wajsmann, E.M.; Alonso, M.E.; Pulst, S.M.; Anders  
 arekiki, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Mart  
 Am. J. Hum. Genet. 51, 998-1014, 1992  
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t

A:Reference number: A44017; MUID:93035397  
 A:Accession: A44017  
 A:Molecule type: DNA  
 A:Residues: 687-692, 'G', 694-718 <KAM1>  
 A:Cross-references: GB:S45135; NID:9257377; PIDN:AA823645.1; PID:9257378  
 A:Experimental source: familial Alzheimer disease family SB  
 A:Note: Sequence extracted from NCBI backbone (NCBIP:115376)  
 A:Accession: B44017  
 A:Molecule type: DNA  
 A:Residues: 687-718 <KAM2>  
 A:Cross-references: GB:S45136; NID:9257379; PIDN:AA823646.1; PID:9257380  
 A:Experimental source: familial Alzheimer disease family LIT  
 A:Note: Sequence extracted from NCBI backbone (NCBIP:115376)  
 A:Note: This sequence has a silent mutation  
 R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.; Nature 325, 733-736, 1987  
 A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface  
 A:Reference number: A03134; MUID:87144572  
 A:Accession: A03134  
 A:Molecule type: mRNA  
 A:Residues: 1-288, 'V', 365-770 <KAN>  
 A:Cross-references: GB:Y00264; NID:928525; PIDN:CAA68374.1; PID:928526  
 A:Note: alternative splice form APP(695)  
 R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.; Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987  
 A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular A  
 A:Reference number: A29030; MUID:87231971  
 A:Accession: A29030  
 A:Molecule type: mRNA  
 A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>  
 A:Cross-references: GB:M16765; NID:9178539; PIDN:AA51722.1; PID:9178540  
 A:Note: the authors translated the codon GAG for residue 647 as Asp  
 R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.; Science 235, 877-880, 1987  
 A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid A  
 A:Reference number: A47584; MUID:87120328  
 A:Accession: A47584  
 A:Molecule type: mRNA  
 A:Residues: 674-756, 'S', 758-770 <GOL>  
 A:Cross-references: GB:M15533; NID:9178706; PIDN:AA53540.1; PID:9178707  
 A:Experimental source: brain  
 R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke Science 235, 880-884, 1987  
 A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th  
 A:Reference number: A47585; MUID:87120329  
 A:Accession: A47585  
 A:Molecule type: mRNA  
 A:Residues: 674-703 <TMN1>  
 A:Cross-references: GB:M15532; NID:9177957; PIDN:AA51564.1; PID:9177958  
 R:Dykes, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle EMBO J. 7, 949-957, 1988  
 A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec  
 A:Reference number: S02638; MUID:88296437  
 A:Accession: S02638  
 A:Molecule type: mRNA  
 A:Residues: 672-678 <DYR>  
 R:Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve Nature 331, 528-530, 1988  
 A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat  
 A:Reference number: S00707; MUID:88122640  
 A:Accession: S00707  
 A:Molecule type: mRNA  
 A:Residues: 286-344, 'I', 365-366 <TMN2>  
 A:Cross-references: EMBL:X06982; NID:928817; PIDN:CAA30042.1; PID:9292612  
 A:Experimental source: promyelocytic leukemia cell line HL60  
 A:Note: alternative splice form APP(751)  
 R:Ponte, P.; Gonzalez-Demhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; De Nature 331, 525-527, 1988  
 A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit  
 A:Reference number: S00925; MUID:88122639  
 A:Accession: S00925  
 A:Molecule type: mRNA  
 A:Residues: 1-344, 'I', 365-770 <PO2>

A:Cross-references: GB:X06989; EMBL:X00297; NID:928720; PIDN:CAA30050.1; PID:928721  
 A:Note: alternative splice form APP(751)  
 R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.; Nature 331, 530-532, 1988  
 A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibi  
 A:Reference number: A38949; MUID:88122641  
 A:Accession: A38949  
 A:Molecule type: mRNA  
 A:Residues: 287-367 <KIT>  
 A:Cross-references: GB:X06981; NID:928816; PIDN:CAA30041.1; PID:9292611  
 A:Experimental source: glioblastoma cell line  
 A:Note: alternative splice form APP(770)  
 R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ash Brain Res. Mol. Brain Res. 4, 121-131, 1988  
 A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three  
 A:Reference number: A30320  
 A:Accession: A30320  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 284-288, 'V', 365-770 <VIT1>  
 A:Accession: B30320  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 122-288, 'V', 365-770 <VIT2>  
 A:Accession: C30320  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 606-770 <VIT3>  
 R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988  
 A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease  
 A:Reference number: A31087; MUID:88124954  
 A:Accession: A31087  
 A:Molecule type: mRNA  
 A:Residues: 507-770 <ZAI>  
 A:Cross-references: GB:M18734; NID:9178572; PIDN:AA51726.1; PID:9178573  
 A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 8 as Val, GTC for residue 609 as Asp, AAT for residue 610 as Gly, and GCT for residue  
 A:Note: the cited Genbank accession number, J03594, is not in release 101.0  
 R:Masters, C.L.; Multhaup, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther,  
 Query Match 100.0%; Score 40; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-34;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 DAEFRHDSGYEVHHOKIVFPAEDVGSNKGATITLWGGV 40  
 DB 672 DAEFRHDSGYEVHHOKIVFPAEDVGSNKGATITLWGGV 711  
 RESULT 11  
 A27485  
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse  
 N:Alternate names: proteinase nexin II  
 C:Species: Mus musculus (house mouse)  
 C:Date: 31-Mar-1989 #sequence, revision 31-Mar-1989 #text, change 13-Aug-1999  
 C:Accession: A27485; S19727; I49485  
 R:Ramada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.; Biochem. Biophys. Res. Commun. 149, 665-671, 1987  
 A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein pr  
 A:Reference number: A27485; MUID:88106489  
 A:Accession: A27485  
 A:Molecule type: mRNA  
 A:Residues: 1-695 <YAM>  
 A:Cross-references: GB:M18373; NID:9191568; PIDN:AA517139.1; PID:9309085  
 A:Experimental source: brain  
 R:de Strooper, B.; van Leuven, F.; van den Berghe, H.; Biochim. Biophys. Acta 1129, 141-143, 1991  
 A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is clos  
 A:Reference number: S19727; MUID:92096458  
 A:Accession: S19727  
 A:Molecule type: mRNA  
 A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>

A:Cross-references: EMBL:X59379  
 R:Rizumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.  
 Gene 112, 189-195, 1992  
 A:Title: Positive and negative regulatory elements for the expression of the Alzheimer's  
 A:Reference number: 149485; MUID:9220998  
 A:Accession: 149485  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-19 <RES>  
 A:Cross-references: GB:D10603; NID:9220328; PIDN:BA01456.1; PID:9220329  
 C:Genetics:  
 A:Map position: 16C3  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 67.5%; Score 27; DB 2; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-21;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 HOKLVFPAEDVGSNKGAITGLMWGVV 40  
 ||||||||||||||||||||||||||||  
 DB 610 HOKLVFPAEDVGSNKGAITGLMWGVV 636

RESULT 12  
 S00550  
 Alzheimer's disease amyloid beta protein precursor - rat  
 M:Alternate names: beta-A4 amyloid protein  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 13-Aug-1999  
 C:Accession: S00550; A41245; A39820; S46251  
 R:Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.  
 EMBO J. 7, 1365-1370, 1988  
 A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain  
 A:Reference number: S00550; MUID:86312583  
 A:Accession: S00550  
 A:Molecule type: mRNA  
 A:Residues: 1-695 <SH1>  
 A:Cross-references: EMBL:X07648; NID:955616; PIDN:CA30488.1; PID:955617  
 R:Schubert, D.; Schroeder, R.; Lacobdierre, M.; Saitoh, T.; Cole, G.  
 Science 241, 223-226, 1988  
 A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core  
 A:Reference number: A41245; MUID:88264430  
 A:Accession: A41245  
 A:Molecule type: protein  
 A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>  
 A:Note: evidence for heparan sulfate attachment  
 R:Hesse, L.; Behner, D.; Masters, C.L.; Multhaup, G.  
 FEBS Lett. 349, 109-116, 1994  
 A:Title: The beta-A4 amyloid precursor protein binding to copper.  
 A:Reference number: S46251; MUID:94320627  
 A:Contents: annotation; copper binding sites  
 A:Note: rat peptides were isolated but not sequenced  
 R:Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.  
 J. Biol. Chem. 266, 8464-8469, 1991  
 A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain  
 A:Reference number: A39820; MUID:91217087  
 A:Accession: A39820  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 18-32 <POT>  
 A:Experimental source: brain  
 C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is ch  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein  
 F:625-648/Domain: transmembrane #status predicted <TM>

Query Match 67.5%; Score 27; DB 2; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-21;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 HOKLVFPAEDVGSNKGAITGLMWGVV 40  
 ||||||||||||||||||||||||||||  
 DB 610 HOKLVFPAEDVGSNKGAITGLMWGVV 636

RESULT 13  
 JH0773  
 Alzheimer's disease amyloid beta protein precursor - African clawed frog  
 C:Species: Xenopus laevis (African clawed frog)  
 C>Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 13-Aug-1999  
 C:Accession: JH0773  
 R:Okado, H.; Okamoto, H.  
 Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992  
 A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: development  
 A:Reference number: JH0773; MUID:93129227  
 A:Accession: JH0773  
 A:Molecule type: mRNA  
 A:Residues: 1-747 <OKA>  
 A:Cross-references: GB:S52417; NID:9263150; PIDN:AAB24853.1; PID:9263151  
 A:Experimental source: larva  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 C:Keywords: alternative splicing; amyloid  
 F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 42.5%; Score 17; DB 2; Length 747;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-10;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 VGSNKGAITGLMWGVV 40  
 ||||||||||||||||||||||||  
 DB 672 VGSNKGAITGLMWGVV 688

RESULT 14  
 S23094  
 beta-amyloid protein precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 03-May-1996  
 C:Accession: S23094  
 R:Kojima, S.; Omori, M.  
 FEBS Lett. 304, 57-60, 1992  
 A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic protein  
 A:Reference number: S23094; MUID:92316198  
 A:Accession: S23094  
 A:Molecule type: protein  
 A:Residues: 1-33 <ROJ>  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

Query Match 37.5%; Score 15; DB 2; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-09;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 HOKLVFPAEDVGSNK 28  
 ||||||||||||||||  
 DB 19 HOKLVFPAEDVGSNK 33

RESULT 15  
 B83880  
 3-oxoacyl-(acyl-carrier protein) reductase B81842 [Imported] - Bacillus halodurans (S  
 C:Species: Bacillus halodurans  
 C>Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 31-Dec-2000  
 C:Accession: B83880  
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H  
 Nucleic Acids Res. 28, 4317-4331, 2000  
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a  
 A:Reference number: A83650; MUID:20263314  
 A:Accession: B83880  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-247 <STO>

A:Cross-references: GB:AP001513; GB:BA000004; NID:G10174345; PIDN:BAB05561.1; GSPDB:GN00  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: BH1842  
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 17.5%; Score 7; DB 2; Length 247;  
Best Local Similarity 100.0%; Pred. No. 5.1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 28 KGAIIGL 34  
|||||  
DB 159 KGAIIGL 165

Search completed: April 24, 2002, 09:23:15  
Job time: 244 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:18:21 : Search time 32.21 seconds  
(without alignments)  
27.946 Million cell updates/sec

Title: US-09-689-469-3

Perfect score: 40  
Sequence: 1 DAEFRHDSGYEVHHQKLVFAEDVSNKGALIGLVGCV 40

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 212252 seqs, 22503292 residues

Word size : 0

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PTOS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 40    | 100.0       | 40     | 1     | US-07-744-767A-1  |
| 2          | 40    | 100.0       | 40     | 1     | US-08-235-400-2   |
| 3          | 40    | 100.0       | 40     | 1     | US-08-476-464A-2  |
| 4          | 40    | 100.0       | 40     | 1     | US-08-304-585-1   |
| 5          | 40    | 100.0       | 40     | 1     | US-08-302-808-3   |
| 6          | 40    | 100.0       | 40     | 2     | US-08-433-734-1   |
| 7          | 40    | 100.0       | 40     | 2     | US-08-609-090-8   |
| 8          | 40    | 100.0       | 40     | 2     | US-07-737-371E-69 |
| 9          | 40    | 100.0       | 40     | 2     | US-08-682-245A-2  |
| 10         | 40    | 100.0       | 40     | 2     | US-08-986-948-3   |
| 11         | 40    | 100.0       | 40     | 2     | US-08-461-216-1   |
| 12         | 40    | 100.0       | 40     | 4     | US-08-959-148-1   |
| 13         | 40    | 100.0       | 40     | 5     | PCT-US92-06700-1  |
| 14         | 40    | 100.0       | 41     | 1     | US-08-302-808-4   |
| 15         | 40    | 100.0       | 41     | 2     | US-08-682-245A-3  |
| 16         | 40    | 100.0       | 41     | 2     | US-08-986-948-4   |
| 17         | 40    | 100.0       | 42     | 1     | US-07-744-767A-2  |
| 18         | 40    | 100.0       | 42     | 1     | US-08-179-574-1   |
| 19         | 40    | 100.0       | 42     | 1     | US-08-347-144-1   |
| 20         | 40    | 100.0       | 42     | 1     | US-08-462-859A-19 |
| 21         | 40    | 100.0       | 42     | 1     | US-08-123-659A-19 |
| 22         | 40    | 100.0       | 42     | 1     | US-08-464-247A-19 |
| 23         | 40    | 100.0       | 42     | 1     | US-08-464-248A-19 |
| 24         | 40    | 100.0       | 42     | 1     | US-08-476-464A-1  |
| 25         | 40    | 100.0       | 42     | 1     | US-08-304-585-2   |
| 26         | 40    | 100.0       | 42     | 1     | US-08-302-808-5   |
| 27         | 40    | 100.0       | 42     | 1     | US-08-268-348A-1  |

|    |    |       |    |   |                   |                    |
|----|----|-------|----|---|-------------------|--------------------|
| 28 | 40 | 100.0 | 42 | 2 | US-08-433-734-2   | Sequence 2, Appl1  |
| 29 | 40 | 100.0 | 42 | 2 | US-08-609-090-9   | Sequence 9, Appl1  |
| 30 | 40 | 100.0 | 42 | 2 | US-07-737-371E-72 | Sequence 72, Appl1 |
| 31 | 40 | 100.0 | 42 | 2 | US-08-422-333-4   | Sequence 4, Appl1  |
| 32 | 40 | 100.0 | 42 | 2 | US-08-682-245A-4  | Sequence 4, Appl1  |
| 33 | 40 | 100.0 | 42 | 2 | US-08-986-948-5   | Sequence 5, Appl1  |
| 34 | 40 | 100.0 | 42 | 3 | US-08-717-551A-2  | Sequence 2, Appl1  |
| 35 | 40 | 100.0 | 42 | 4 | US-09-388-890-1   | Sequence 1, Appl1  |
| 36 | 40 | 100.0 | 42 | 4 | US-09-005-215-20  | Sequence 20, Appl1 |
| 37 | 40 | 100.0 | 42 | 5 | PCT-US92-06700-2  | Sequence 2, Appl1  |
| 38 | 40 | 100.0 | 42 | 5 | PCT-US93-00325-1  | Sequence 1, Appl1  |
| 39 | 40 | 100.0 | 43 | 1 | US-08-235-400-1   | Sequence 1, Appl1  |
| 40 | 40 | 100.0 | 43 | 1 | US-08-437-067-1   | Sequence 1, Appl1  |
| 41 | 40 | 100.0 | 43 | 1 | US-08-302-808-6   | Sequence 6, Appl1  |
| 42 | 40 | 100.0 | 43 | 1 | US-08-079-511-1   | Sequence 1, Appl1  |
| 43 | 40 | 100.0 | 43 | 1 | US-08-467-607-1   | Sequence 1, Appl1  |
| 44 | 40 | 100.0 | 43 | 2 | US-08-404-831-1   | Sequence 1, Appl1  |
| 45 | 40 | 100.0 | 43 | 3 | US-08-976-179-1   | Sequence 1, Appl1  |

#### ALIGNMENTS

```
RESULT 1
US-07-744-767A-1
; Sequence 1, Application US/07744767A
; Patent No. 5434050
;
GENERAL INFORMATION:
; APPLICANT: Maglio, John E.
; APPLICANT: Mantyh, Patrick W.
; TITLE OF INVENTION: Labelled -Amyloid Peptide and Methods
; TITLE OF INVENTION: for Use in Detecting Alzheimer's Disease
; NUMBER OF SEQUENCES: 3
;
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner, P.A.
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07744,767A
; FILING DATE: 13-AUG-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muelling, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 600.226-US-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
;
INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-07-744-767A-1
```

Query Match 100.0%; Score 40; DB 1; Length 40;  
Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVSNKGALIGLVGCV 40  
|||||  
Db 1 DAEFRHDSGYEVHHQKLVFAEDVSNKGALIGLVGCV 40

RESULT 2  
US-08-235-400-2  
Sequence 2, Application US/08235400  
Patent No. 5552426  
GENERAL INFORMATION:  
APPLICANT: Lunn, William H.  
APPLICANT: Moon, James A.  
APPLICANT: Zimmerman, Dennis M.  
TITLE OF INVENTION: METHODS FOR TREATING A PHYSIOLOGICAL  
TIME OF INVENTION: DISORDER ASSOCIATED WITH BETA AMYLOID PEPTIDE  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center/1104  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/235,400  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36, 808  
REFERENCE/DOCKET NUMBER: X-9507  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-235-400-2

Query Match 100.0%; Score 40; DB 1; Length 40;  
Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40  
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 3  
US-08-476-464A-2  
Sequence 2, Application US/08476464A  
Patent No. 5707821  
GENERAL INFORMATION:  
APPLICANT: RYDEL, RUSSELL E.  
APPLICANT: DAPPEN, MICHAEL S.  
TITLE OF INVENTION: THERAPEUTIC INHIBITION OF PHOSPHOLIPASE  
TITLE OF INVENTION: A2 IN A-BETA PEPTIDE-MEDIATED NEURODEGENERATIVE DISEASE  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP  
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: U.S.A.  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,464A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: STORELLA, JOHN R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 15270-002300  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)326-2400  
TELEFAX: (415)576-0300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-476-464A-2

Query Match 100.0%; Score 40; DB 1; Length 40;  
Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40  
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 4  
US-08-304-585-1  
Sequence 1, Application US/08304585  
Patent No. 5721106  
GENERAL INFORMATION:  
APPLICANT: Maggio, John E.  
APPLICANT: Mantlyn, Patrick W.  
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND  
TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Muelting, Raasch, Gebhardt & Schwappach, P.A.  
STREET: P.O. Box 581415  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55458-1415  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/304,585  
FILING DATE: 12-SEP-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Muelting, Ann M.  
REGISTRATION NUMBER: 33,977  
REFERENCE/DOCKET NUMBER: 110,00010120  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-305-1217  
TELEFAX: 612-305-1228  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide

US-08-304-585-1

Query Match 100.0%; Score 40; DB 1; Length 40;  
Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGEYVHHOKLVFAEDVGSNKGAIIGLMWGVV 40  
|||||  
DB 1 DAEFRHDSGEYVHHOKLVFAEDVGSNKGAIIGLMWGVV 40

RESULT 5

US-08-302-808-3

; Sequence 3, Application US/08302808

; Patent No. 5750349

; GENERAL INFORMATION:

; APPLICANT: SUZUKI, No. 5750349uhlro

; APPLICANT: ODAKA, Asano

; APPLICANT: KITADA, Chieko

; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR

; TITLE OF INVENTION: DERIVATIVES AND USE THEREOF

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS &amp; CUSHMAN

; STREET: 130 WATER STREET

; CITY: BOSTON

; STATE: MA

; COUNTRY: USA

; ZIP: 02019

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/302.808

; FILING DATE: 15-SEP-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/JP94/00089

; FILING DATE: 24-JAN-1994

; APPLICATION NUMBER: 010132/1993

; FILING DATE: 25-JAN-1993

; APPLICATION NUMBER: 019035/1993

; FILING DATE: 05-FEB-1993

; APPLICATION NUMBER: 286865/1993

; FILING DATE: 16-NOV-1993

; APPLICATION NUMBER: 334773/1993

; FILING DATE: 28-DEC-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: DAVID, RESNICK S

; REGISTRATION NUMBER: 34,235

; REFERENCE/DOCKET NUMBER: 44631

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-523-3400

; TELEFAX: 617-523-6440

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 40 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: N-terminal

; ORIGINAL SOURCE:

; US-08-302-808-3

Query Match 100.0%; Score 40; DB 1; Length 40;

Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGEYVHHOKLVFAEDVGSNKGAIIGLMWGVV 40  
|||||  
DB 1 DAEFRHDSGEYVHHOKLVFAEDVGSNKGAIIGLMWGVV 40

RESULT 6

US-08-433-734-1

; Sequence 1, Application US/08433734

; Patent No. 5837473

; GENERAL INFORMATION:

; APPLICANT: Magglio, John E.

; APPLICANT: Mantyh, Patrick W. -Amyloid Peptide and Methods

; TITLE OF INVENTION: Labelled for Use in Detecting Alzheimer's Disease

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Muelting, Raasch, Gebhardt &amp; Schwappach, P.A.

; STREET: P.O. Box 581415

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55458-1415

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/433,734

; FILING DATE: 03-MAY-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Muelting, Ann M.

; REGISTRATION NUMBER: 33,977

; REFERENCE/DOCKET NUMBER: 110.00010102

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 612-305-1220

; TELEFAX: 612-305-1228

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 40 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-433-734-1

Query Match 100.0%; Score 40; DB 2; Length 40;  
Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGEYVHHOKLVFAEDVGSNKGAIIGLMWGVV 40  
|||||  
DB 1 DAEFRHDSGEYVHHOKLVFAEDVGSNKGAIIGLMWGVV 40

RESULT 7

US-08-609-090-8

; Sequence 8, Application US/08609090

; Patent No. 5840838

; GENERAL INFORMATION:

; APPLICANT: HENSLEY, Kenneth

; APPLICANT: BUTTERFIELD, D. A.

; APPLICANT: CARNEY, John M.

; APPLICANT: AKSENOV, Michael

; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF

; TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LOWE PRICE LEBLANC &amp; BECKER

Query Match 100.0%; Score 40; DB 1; Length 40;

STREET: 99 Canal Center Plaza, Suite 300  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/609,090  
FILING DATE: 29-FEB-1996  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: KRAUS, ERIC J.  
REGISTRATION NUMBER: 36,190  
REFERENCE/DOCKET NUMBER: 434-059  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-684-1111  
TELEFAX: 703-684-1124  
INFORMATION FOR SEQ. ID NO.: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-609-090-8

Query Match 100.0%; Score 40; DB 2; Length 40;  
Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMVGVV 40  
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMVGVV 40

RESULT 8  
US-07-737-371E-69  
Sequence 69, Application US/07737371E  
Patent No. 5876948  
GENERAL INFORMATION:  
APPLICANT: Yankner, Bruce A.  
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/737,371E  
FILING DATE: 29-JUL-1991  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/559,172  
FILING DATE: 27-JUL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 00108/028002  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ. ID NO.: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-737-371E-69

Query Match 100.0%; Score 40; DB 2; Length 40;  
Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMVGVV 40  
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMVGVV 40

RESULT 9  
US-08-682-245A-2  
Sequence 2, Application US/08682245A  
Patent No. 5919631  
GENERAL INFORMATION:  
APPLICANT: GOYAL, SHERPAL  
APPLICANT: PAUL, JOSEPH W.  
APPLICANT: RIEDEL, NORBERT G.  
APPLICANT: SAHASRABUDHE, SUDHIR  
TITLE OF INVENTION: A METHOD OF DETERMINING THE DEGREE OF  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOECHST MARION ROUSSEL, INC.  
STREET: 2110 E. GALBRAITH RD., P.O. BOX 156300  
CITY: CINCINNATI  
STATE: OHIO  
COUNTRY: U.S.A.  
ZIP: 45215-6300  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/682,245A  
FILING DATE: 17-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/039,414  
FILING DATE: 16-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: LENTZ, NELSEN L.  
REGISTRATION NUMBER: 38,537  
REFERENCE/DOCKET NUMBER: HR-1257A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 513-948-7369  
TELEFAX: 513-948-7961 OR 4681  
TELEX: 214320  
INFORMATION FOR SEQ. ID NO.: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-682-245A-2

Query Match 100.0%; Score 40; DB 2; Length 40;  
Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAITGLMWGVV 40  
DB 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAITGLMWGVV 40

RESULT 10  
US-08-986-948-3  
; Sequence 3, Application US/08986948  
; Patent No. 5955317  
; GENERAL INFORMATION:  
; APPLICANT: SUZUKI, No. 5955317unhito  
; APPLICANT: ODAKA, Asano  
; APPLICANT: KITADA, Chieko  
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR  
; TITLE OF INVENTION: DERIVATIVES AND USE THEREOF  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02019  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/986,948  
; FILING DATE:  
; CLASSIFICATION:  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/302,808  
; FILING DATE: 15-SEP-1994  
; APPLICATION NUMBER: PCT/JP94/00089  
; FILING DATE: 24-JAN-1994  
; APPLICATION NUMBER: 010132/1993  
; FILING DATE: 25-JAN-1993  
; APPLICATION NUMBER: 019035/1993  
; FILING DATE: 05-FEB-1993  
; APPLICATION NUMBER: 286985/1993  
; FILING DATE: 16-NOV-1993  
; APPLICATION NUMBER: 334773/1993  
; FILING DATE: 28-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DAVID, RESNICK S  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 44631  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELETYPE: 200291 STRE  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; US-08-986-948-3

Query Match 100.0%; Score 40; DB 2; Length 40;  
Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAITGLMWGVV 40

DB 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAITGLMWGVV 40

RESULT 11  
US-08-461-216-1  
; Sequence 1, Application US/08461216  
; Patent No. 5958883  
; GENERAL INFORMATION:  
; APPLICANT: SNOW, A. D.  
; TITLE OF INVENTION: ANIMAL MODELS OF HUMAN AMYLOIDOSES  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness  
; STREET: 1420 Fifth Avenue, Suite 2800  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101-2347  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette-5.25 inch, 1.2mb storage  
; OPERATING SYSTEM: MS-DOS 4.01  
; SOFTWARE: Word for Windows-t  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461,216  
; FILING DATE:  
; CLASSIFICATION:  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 07/969,734  
; FILING DATE: October 23, 1992  
; APPLICATION NUMBER: 07/950,417  
; FILING DATE: September 23, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Broderick, Thomas F.  
; REGISTRATION NUMBER: 31,332  
; REFERENCE/DOCKET NUMBER: UOEW-1-6707  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 1-206-682-8100; 1-206-224-0709 (direct)  
; TELEFAX: 1-206-224-0779  
; TELETYPE: 4938023  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; DESCRIPTION: (SYMBOL 98 \f "symbol")/A4(1-40);  
; DESCRIPTION: FIGURES 23-29  
; US-08-461-216-1

Query Match 100.0%; Score 40; DB 2; Length 40;  
Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAITGLMWGVV 40  
DB 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAITGLMWGVV 40

RESULT 12  
US-08-959-148-1  
; Sequence 1, Application US/08959148  
; Patent No. 6172277  
; GENERAL INFORMATION:  
; APPLICANT: Tate, Barbara A.  
; APPLICANT: Majocha, Ronald  
; APPLICANT: Newton, Julie L.  
; TITLE OF INVENTION: NON-TRANSGENIC ANIMAL MODEL OF ALZHEIMER'S DISEASE  
; FILE REFERENCE: 04930/022001  
; CURRENT APPLICATION NUMBER: US/08/959,148

;; CURRENT FILING DATE: 1997-10-28  
;; NUMBER OF SEQ ID NOS: 2  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO: 1  
;; LENGTH: 40  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-08-959-148-1

Query Match 100.0%; Score 40; DB 4; Length 40;  
Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40  
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

## RESULT 13

PCT-US92-06700-1  
; Sequence 1, Application PC/TUS9206700  
; GENERAL INFORMATION:  
; APPLICANT: Mantyh, Patrick W.  
; APPLICANT: Magglo, John E.  
; TITLE OF INVENTION: Labelled -Amyloid Peptide  
; TITLE OF INVENTION: and Alzheimer's Disease Detection  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 3100 Northwest Center  
; CITY: Minneapolis  
; STATE: Minnesota  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb  
; COMPUTER: Northgate 386  
; OPERATING SYSTEM: DOS 4.0  
; SOFTWARE: WordPerfect 5.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/06700  
; FILING DATE: 19920810  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kowalczyk, Alan W.  
; REGISTRATION NUMBER: 31,535  
; REFERENCE/DOCKET NUMBER: 600.226-WO-01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (612) 332-5300  
; TELEFAX: (612) 332-9081  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40 amino acid residues  
; TYPE: AMINO ACID  
; TOPOLOGY: Linear  
; MOLECULE TYPE: Peptide  
; FRAGMENT TYPE: Internal Fragment  
; ORIGINAL SOURCE: Synthetically Derived  
; FEATURE:  
; NAME/KEY: Internal fragment of the -  
; NAME/KEY: amyloid peptide precursor  
; LOCATION: sequence of 40 amino acid residues  
; LOCATION: the -amyloid peptide precursor  
PCT-US92-06700-1

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40  
Query Match 100.0%; Score 40; DB 5; Length 40;  
Best Local Similarity 100.0%; Pred. No. 1.8e-34;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

## RESULT 14

US-08-302-808-4  
; Sequence 4, Application US/08302808  
; Patent No. 5750349  
; GENERAL INFORMATION:  
; APPLICANT: SUZUKI, No. 5750349uhiro  
; APPLICANT: ODAKA, Asano  
; APPLICANT: KITADA, Chieko  
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR  
; TITLE OF INVENTION: DERIVATIVES AND USE THEREOF  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02019  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/302, 808  
; FILING DATE: 15-SEP-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP94/00089  
; FILING DATE: 24-JAN-1994  
; APPLICATION NUMBER: 010132/1993  
; FILING DATE: 25-JAN-1993  
; APPLICATION NUMBER: 019035/1993  
; FILING DATE: 05-FEB-1993  
; APPLICATION NUMBER: 286985/1993  
; FILING DATE: 16-NOV-1993  
; APPLICATION NUMBER: 334773/1993  
; FILING DATE: 28-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DAVID, RESNICK S  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 44631  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELEX: 200291 SPRE  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 41 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
US-08-302-808-4

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40  
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40  
Query Match 100.0%; Score 40; DB 1; Length 41;  
Best Local Similarity 100.0%; Pred. No. 1.9e-34;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 15
US-08-682-245A-3
Sequence 3, Application US/08682245A
Patent No. 5919631
GENERAL INFORMATION:
APPLICANT: GOYAL, SHEFALI
APPLICANT: PAUL, JOSEPH W
APPLICANT: RIEDEL, NORBERT G
APPLICANT: SAHASRABDHE, SODHIR
TITLE OF INVENTION: A METHOD OF DETERMINING THE DEGREE OF
TITLE OF INVENTION: AGGREGATION OF THE BAA PEPTIDE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOECHST MARION ROUSSEL, INC.
STREET: 2110 E. GALBRAITH RD., P.O. BOX 156300
CITY: CINCINNATI
STATE: OHIO
COUNTRY: U.S.A
ZIP: 45215-6300
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,245A
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,414
FILING DATE: 16-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: LENTZ, NELSEN L
REGISTRATION NUMBER: 38,537
REFERENCE/DOCKET NUMBER: HR-1257A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-948-7369
TELEFAX: 513-948-7961 OR 4681
TELEX: 214320
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-682-245A-3

```

|                       |                 |  |           |            |
|-----------------------|-----------------|--|-----------|------------|
| Query Match           | 100.0%          | Score 40;                              | DB 2;     | Length 41; |
| Best Local Similarity | 100.0%          | Pred. No. 1,9e-34;                     |           |            |
| Matches 40;           | Conservative 0; | Mismatches 0;                          | Indels 0; | Gaps 0;    |
| QY                    | 1               | DAEFRHDSGYEYHHOKLVEFAEDVGSNKGATIGLVGCV | 40        |            |
|                       |                 |  |           |            |
| Db                    | 1               | DAEFRHDSGYEYHHOKLVEFAEDVGSNKGATIGLVGCV | 40        |            |

Search completed: April 24, 2002, 09:22:29  
Job time: 248 sec

**THIS PAGE BLANK (USPTO)**



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:20:47 ; Search time 21.46 Seconds  
(without alignments)  
68.341 Million cell updates/sec

Title: US-09-689-469-3

Perfect score: 40

Sequence: 1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGATIGLVAGVY 40

Scoring table: OLIGO

Searched: 100059 seqs, 36664827 residues

Word size: 0

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID         | Description         |
|------------|-------|-------------|--------|------------|---------------------|
| 1          | 40    | 100.0       | 57     | A4_PIG     | Q29023 sus scrofa   |
| 2          | 40    | 100.0       | 57     | A4_URMA    | Q29149 ursus marit  |
| 3          | 40    | 100.0       | 58     | A4_CANFA   | Q28280 canis fami1  |
| 4          | 40    | 100.0       | 58     | A4_RABIT   | Q28748 oryctolagus  |
| 5          | 40    | 100.0       | 58     | A4_SHEEP   | Q28757 ovis aries   |
| 6          | 40    | 100.0       | 59     | A4_BOVIN   | Q28053 bos taurus   |
| 7          | 40    | 100.0       | 751    | A4_SATSC   | Q95241-salmi1r1 sci |
| 8          | 40    | 100.0       | 770    | A4_HUMAN   | P05067 homo sapien  |
| 9          | 27    | 67.5        | 770    | A4_MOUSE   | P18023 mus musculu  |
| 10         | 27    | 67.5        | 770    | A4_RAT     | P24077 escherichia  |
| 11         | 17.5  | 416         | 1      | VBDA_ECOLI | Q24077 escherichia  |
| 12         | 7     | 17.5        | 546    | UBIB_SALTY | Q916m4 salmonella   |
| 13         | 6     | 15.0        | 64     | EPVA_STRPN | Q03159 streptococc  |
| 14         | 6     | 15.0        | 130    | PROF_ENTHI | P49230 entamoeba h  |
| 15         | 6     | 15.0        | 173    | NT6M_CEPCC | P43197 cephus col   |
| 16         | 6     | 15.0        | 184    | MP20_DROME | P14318 dtrosophila  |
| 17         | 6     | 15.0        | 199    | NP25_MOUSE | Q9198 mus musculu   |
| 18         | 6     | 15.0        | 213    | AAT_STRGR  | P36692 streptomyc   |
| 19         | 6     | 15.0        | 214    | ACUB_BACSU | P33066 bacillus su  |
| 20         | 6     | 15.0        | 219    | NP25_RAT   | P37805 rattus norv  |
| 21         | 6     | 15.0        | 262    | FLGQ_RHIME | Q52946 rhizobium m  |
| 22         | 6     | 15.0        | 282    | NP25_HUMAN | Q94115 homo sapien  |
| 23         | 6     | 15.0        | 284    | POLG_PVITO | P11897 potato viru  |
| 24         | 6     | 15.0        | 287    | LEP4_LEGPN | Q57695 methanococ   |
| 25         | 6     | 15.0        | 289    | DAPA_METJA | P26932 gallus galli |
| 26         | 6     | 15.0        | 292    | CLPO_CHICK | P51991 homo sapien  |
| 27         | 6     | 15.0        | 297    | CLP1_HUMAN | Q08091 mus musculu  |
| 28         | 6     | 15.0        | 297    | CLP1_MOUSE | Q08092 sus scrofa   |
| 29         | 6     | 15.0        | 297    | CLP1_PIG   | Q08092 sus scrofa   |
| 30         | 6     | 15.0        | 297    | CLP1_RAT   | Q08092 sus scrofa   |
| 31         | 6     | 15.0        | 321    | CYE_GUTTH  | Q07894 guillardia   |
| 32         | 6     | 15.0        | 321    | EUMI_EURMA | P25780 eurogiylphus |
| 33         | 6     | 15.0        | 321    | PUR_MOUSE  | P42669 mus musculu  |

|    |   |      |     |   |            |                    |
|----|---|------|-----|---|------------|--------------------|
| 34 | 6 | 15.0 | 322 | 1 | PUR_HUMAN  | Q00577 homo sapien |
| 35 | 6 | 15.0 | 327 | 1 | POLG_PVICH | P21294 potato viru |
| 36 | 6 | 15.0 | 330 | 1 | COTL_PEMV  | P07993 pepper molt |
| 37 | 6 | 15.0 | 339 | 1 | IC11_TRIFA | P34053 trichoderma |
| 38 | 6 | 15.0 | 387 | 1 | CTRB_NEIMB | P32014 neisseria m |
| 39 | 6 | 15.0 | 391 | 1 | CPSD_STRAG | Q04664 streptococc |
| 40 | 6 | 15.0 | 397 | 1 | AAT_STRAG  | Q06013 streptomyc  |
| 41 | 6 | 15.0 | 405 | 1 | GSPE_PSEAE | Q00513 pseudomonas |
| 42 | 6 | 15.0 | 428 | 1 | CPYL_PSESP | P33006 pseudomonas |
| 43 | 6 | 15.0 | 429 | 1 | AROQ_CORGL | Q92470 corynebacte |
| 44 | 6 | 15.0 | 442 | 1 | CEN1_YEAST | P39525 saccharomyc |
| 45 | 6 | 15.0 | 450 | 1 | AROQ_MYCTU | P22487 mycobacteri |

## ALIGNMENTS

| RESULT | ID   | STANDARD                                | PRT | 57 AA                             |
|--------|--|---|-----|-----------------------------------|
| 1      | A4_PIG   |   |     |                                   |
| AC     | Q29023:  |   |     |                                   |
| DT     | 01-NOV-1997 (Rel. 35, Created)   |   |     |                                   |
| DT     | 01-NOV-1997 (Rel. 35, Last sequence update)  |   |     |                                   |
| DT     | 20-AUG-2001 (Rel. 40, Last annotation update)  |   |     |                                   |
| DE     | ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).  |   |     |                                   |
| GN     | APP.   |   |     |                                   |
| OS     | Sus. scrofa (Pig).   |   |     |                                   |
| OC     | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  |   |     |                                   |
| OC     | Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  |   |     |                                   |
| OX     | NCBI_TaxID=9823;   |   |     |                                   |
| RN     | [1]  |   |     |                                   |
| RP     | SEQUENCE FROM N.A.   |   |     |                                   |
| RC     | TISUE=Brain;   |   |     |                                   |
| RX     | MEDLINE=92017079; PubMed=1656157;  |   |     |                                   |
| RA     | Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;   |   |     |                                   |
| RT     | "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis."   |   |     |                                   |
| RL     | Brain Res. Mol. Brain Res. 10:299-305(1991).   |   |     |                                   |
| RT     | FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO GPCR (BY SIMILARITY).  |   |     |                                   |
| CC     | INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN GPCR (BY SIMILARITY).  |   |     |                                   |
| CC     | - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.   |   |     |                                   |
| CC     | - SIMILARITY: BELONGS TO THE APP FAMILY.   |   |     |                                   |
| CC     | -----  |   |     |                                   |
| CC     | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ). |   |     |                                   |
| CC     | -----  |   |     |                                   |
| DR     | EMBL: X56127; CAA39592.1; -  |   |     |                                   |
| DR     | HSSP: P05067; 1AML.  |   |     |                                   |
| DR     | InterPro: IPR001868; A4_APP.   |   |     |                                   |
| DR     | PROSITE: PS00319; A4_EXTRA; PARTIAL.   |   |     |                                   |
| DR     | PROSITE: PS00320; A4_INTRA; PARTIAL.   |   |     |                                   |
| KW     | Glycoprotein; Amyloid; Neurone; Transmembrane.   |   |     |                                   |
| FT     | NON_TER  | 1                                       |     |                                   |
| FT     | CHAIN  | 6                                       | 48  | BETA-AMYLOID PROTEIN (POTENTIAL). |
| FT     | DOMAIN   | <1                                      | 33  | EXTRACELLULAR (POTENTIAL).        |
| FT     | TRANSMEM   | 34                                      | 57  | POTENTIAL.                        |
| FT     | NON_TER  | 57                                      |     |                                   |
| SQ     | SEQUENCE   | 57 AA; 6172 MW; 84209D88BBA82DFA CRC64; |     |                                   |

Query Match 100.0%; Score 40; DB 1; Length 57;  
Best Local Similarity 100.0%; Pred. No. 1.2e-34;  
Matches 40; Conservative 0; Mismatches 0; Gaps 0;

DB 6 DAERFHDGSEVHHOKLVFAEDVGSNKGAIIGLMVGVV 45

## RESULT 2

A4\_URSMA STANDARD; PRT; 57 AA.

AC Q29149;  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID  
 DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).  
 GN APP.  
 OS Ursus maritimus (Polar bear) (Thalarcos maritimus).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.  
 OX NCBI\_TaxID=29073;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Brain;  
 RX MEDLINE=92017079; PubMed=1656157;  
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
 RT "Conservation of the sequence of the Alzheimer's disease amyloid  
 RT peptide in dog, polar bear and five other mammals by cross-species  
 RT polymerase chain reaction analysis."  
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
 CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
 CC G(O) (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: X56128; CAA39593.1; -.  
 CC DR HSSP: P05067; IAML.  
 CC DR Interpro: IPR001868; A4\_APP.  
 CC DR PROSITE: PS00319; A4\_EXTRA; PARTIAL.  
 CC DR PROSITE: PS00320; A4\_INTRA; PARTIAL.  
 CC KM Glycoprotein; Amyloid; Neurone; Transmembrane.  
 CC FT NON\_TER 1 1  
 CC FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).  
 CC FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 34 57 POTENTIAL.  
 CC FT NON\_TER 57 57  
 CC SQ SEQUENCE 57 AA; 6172 MW; 84209D808BEA82DFA CRC64;

Query Match 100.0%; Score 40; DB 1; Length 57;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-34;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAERFHDGSEVHHOKLVFAEDVGSNKGAIIGLMVGVV 40  
 DB 6 DAERFHDGSEVHHOKLVFAEDVGSNKGAIIGLMVGVV 45

## RESULT 3

A4\_CANFA STANDARD; PRT; 58 AA.

AC Q28280;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID  
 DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).

GN APP.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Kidney;  
 RX MEDLINE=92017079; PubMed=1656157;  
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
 RT "Conservation of the sequence of the Alzheimer's disease amyloid  
 RT peptide in dog, polar bear and five other mammals by cross-species  
 RT polymerase chain reaction analysis."  
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
 CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
 CC G(O) (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
 CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

CC EMBL: X56125; CAA39590.1; -.  
 CC DR HSSP: P05067; IAML.  
 CC DR Interpro: IPR001868; A4\_APP.  
 CC DR PROSITE: PS00319; A4\_EXTRA; PARTIAL.  
 CC DR PROSITE: PS00320; A4\_INTRA; PARTIAL.  
 CC KM Glycoprotein; Amyloid; Neurone; Transmembrane.  
 CC FT NON\_TER 1 1  
 CC FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).  
 CC FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 35 58 POTENTIAL.  
 CC FT NON\_TER 58 58  
 CC SQ SEQUENCE 58 AA; 6285 MW; 8469DA88A2E12DFA CRC64;

Query Match 100.0%; Score 40; DB 1; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-34;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAERFHDGSEVHHOKLVFAEDVGSNKGAIIGLMVGVV 40  
 DB 7 DAERFHDGSEVHHOKLVFAEDVGSNKGAIIGLMVGVV 46

## RESULT 4

A4\_RABIT STANDARD; PRT; 58 AA.

AC Q28748;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID  
 DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).  
 GN APP.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Brain;  
 RX MEDLINE=92017079; PubMed=1656157;  
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
 RT "Conservation of the sequence of the Alzheimer's disease amyloid  
 RT peptide in dog, polar bear and five other mammals by cross-species  
 RT polymerase chain reaction analysis.";

|    |               |  |
|----|---------------|--|
| RL |               | Brain Res. Mol. Brain Res. 10:299-305(1991).   |
| CC | -I-           | FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  |
| CC |               | INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  |
| CC | G(O)          | (BY SIMILARITY).   |
| CC | -I-           | SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.   |
| CC | -I-           | SIMILARITY: BELONGS TO THE APP FAMILY.   |
| CC |               | -----  |
| CC |               | This SWISS-PROT entry is copyright. It is produced through a collaboration   |
| CC |               | between the Swiss Institute of Bioinformatics and the EMBL outstation -  |
| CC |               | the European Bioinformatics Institute. There are no restrictions on its  |
| CC |               | use by non-profit institutions as long as its content is in no way   |
| CC |               | modified and this statement is not removed. Usage by and for commercial  |
| CC |               | entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> |
| CC |               | or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).  |
| CC |               | -----  |
| DR | EMBL:         | X56129; CAA39594.1; .  |
| DR | HSSP:         | P05067; JMWL.  |
| DR | InterPro:     | IPIR001868; A4_APP.  |
| DR | PROSITE:      | PS00319; A4_EXTRA; PARTIAL.  |
| DR | PROSITE:      | PS00320; A4_INTRA; PARTIAL.  |
| KW | Glycoprotein; | Amyloid; Neurope; Transmembrane.   |
| FT | NON_TER       | 1  |
| FT | CHAIN         | 1  |
| FT |               | 6 48   |
| FT | DOMAIN        | <1 33 BETA-AMYLOID PROTEIN (POTENTIAL).  |
| FT | TRANSMEM      | 34 57 EXTRACELLULAR (POTENTIAL).   |
| FT | DOMAIN        | 58 >58 POTENTIAL.  |
| FT | NON_TER       | 58 58 CYTOPLASMIC (POTENTIAL).   |
| SO | SEQUENCE      | 58 AA: 6300 MW: F434209D88EBA82D CRC64:  |

|                       |                 |               |           |            |
|-----------------------|-----------------|---------------|-----------|------------|
| Query Match           | 100.0%          | Pred. 40;     | DB 1;     | Length 58; |
| Best Local Similarity | 100.0%          | Pred. No. 1   | 2e-34;    |            |
| Matches 40;           | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0;    |

```
QY      1 DAEFRHDSGEVHHOKLVFFAEDVSNKGAIIGLMGCV 40
        |||||
Db       6 DAERHDSGEVHHOKLVFFAEDVSNKGAIIGLMGCV 45
```

| CC | RESULT | 5   |           |             |
|----|--------|---|-----------|-------------|
| CC | ID     | A4_SHEEP  | STANDARD: | PRT: 58 AA. |
| CC | AC     | Q28757;   |           |             |
| CC | DT     | 01-NOV-1997 (Rel. 35, Created)  |           |             |
| CC | DT     | 01-NOV-1997 (Rel. 35, Last sequence update)   |           |             |
| CC | DT     | 30-MAY-2000 (Rel. 39, Last annotation update)   |           |             |
| CC | DE     | ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT). |           |             |
| CC | DE     | APP.  |           |             |
| CC | OS     | Ovis aries (Sheep).   |           |             |
| CC | OC     | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |           |             |
| CC | OC     | Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;   |           |             |
| CC | OC     | Bovidae; Caprinae; Ovis.  |           |             |
| CC | OX     | NCBI_TaxID:9940;  |           |             |
| CC | RN     | [1]   |           |             |
| CC | RP     | SEQUENCE FROM N.A.  |           |             |
| CC | RC     | TISSUE=Heart;   |           |             |
| CC | RX     | MEDLINE=92017079; PubMed=1656157;   |           |             |
| CC | RA     | Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  |           |             |
| CC | RT     | "Conservation of the sequence of the Alzheimer's disease amyloid  |           |             |
| CC | RT     | peptide in dog, polar bear and five other mammals by cross-species  |           |             |
| CC | RT     | polymerase chain reaction analysis.";   |           |             |
| CC | RL     | Brain Res. Mol. Brain Res. 10:299-305(1991).  |           |             |
| CC | -I-    | FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO   |           |             |
| CC |        | INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN   |           |             |
| CC |        | G(O) (BY SIMILARITY).   |           |             |
| CC | -I-    | SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  |           |             |
| CC | -I-    | SIMILARITY: BELONGS TO THE APP FAMILY.  |           |             |
| CC | CC     | -----   |           |             |
| CC | CC     | This SWISS-PROT entry is copyright. It is produced through a collaboration                                      |           |             |
| CC | CC     | between the Swiss Institute of Bioinformatics and the EMBL outstation -   |           |             |
| CC | CC     | the European Bioinformatics Institute. There are no restrictions on its   |           |             |
| CC | CC     | use by non-profit institutions as long as its content is in no way  |           |             |

```
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.lsb-sib.ch/announce/
CC or send an email to license@lsb-sib.ch).
CC -----
DR EMBL; X56130; CAA39595.1; -.
DR HSSP; P05067; 1AML.
DR InterPro; IPR001868; A4_APP.
DR PROSITE; PS003019; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neutrine; Transmembrane.
FT NON_TER 1
FT CHAIN 1
FT DOMAIN 6
FT DOMAIN <1 33 BETA-AMYLOID PROTEIN (POTENTIAL).
FT TRANSMEM 34 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 57 POTENTIAL.
FT NON_TER 58 CYTOPLASMIC (POTENTIAL).
FT 58
FT SEQUENCE 58 AA; 6300 MW; F434209D88BBA82D CRC64;
```

|                       |                |              |          |           |
|-----------------------|----------------|--------------|----------|-----------|
| Query Match           | 100.0%         | Score 40     | DB 1     | Length 58 |
| Best Local Similarity | 100.0%         | Pred. No. 1  | 2e-34    |           |
| Matches 40            | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0    |

QY 1 DAERHDSGYEVHOKLVFAEDVGSNKGATITGMGGV 40  
| | | | | | | | | | | | | | | | | | | | | |  
Db 6 DAERHDSGYEVHOKLVFAEDVGSNKGATITGMGGV 45

```

A4_RESULT 6
A4_BOVIN
ID A4_BOVIN STANDARD: PRT: 59 AA.
AC Q28053.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).
GN APP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RC MEDLINE=92017079; PubMed=1656157;
RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RA "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on les-
CC use by non-profit institutions as long as their content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X56124; CAA39589.1; -
DR EMBL; X56126; CAA39591.1; -
DR HSSP; P05067; IAML.
DR InterPro; IPR001868; A4_APP.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.

```

```

FT  NON_TER      1      1
FT  CHAIN         7      49
FT  DOMAIN        <1     34
FT  TRASNEM       35     58
FT  DOMAIN        59     59
FT  NON_TER       59     59
SQ  SEQUENCE      59 AA: 6414 MW: F43469D48A2E12D CRC64;

Query Match      100.0%; Score 40; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.2e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 DAEFRHDSGYEVHHOKLVFEADVGSNKGAIIGLMVGVV 40
    |||
DB  7 DAEFRHDSGYEVHHOKLVFEADVGSNKGAIIGLMVGVV 46

RESULT 7
A4_SAIISC STANDARD; PRT; 751 AA.
AC  095241;
DT  15-DEC-1998 (Rel. 37, Created)
DT  15-DEC-1998 (Rel. 37, Last sequence update)
DT  20-AUG-2001 (Rel. 40, Last annotation update)
DE  ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR [CONTAINS: BETA-
DE  AMYLOID PROTEIN (BETA-APP) (A-BETA)].
GN  APP.
OS  Saimiri sciureus (Common squirrel monkey).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
OX  NCBI_TaxID=9521;
RN  [1];
RP  SEQUENCE FROM N.A.
RC  TISSUE=Liver, and kidney;
RX  MEDLINE=96108492; PubMed=8532114;
RA  Levy E., Amotim A., Frangione B., Walker L.C.;
RT  "Beta-amyloid precursor protein gene in squirrel monkeys with
RT  cerebral amyloid angiopathy.";
RL  Neurobiol. Aging 16:805-808(1995).
CC  -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC  INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC  G(O).
CC  -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC  -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC  WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC  RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC  NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC  PHOSPHORYLATION (BY SIMILARITY).
CC  -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC  -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use. By non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@sib-sib.ch).
CC  -----
DR  EMBL: S81024; AAD14347.1; -
DR  InterPro: IPR001868; A4_APP.
DR  InterPro: IPR002223; Kunitz_BPTI.
DR  Pfam: PF02177; A4_EXTRA; 1.
DR  Pfam: PF00014; Kunitz_BPTI; 1.
DR  PRINTS: PR00203; AMYLOID14.
DR  PRINTS: PR00204; BETAAMYLOID.
DR  PRINTS: PR00759; BASICPTASE.
DR  SMART: SM00006; A4_EXTRA; 1.
DR  SMART: SM00131; KU; 1.
DR  PROSITE: PS00319; A4_EXTRA; 1.
DR  PROSITE: PS00320; A4_INTRA; 1.
DR  PROSITE: PS00280; BPTI_KUNITZ_1; 1.

```

```

DR  PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KM  Glycoprotein: Amyloid; Neurone; Transmembrane; Alternative splicing;
KW  Signal; Serine protease inhibitor.
FT  SIGNAL        1      17
FT  CHAIN         18     751
FT  DOMAIN        653     695
FT  TRASNEM       18     680
FT  DOMAIN        681     704
FT  TRASNEM       705     751
FT  DOMAIN        287     345
FT  SITE          740     743
FT  ACT_SITE      301     302
FT  DISULFID      291     341
FT  DISULFID      300     324
FT  DISULFID      316     337
FT  CARBOHYD      523     523
FT  CARBOHYD      552     552
SQ  SEQUENCE      751 AA: 84893 MW: 6C3E431089569049 CRC64;

Query Match      100.0%; Score 40; DB 1; Length 751;
Best Local Similarity 100.0%; Pred. No. 9.6e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 DAEFRHDSGYEVHHOKLVFEADVGSNKGAIIGLMVGVV 40
    |||
DB  653 DAEFRHDSGYEVHHOKLVFEADVGSNKGAIIGLMVGVV 692

RESULT 8
A4_HUMAN STANDARD; PRT; 770 AA.
ID  A4_HUMAN
AC  P05067; P09000; Q16011;
DT  13-AUG-1987 (Rel. 05, Created)
DT  01-NOV-1991 (Rel. 20, Last sequence update)
DT  20-AUG-2001 (Rel. 40, Last annotation update)
DE  ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR (PROTEASE NEXIN-II)
DE  (PN-II) (APP) [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)].
GN  APP OR A4 OR CVAP OR ADL.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1];
RP  SEQUENCE FROM N.A.
RC  TISSUE=Brain;
RX  MEDLINE=87144572; PubMed=2881207;
RA  Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA  Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT  "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RT  cell-surface receptor.";
RL  Nature 325:733-736(1987).
RN  [2];
RP  SEQUENCE FROM N.A.
RX  MEDLINE=88122639; PubMed=2893289;
RA  Ponte P., Gonzalez-Dewhilt P., Schilling J., Miller J., Hsu D.,
RA  Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA  Cordell B.;
RT  "A new A4 amyloid mRNA contains a domain homologous to serine
RT  proteinase inhibitors.";
RL  Nature 331:525-527(1988).
RN  [3];
RP  SEQUENCE FROM N.A.
RX  MEDLINE=89128427; PubMed=2783775;
RA  Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA  Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT  "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
RT  is encoded by 16 exons.";
RL  Nucleic Acids Res. 17:517-522(1989).
RN  [4];
RP  SEQUENCE FROM N.A.
RX  MEDLINE=97263807; PubMed=9108164;
RA  Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,

```

RA Saito M., Tsukuni S., Sakaki Y.;  
 RT "A novel method for making nested deletions and its application for  
 RT sequencing of a 300 kb region of human APP locus."; *Nucleic Acids Res.* 25:1802-1808(1997).  
 RN [5]  
 RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.  
 RX MEDLINE-88122640; PubMed-2893290;  
 RA Tanzi R.E., McClatchey A.I., Lampert I.D., Villa-Komaroff L.,  
 RA Gusella J.F., Neve R.L.;  
 RT "Protease inhibitor domain encoded by an amyloid protein precursor  
 RT mRNA associated with Alzheimer's disease."; *Nature* 331:528-530(1988).  
 RN [6]  
 RP SEQUENCE OF 287-367 FROM N.A.  
 RX MEDLINE-88122641; PubMed-2893291;  
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;  
 RT "Novel precursor of Alzheimer's disease amyloid protein shows  
 RT protease inhibitory activity."; *Nature* 331:530-532(1988).  
 RN [7]  
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.  
 RX MEDLINE-87231971; PubMed-3035574;  
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;  
 RT "Molecular cloning and characterization of a cDNA encoding the  
 RT cerebrovascular and the neuritic plaque amyloid peptides."; *Proc. Natl. Acad. Sci. U.S.A.* 84:4190-4194(1987).  
 RN [8]  
 RP SEQUENCE OF 507-770 FROM N.A.  
 RX MEDLINE-88124954; PubMed-2893379;  
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,  
 RA Marotta C.A.;  
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer  
 RT disease brain: coding and noncoding regions of the fetal precursor  
 RT mRNA are expressed in the cortex."; *Proc. Natl. Acad. Sci. U.S.A.* 85:929-933(1988).  
 RN [9]  
 RP SEQUENCE OF 672-681.  
 RX MEDLINE-88035004; PubMed-3312495;  
 RA Partridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,  
 RA Tountouloute W.W., Huebner V., Shively J.E.;  
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition  
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical  
 RT microvessels."; *J. Neurochem.* 49:1394-1401(1987).  
 RN [10]  
 RP SEQUENCE OF 739-770 FROM N.A.  
 RX MEDLINE-90236318; PubMed-2110105;  
 RA Yoshikawa S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;  
 RT "Genomic organization of the human amyloid beta-protein precursor  
 RT gene."; *Gene* 87:257-263(1990).  
 RN [11]  
 RP SEQUENCE OF 1-10 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE-89016647; PubMed-3140222;  
 RA Schon E.A., Mila S., Sadlo J., Herbert J.;  
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)  
 RT encodes a 95-kDa polypeptide."; *Nucleic Acids Res.* 16:9351-9351(1988).  
 RN [12]  
 RP SEQUENCE OF 18-50.  
 RX MEDLINE-87250462; PubMed-3597385;  
 RA van Nostrand W.E., Cunningham D.D.;  
 RT "Purification of protease nexin II from human fibroblasts."; *J. Biol. Chem.* 262:8508-8514(1987).  
 RN [13]  
 RP IDENTITY OF APP WITH NEXIN-II.  
 RX MEDLINE-89384866; PubMed-2506449;  
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,  
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,  
 RA Sinha S.;  
 RT "The secreted form of the Alzheimer's amyloid precursor protein with  
 RT the Kunitz domain is protease nexin-II.";

RL Nature 341:144-147(1989).  
 RN [14]  
 RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.  
 RX MEDLINE-90211252; PubMed-1969731;  
 RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;  
 RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's  
 RT disease amyloid protein precursor."; *Biochem. Biophys. Res. Commun.* 167:716-721(1990).  
 RN [15]  
 RP COMPLEX WITH G(O).  
 RX MEDLINE-93188965; PubMed-8446172;  
 RA Nishimoto I., Okamoto T., Matsura Y., Takahashi S., Okamoto T.,  
 RA Murayama Y., Ogata E.;  
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding  
 RT protein G(O)"; *Nature* 362:75-79(1993).  
 RN [16]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.  
 RX MEDLINE-99215582; PubMed-10201399;  
 RA Rossjohn J., Cappai R., Fell S.C., Henry A., McKinsty W.J.,  
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,  
 RA Parker M.W.;  
 RT "Crystal structure of the N-terminal, growth factor-like domain of  
 RT Alzheimer amyloid precursor protein."; *Nat. Struct. Biol.* 6:327-331(1999).  
 RN [17]  
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.  
 RX MEDLINE-91104913; PubMed-2125487;  
 RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrodt C., Kossiakof A.A.;  
 RT "X-ray crystal structure of the protease inhibitor domain of  
 RT Alzheimer's amyloid beta-protein precursor."; *Biochemistry* 29:10018-10022(1990).  
 RN [18]  
 RP STRUCTURE BY NMR OF 289-344.  
 RX MEDLINE-92031488; PubMed-1718421;  
 RA Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayney R.M.,  
 RA Kamarc K.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,  
 RA Tamburini P.P.;  
 RT "Sequential NMR resonance assignment and structure determination of  
 RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid  
 RT precursor protein."; *Biochemistry* 30:10467-10478(1991).  
 RN [19]  
 RP STRUCTURE BY NMR OF 672-699.  
 RX MEDLINE-94281210; PubMed-7516706;  
 RA Talafous J., Marchowski K.J., Klopman G., Zagorski M.G.;  
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide."; *Biochemistry* 33:7788-7796(1994).  
 RN [20]  
 RP STRUCTURE BY NMR OF 696-706.  
 RX MEDLINE-97128622; PubMed-8973180;  
 RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;  
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in  
 RT membrane-mimicking environment."; *Biochemistry* 35:16094-16104(1996).  
 RN [21]  
 RP STRUCTURE BY NMR OF 672-711.  
 RX MEDLINE-98359783; PubMed-9693002;  
 RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;  
 RT "Solution structure of amyloid beta-peptide(1-40) in a water-miscible  
 RT environment. Is the membrane-spanning domain where we think it is?"; *Biochemistry* 37:11064-11077(1998).  
 RN [22]  
 RP STRUCTURE BY NMR OF 672-699.  
 RX MEDLINE-20400066; PubMed-10940222;  
 RA Poulsen S.-A., Watson A.A., Craik D.J.;  
 RT "Solution structures in aqueous SDS micelles of two amyloid beta  
 RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage  
 RT site."; *J. Struct. Biol.* 130:142-152(2000).  
 RN [23]  
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.  
 RX MEDLINE-88296437; PubMed-2900137;

RA Dykx T., Weidemann A., Multhaupt G., Salbaum J.M., Lemaire H.-G.,  
 RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;  
 RT "Identification, transmembrane orientation and biogenesis of the  
 RT amyloid A4 precursor of Alzheimer's disease.";  
 RL EMO J. 7:949-957(1988).  
 RN [24]  
 RP REVIEW.  
 RX MEDLINE-92271194; PubMed=1589757;  
 RA Kosik K.S.;  
 RT "Alzheimer's disease: a cell biological perspective.";  
 RL Science 256:780-783(1992).  
 RN [25]  
 Query Match 100.0%; Score 40; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-34;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 672 DAEFRHDSGEVHHOKLVFAEDVGSNKGAIIGLWGVV 40  
 QY 1 DAEFRHDSGEVHHOKLVFAEDVGSNKGAIIGLWGVV 40  
 DB 672 DAEFRHDSGEVHHOKLVFAEDVGSNKGAIIGLWGVV 711  
 RESULT 9  
 A4\_MOUSE STANDARD; PRT; 770 AA.  
 AC P12023;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR  
 DE (AMYLOIDOGENIC GLYCOPROTEIN) (AG).  
 GN APP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.  
 RC STRAIN-BALB/C; TISSUE-Brain;  
 RX MEDLINE-92096458; PubMed=1756177;  
 RA de Strooper B., van Leuven F., van den Bergh H.;  
 RT "The amyloid beta protein precursor or protease nexin II from mouse  
 RT is closer related to its human homolog than previously reported.";  
 RL Biochim. Biophys. Acta 1129:141-143(1991).  
 RN [2]  
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.  
 RC TISSUE-Brain;  
 RX MEDLINE-88106489; PubMed=3322280;  
 RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;  
 RT "Complementary DNA for the mouse homolog of the human amyloid beta  
 RT protein precursor.";  
 RL Biochem. Biophys. Res. Commun. 149:665-671(1987).  
 RN [3]  
 RP REVISIONS.  
 RA Yamada T.;  
 RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 289-364 FROM N.A.  
 RC STRAIN-CD-1; TISSUE-Placenta;  
 RX MEDLINE-89345111; PubMed=2569710;  
 RA Fukuchi K., Martin G.M., Deeb S.S.;  
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein  
 RT precursor of Mus domestica.";  
 RL Nucleic Acids Res. 17:5396-5396(1989).  
 RN [5]  
 RP SEQUENCE OF 1-19 FROM N.A.  
 RX MEDLINE-92209998; PubMed=1555768;  
 RA Izumi R., Yamada T., Yoshikaki S.I., Sasaki H., Hattori M.,  
 RA Sakai Y.;  
 RT "Positive and negative regulatory elements for the expression of the  
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";  
 RL Gene 112:189-195(1992).  
 RN [6]

RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.  
 RC TISSUE-Brain, and Kidney;  
 RX MEDLINE-89149813; PubMed=2493250;  
 RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;  
 RT "Structure and expression of the alternatively spliced forms of mRNA  
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein  
 RT precursor.";  
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(695),  
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING.  
 CC -1- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS  
 CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND  
 CC LIVER.  
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION  
 CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC  
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE  
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF  
 CC PHOSPHORYLATION (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.  
 CC -----  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: X59379; NOT ANNOTATED\_CDS.  
 DR EMBL: M18373; AAA37139.1; -;  
 DR EMBL: X15210; CAA33280.1; -;  
 DR EMBL: D10603; BAA01436.1; -;  
 DR EMBL: M24397; AAA39929.1; -;  
 DR PIR: A27485; A27485.  
 DR PIR: S04855; S04855.  
 DR PIR: S19727; S19727.  
 DR MGI: 88059; App.  
 DR InterPro: IPR001868; A4\_APP.  
 DR InterPro: IPR002223; Kunitz\_BPTI.  
 DR Pfam: PF02177; A4\_EXTRA; 1.  
 DR Pfam: PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS: PRO0203; AMYLOIDA4.  
 DR PRINTS: PRO0204; BETAMAMLOID.  
 DR PRINTS: PRO0759; BASICPTASE.  
 DR SMART: SM00131; KU; 1.  
 DR SMART: SM00131; KU; 1.  
 DR PROSITE: PS00319; A4\_EXTRA; 1.  
 DR PROSITE: PS00320; A4\_INTRA; 1.  
 DR PROSITE: PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE: PS0279; BPTI\_KUNITZ\_2; 1.  
 DR PROSITE: PS0279; BPTI\_KUNITZ\_2; 1.  
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;  
 KW Alternative splicing; Serine protease inhibitor.  
 FT SIGNAL 1 17  
 FT CHAIN 18 770  
 FT FT  
 FT DOMAIN 18 699  
 FT TRANSMEM 700 723  
 FT DOMAIN 724 770  
 FT DOMAIN 673 715  
 FT DOMAIN 287 345  
 FT SITE 759 762  
 FT SITE 291 341  
 FT DISULFID 300 324  
 FT DISULFID 316 337  
 FT CARBOHYD 542 542  
 FT CARBOHYD 571 571  
 FT CARBOHYD 289 289  
 FT VARSPPLIC 290 364  
 FT VARSPPLIC 346 380  
 FT SEQUENCE 770 AA; 86752 MW; 26C50DE0890CAF7A CRC64;  
 SO

Query Match 67.5%; Score 27; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-20;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 HOKLVEFADVGSKNGAIIGLWGVV 40  
 |||||  
 DB 685 HOKLVEFADVGSKNGAIIGLWGVV 711

RESULT 10  
 A4\_RAT STANDARD; PRT: 770 AA.

AC P08592;  
 DT 01-AUG-1988 (rel. 08, Created)  
 DT 01-DEC-1992 (rel. 24, Last sequence update)  
 DT 20-AUG-2001 (rel. 40, Last annotation update)  
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR  
 DE (AMYLOIDGENIC GLYCOPROTEIN) (AG).  
 GN APP.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=88312583; PubMed=2900758;  
 RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,  
 RA Seeburg P.H.;  
 RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern  
 RT in rat brain suggests a role in cell contact.";  
 RL EMBO J. 7:1365-1370(1988).  
 RN [2]  
 RP SEQUENCE OF 289-364 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=89183625; PubMed=2648331;  
 RA Kang J., Mueller-Hill B.;  
 RT "The sequence of the two extra exons in rat preA4.";  
 RL Nucleic Acids Res. 17:2130-2130(1989).  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695),  
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING.  
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION  
 CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC  
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE  
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF  
 CC PHOSPHORYLATION (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 BPT/KUNITZ INHIBITOR DOMAIN.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: X07648; CAA30488.1; -  
 DR EMBL: X14066; CAA32229.1; -  
 DR PIR: S00550; S00550.  
 DR PIR: S03607; S03607.  
 DR InterPro: IPR001868; A4\_APP.  
 DR InterPro: IPR002223; Kunitz\_BPTI.  
 DR Pfam: PF02177; A4\_EXTRA; 1.  
 DR Pfam: PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS: PR00203; AMYLOIDA4.  
 DR PRINTS: PR00204; BETAMYLOID.  
 DR PRINTS: PR00759; BASICPASE.  
 DR SMART; SM00006; A4\_EXTRA; 1.

DR SMART; SM00131; KU; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE; PS00279; BPTI\_KUNITZ\_2; 1.  
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;  
 KW Alternative splicing; Serine protease inhibitor.  
 FT SIGNAL 1 17  
 FT CHAIN 18 770  
 FT FT  
 FT DOMAIN 18 699  
 FT TRANSMEM 700 723  
 FT DOMAIN 724 770  
 FT DOMAIN 673 715  
 FT DOMAIN 287 345  
 FT SITE 759 762  
 FT DISULFID 291 341  
 FT DISULFID 300 324  
 FT DISULFID 316 337  
 FT CARBOHYD 542 542  
 FT CARBOHYD 571 571  
 FT CARBOHYD 289 289  
 FT VARSPLIC 290 364  
 FT SEQUENCE 770 AA; 86704 MW; C26C9D6B2D929A7 CRC64;

Query Match 67.5%; Score 27; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-20;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 HOKLVEFADVGSKNGAIIGLWGVV 40  
 |||||  
 DB 685 HOKLVEFADVGSKNGAIIGLWGVV 711

RESULT 11  
 YBDA\_ECOLI STANDARD; PRT: 416 AA.

ID YBDA\_ECOLI  
 AC P24077;  
 DT 01-MAR-1992 (rel. 21, Created)  
 DT 01-NOV-1997 (rel. 35, Last sequence update)  
 DT 20-AUG-2001 (rel. 40, Last annotation update)  
 DE HYPOTHETICAL MEMBRANE PROTEIN P43.  
 GN YBDA OR B0591.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=92157868; PubMed=1838574;  
 RA Shea C.M., McIntosh M.A.;  
 RT "Nucleotide sequence and genetic organization of the ferric  
 RT enterobactin transport system: homology to other periplasmic binding  
 RT protein-dependent systems in Escherichia coli.";  
 RL Mol. Microbiol. 5:1415-1428(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=92157867; PubMed=1787794;  
 RA Chenaault S.S., Earhart C.F.;  
 RT "Organization of genes encoding membrane proteins of the Escherichia  
 RT coli ferriterobactin permease.";  
 RL Mol. Microbiol. 5:1405-1413(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Berna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;

RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 RN [41]  
 RP SEQUENCE FROM N.A.  
 RA Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,  
 RA Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,  
 RA Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: X57470; CAA40706.1; -  
 CC EMBL: X59402; CAA42044.1; -  
 CC EMBL: AE000164; AAC73692.1; -  
 CC EMBL: U82598; AAB40790.1; -  
 CC PIR: S16295; S16295.  
 CC PIR: S16306; S16306.  
 CC PIR: S14850; S14850.  
 CC Ecogene: EG11104; Ybda.  
 CC Hypothetical protein: Transmembrane: Complete proteome.  
 KM TRANSMEM 22 42 POTENTIAL.  
 FT TRANSMEM 36 76 POTENTIAL.  
 FT TRANSMEM 96 116 POTENTIAL.  
 FT TRANSMEM 119 139 POTENTIAL.  
 FT TRANSMEM 157 177 POTENTIAL.  
 FT TRANSMEM 179 199 POTENTIAL.  
 FT TRANSMEM 219 239 POTENTIAL.  
 FT TRANSMEM 257 277 POTENTIAL.  
 FT TRANSMEM 301 321 POTENTIAL.  
 FT TRANSMEM 357 377 POTENTIAL.  
 FT TRANSMEM 379 399 POTENTIAL.  
 FT TRANSMEM 123 123 F -> S (IN REF. 1).  
 SO CONFLICT 123 123  
 SO SEQUENCE 416 AA; 43282 MW; 64PCCF9AF99AC25A CRC64;  
 QY 33 GLMVGCV 39  
 DB 68 GLMVGCV 74  
 ID UBIB\_SALTY STANDARD: PRT; 546 AA.  
 AC Q9L6M4;  
 DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE PROBABLE UBIQUINONE BIOSYNTHESIS PROTEIN UBIB.  
 GN UBIB OR AARP OR STWD1.17.  
 OS Salmonella typhimurium.  
 OC Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 CC Salmonella.  
 OX NCBI\_TaxID=602;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LT2 / SGGC1412;  
 RA Waterston R.;  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: REQUIRED, PROBABLY INDIRECTLY, FOR THE HYDROXYLATION OF  
 CC 2-OCTAPRENYLPHENOL TO 2-OCTAPRENYL-6-HYDROXY-PHENOL, THE FOURTH  
 CC STEP IN UBIQUINONE BIOSYNTHESIS (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE ABCI FAMILY. UBIB SUBFAMILY.

CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: AF233324; AAF3420.1; -  
 CC Scygene: SG77777; ubib.  
 KW Ubiquinone biosynthesis.  
 SQ SEQUENCE 546 AA; 63238 MW; 362873022A808F1A CRC64;  
 QY 34 LMVGCV 40  
 DB 530 LMVGCV 536  
 ID EPUA\_STRPN STANDARD: PRT; 64 AA.  
 AC Q03159;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last annotation update)  
 DE EPUA PROTEIN.  
 GN EPUA.  
 OS Streptococcus pneumoniae  
 OC Bacteria: Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1313;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=470;  
 RC MEDLINE=90294291; PubMed=2359120;  
 RA Puyet A., Greenberg B., Lacks S.A.;  
 RT "Genetic and structural characterization of end. A membrane-bound  
 RT nuclease required for transformation of Streptococcus pneumoniae.";  
 RL J. Mol. Biol. 213:727-738(1990).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: X54225; CAA38133.1; -  
 CC PIR: S10640; S10640.  
 SO SEQUENCE 64 AA; 7037 MW; DE5727DA7B5EBB92 CRC64;  
 QY 32 IGLMVG 37  
 DB 30 IGLMVG 35  
 ID PROF\_ENTHI STANDARD: PRT; 130 AA.  
 AC P49230;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 QY 32 IGLMVG 37  
 DB 30 IGLMVG 35  
 ID PROF\_ENTHI STANDARD: PRT; 130 AA.  
 AC P49230;  
 DT 01-FEB-1996 (Rel. 33, Created)



```

DT 01-FEB-1996 (Rel. 33, last sequence update)
DT 15-DEC-1998 (Rel. 37, last annotation update)
DE PROFILIN.
OS Entamoeba histolytica.
CC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 74-84 AND 86-94.
RC STRAIN=SEF-3;
RX MEDLINE=96085166; PubMed=8521867;
RA Blinder M., Ortner S., Erben H., Scheiner O., Wiedermann G.,
  Valenta R., Duchen M.;
RT "The basic isoform of profilin in pathogenic Entamoeba histolytica.
  cDNA cloning, heterologous expression, and actin-binding
  properties."
RL Eur. J. Biochem. 233:976-981(1995).
CC -!- FUNCTION: BINDS TO ACTIN AND AFFECTS THE STRUCTURE OF THE
  CYTOSKELETON. AT HIGH CONCENTRATIONS, PROFILIN PREVENTS THE
  POLYMERIZATION OF ACTIN, WHEREAS IT ENHANCES IT AT LOW
  CONCENTRATIONS. BY BINDING TO PIP2, IT INHIBITS THE FORMATION OF
  IP3 AND DG.
CC -!- SUBUNIT: OCCURS IN MANY KINDS OF CELLS AS A COMPLEX WITH MONOMERIC
  ACTIN IN A 1:1 RATIO.
CC -!- SIMILARITY: BELONGS TO THE PROFILIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X90911; CA62418.1;
DR HSSP: P07274; 1YPR.
DR InterPro: IPR002097; Profilin.
DR Pfam: PF00235; Profilin; 1.
DR SMART: SM00392; PROF; 1.
DR PROSITE: PS00414; PROFILIN; 1.
KW Actin-binding; Cytoskeleton.
SQ SEQUENCE 130 AA; 13237 MW; AF50A8E08FA00A6F CRC64;

Query Match 15.0%; Score 6; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 29 GATIGL 34
    |||||
Db 20 GATIGL 25

RESULT 15
NO6M_CEPKO STANDARD: PRT; 173 AA.
AC P43197;
DT 01-NOV-1995 (Rel. 32, created)
DT 01-NOV-1995 (Rel. 32, last sequence update)
DT 15-JUL-1998 (Rel. 36, last annotation update)
DE MADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6 (EC 1.6.5.3).
MT MTND6 OR ND6 OR NADH6.
OS Cepphus columba (Pigeon guillemot).
CC Mitochondrion.
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Archosauia; Aves; Neognathae; Charadriiformes; Alcidae; Cepphus.
OX NCBI_TaxID=28696;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94363783; PubMed=8082208;
RA Moun T., Willassen N.P., Johansen S.;
RT "Intergenic rearrangements in the mitochondrial MADH dehydrogenase
  subunit 6 gene of vertebrates."
RL Curr. Genet. 25:554-557(1994).

```

```

CC -!- CATALYTIC ACTIVITY: MADH + UBIQUINONE = NAD(+) + UBIQUINOL.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X73918; CA52123.1;
DR InterPro: IPR001457; Oxidored_q3.
DR Pfam: PF00499; oxidored_q3; 1.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ SEQUENCE 173 AA; 17982 MW; AAAP84636E040DF8 CRC64;

Query Match 15.0%; Score 6; DB 1; Length 173;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 LMWGV 39
    |||||
Db 98 LMWGV 103

```

Search completed: April 24, 2002, 09:24:53  
 Job time: 246 sec





FT NON\_TER 1 1  
SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match 100.0%; Score 40; DB 4; Length 82;  
Best Local Similarity 100.0%; Pred. No. 2e-35;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLWGVV 40  
DB 17 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLWGVV 56

RESULT 2

ID 016014 PRELIMINARY; PRT: 82 AA.

AC 016014; 01-NOV-1996 (TREMBLREL. 01, Created)  
DT 01-NOV-1996 (TREMBLREL. 01, last sequence update)  
DE 01-MAR-2001 (TREMBLREL. 16, last annotation update)  
GN BETA-AMYLLOID PEPTIDE PRECURSOR (FRAGMENT).

OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.

RX MEDLINE=93236601; PubMed=8476439;  
RA Denman R.B., Rosenzwaig R., Miller D.L.;  
RT "A system for studying the effect(s) of familial Alzheimer disease  
mutations on the processing of the beta-amyloid peptide precursor.";  
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
DR EMBL; S60721; AAB26263.2; -  
DR HSSP; P05067; IBA4.

FT NON\_TER 1 1  
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 100.0%; Score 40; DB 4; Length 82;  
Best Local Similarity 100.0%; Pred. No. 2e-35;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLWGVV 40  
DB 18 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLWGVV 57

RESULT 3

ID 016019 PRELIMINARY; PRT: 82 AA.

AC 016019; 01-NOV-1996 (TREMBLREL. 01, Created)  
DT 01-NOV-1996 (TREMBLREL. 01, last sequence update)  
DE 01-MAR-2001 (TREMBLREL. 16, last annotation update)  
GN BETA-AMYLLOID PEPTIDE PRECURSOR (FRAGMENT).

OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.

RX MEDLINE=93236601; PubMed=8476439;  
RA Denman R.B., Rosenzwaig R., Miller D.L.;  
RT "A system for studying the effect(s) of familial Alzheimer disease  
mutations on the processing of the beta-amyloid peptide precursor.";  
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
DR EMBL; S61380; AAB26264.2; -  
DR HSSP; P05067; IBA4.

FT NON\_TER 1 1  
SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match 100.0%; Score 40; DB 4; Length 82;  
Best Local Similarity 100.0%; Pred. No. 2e-35;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLWGVV 40  
DB 18 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLWGVV 57

RESULT 4

ID 016020 PRELIMINARY; PRT: 82 AA.

AC 016020; 01-NOV-1996 (TREMBLREL. 01, Created)  
DT 01-NOV-1996 (TREMBLREL. 01, last sequence update)  
DE 01-MAR-2001 (TREMBLREL. 16, last annotation update)  
GN BETA-AMYLLOID PEPTIDE PRECURSOR (FRAGMENT).

OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.

RX MEDLINE=93236601; PubMed=8476439;  
RA Denman R.B., Rosenzwaig R., Miller D.L.;  
RT "A system for studying the effect(s) of familial Alzheimer disease  
mutations on the processing of the beta-amyloid peptide precursor.";  
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
DR EMBL; S61383; AAB26265.2; -  
DR HSSP; P05067; IBA4.

FT NON\_TER 1 1  
SQ SEQUENCE 82 AA; 8882 MW; F534AA5AB5D9230A CRC64;

Query Match 100.0%; Score 40; DB 4; Length 82;  
Best Local Similarity 100.0%; Pred. No. 2e-35;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLWGVV 40  
DB 18 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLWGVV 57

RESULT 5

ID 093296 PRELIMINARY; PRT: 534 AA.

AC 093296; 01-NOV-1998 (TREMBLREL. 08, Created)  
DT 01-NOV-1998 (TREMBLREL. 08, last sequence update)  
DE 01-JUN-2001 (TREMBLREL. 17, last annotation update)  
GN AMYLLOID PRECURSOR PROTEIN (FRAGMENT).

OS Gallus gallus (Chicken)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Barnes N.Y., Ling L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,  
RT "Increased production of amyloid precursor protein provides a  
substrate for Caspase 3 in dying motoneurons.";  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBD databases.  
DR EMBL; AF042098; AAC25052.1; -  
DR HSSP; P05067; IBA4.

DR InterPro; IPR001868; A4\_APP.  
DR PRINTS; PR00203; AMYLLOIDA4.  
DR PROSITE; PS00319; A4\_EXTRA; 1.  
DR PROSITE; PS00320; A4\_INTRA; 1.

FT NON\_TER 1 1  
SQ SEQUENCE 534 AA; 60597 MW; FB53EC2E66D4C92 CRC64;

Query Match  
Best Local Similarity 100.0%; Score 40; DB 13; Length 534;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMGVV 40  
DB 436 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMGVV 475

RESULT 6  
ID Q9PVL1 PRELIMINARY; PRT; 569 AA.

AC Q9PVL1  
DT 01-MAY-2000 (TREMblrel. 13, Created)  
DT 01-MAY-2000 (TREMblrel. 13, last sequence update)  
DE AMYLOID PROTEIN PRECURSOR (FRAGMENT).  
GN APP.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BRAIN;  
RA Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;  
RT "What the evolution of the amyloid protein precursor supergene family  
RT tells us about its function."  
RL Neurochem. Int. 0:0-0(2000).  
DR EMBL: AF030341; AAF12698.1; -.  
DR HSSP: P05067; 1BA4.  
DR InterPro: IPR001868; A4\_APP.  
DR Pfam: PF02177; A4\_EXTRA; 1.  
DR PRINTS: PR00203; AMYLOIDA4.  
DR SMART: SM00006; A4\_EXTRA; 1.  
DR PROSITE: PS00319; A4\_EXTRA; 1.  
DR PROSITE: PS00320; A4\_INTRA; 1.  
FT NON\_TER 1  
SQ SEQUENCE 569 AA; 64753 MW; 0AB8B851863A19D CRC64;

Query Match  
Best Local Similarity 100.0%; Score 40; DB 13; Length 569;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMGVV 40  
DB 472 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMGVV 511

RESULT 7  
ID Q60496 PRELIMINARY; PRT; 695 AA.  
AC Q60496;  
DT 01-NOV-1996 (TREMblrel. 01, Created)  
DT 01-NOV-1996 (TREMblrel. 01, last sequence update)  
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriognathii; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BRAIN;  
RA Beck M., Mueller D., Bigl V.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO

CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
CC G(O).  
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -!- SIMILARITY: TO OTHER SPECIES APP ANALOGUES.

DR EMBL: X97631; CA66230.1; -.  
DR HSSP: P05067; 1BA4.  
DR InterPro: IPR001868; A4\_APP.  
DR Pfam: PF02177; A4\_EXTRA; 1.  
DR PRINTS: PR00203; AMYLOIDA4.  
DR SMART: SM00006; A4\_EXTRA; 1.  
DR PROSITE: PS00319; A4\_EXTRA; 1.  
DR PROSITE: PS00320; A4\_INTRA; 1.  
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match  
Best Local Similarity 100.0%; Score 40; DB 11; Length 695;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMGVV 40  
DB 597 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMGVV 636

RESULT 8  
ID Q9DGJ8 PRELIMINARY; PRT; 695 AA.

AC Q9DGJ8  
DT 01-MAR-2001 (TREMblrel. 16, Created)  
DT 01-MAR-2001 (TREMblrel. 16, last sequence update)  
DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOROM.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sarasa M., Rodolosse A., Sorribas V.;  
RT "Cloning of full-length chicken beta-amyloid precursor protein  
RT isoforms."  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF289218; AAG00593.1; -.  
DR InterPro: IPR001868; A4\_APP.  
DR Pfam: PF02177; A4\_EXTRA; 1.  
DR PRINTS: PR00203; AMYLOIDA4.  
DR SMART: SM00006; A4\_EXTRA; 1.  
DR PROSITE: PS00319; A4\_EXTRA; 1.  
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match  
Best Local Similarity 100.0%; Score 40; DB 13; Length 695;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMGVV 40  
DB 597 DAEFRHDSGYEVHHQKLVFAEDVGSNKGALIGLMGVV 636

RESULT 9  
ID Q9DGJ7 PRELIMINARY; PRT; 751 AA.  
AC Q9DGJ7;  
DT 01-MAR-2001 (TREMblrel. 16, Created)  
DT 01-MAR-2001 (TREMblrel. 16, last sequence update)  
DE BETA-AMYLOID PRECURSOR PROTEIN 751 ISOROM.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.

```

OX NCB1_TaxID=9031;
RN
RP SEQUENCE FROM N.A.
RA Sarraa M., Rodolose A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO PANCREATIC TRYPsin INHIBITOR (KUNITZ) DOMAIN.
DR EMBL; AF289219; AAC00594.1; -.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KM Serine protease inhibitor.
SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match
Best Local Similarity 100.0%; Score 40; DB 13; Length 751;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAERHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVV 40
Db 653 DAERHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVV 692

RESULT 10
O9TUIO
ID O9TUIO PRELIMINARY; PRT; 770 AA.
AC O9TUIO;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE AMYLOID PRECURSOR PROTEIN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCB1_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid Precursor Protein 770."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO PANCREATIC TRYPsin INHIBITOR (KUNITZ) DOMAIN.
DR EMBL; AB032550; BAA84580.1; -.
DR HSSP; P05067; IAAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS50280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KM Serine protease inhibitor.
SQ SEQUENCE 770 AA; 86961 MW; 5F7A1DCB2BCC583E CRC64;

Query Match
Best Local Similarity 100.0%; Score 40; DB 6; Length 770;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAERHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVV 40

```

```

Db 672 DAERHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVV 711

RESULT 11
O13778
ID O13778 PRELIMINARY; PRT; 97 AA.
AC O13778;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE AMYLOID PROTEIN (AD-AP) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87120328; PubMed=3810169;
RA Goldhaber D., Lerman M.I., McBride O.W., Saffioti U., Gajdusek D.C.;
RT "Characterization and chromosomal localization of a cDNA encoding
RT brain amyloid of Alzheimer's disease."
RL Science 235:877-880(1987).
DR EMBL; M15533; AAA35540.1; -.
DR HSSP; P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR PRINTS; PR00203; AMYLOIDA4.
DR NON_TER 1 1
SQ SEQUENCE 97 AA; 10884 MW; E528CDB448DE474E CRC64;

Query Match
Best Local Similarity 100.0%; Score 38; DB 4; Length 97;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 EFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVV 40
Db 1 EFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVV 38

RESULT 12
O9UC33
ID O9UC33 PRELIMINARY; PRT; 33 AA.
AC O9UC33;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93024877; PubMed=1406936;
RA Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
RA Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
RT "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT biological fluids."
RL Nature 359:325-327(1992).
DR HSSP; P05067; IBA4.
SQ SEQUENCE 33 AA; 3674 MW; B1DEF2F4167ABD0 CRC64;

Query Match
Best Local Similarity 100.0%; Score 33; DB 4; Length 33;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAERHDSGYEVHHOKLVFAEDVGSNKGAIIG 33
Db 1 DAERHDSGYEVHHOKLVFAEDVGSNKGAIIG 33

```

RESULT 13

ID 073683 PRELIMINARY; PRT; 780 AA.

AC 073683;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)].

GN APP.

OS Tetraodon fluviatilis (Puffer fish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; OC Acanthomorphae; Acanthopterygii; Percomorpha; Tetraodontiformes; OC Tetraodontidae; Tetraodon.

OX NCBI\_TaxID=47145;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98252138; PubMed=9599080;

RA Villalad L., Tassone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;

RT "Analysis of pufferfish homologues of the At-rich human APP gene.";

RL Gene 210:17-24(1998).

CC -I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).

CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -I- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).

CC -I- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -I- SIMILARITY: CONTAINS 1 PROTEASE INHIBITOR DOMAIN BELONGING TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.

DR EMBL; AF018165; AAC41275.1; -.

DR HSSP; P05067; 1QCM.

DR InterPro; IPR001868; A4\_APP.

DR InterPro; IPR002223; Kunitz\_BPTI.

DR Pfam; PF02177; A4\_EXTRAI.1.

DR Pfam; PF00014; Kunitz\_BPTI.1.

DR PRINTS; PR00203; AMYLOIDA4.

DR PRINTS; PR00759; BASICPTASE.

DR SMART; SM00106; A4\_EXTRA.1.

DR SMART; SM00131; KU; 1.

DR PROSITE; PS00319; A4\_EXTRA.1.

DR PROSITE; PS00320; A4\_INTRA.1.

DR PROSITE; PS00280; BPTI\_KUNITZ.1; FALSE\_NEG.

DR PROSITE; PS50279; BPTI\_KUNITZ\_2; 1.

KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;

KW Serine protease inhibitor.

FT SIGNAL 1 18 POTENTIAL.

FT CHAIN 19 780 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN

FT 682 724 HOMOLOG.

FT DOMAIN 19 711 BETA-AMYLOID PROTEIN (POTENTIAL).

FT TRANSMEM 712 732 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 733 780 POTENTIAL.

FT DOMAIN 323 382 CYTOPLASMIC (POTENTIAL).

FT SITE 769 772 BPTI/KUNITZ INHIBITOR.

FT DISULFID 327 378 CLATHRIN-BINDING (BY SIMILARITY).

FT DISULFID 336 361 BY SIMILARITY.

FT CARBOHYD 560 560 N-LINKED (GLCNAC. . .) (POTENTIAL).

SO SEQUENCE 780 AA; 88238 MW; 60071BE94520191D CRC64;

Query Match 77.5%; Score 31; DB 13; Length 780;

Best Local Similarity 100.0%; Pred. No. 7.1e-25;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEYHHOKLVEFAEDVGSNGKAITGLMWGSV 40

DB 691 YEYHHOKLVEFAEDVGSNGKAITGLMWGSV 721

RESULT 14

ID 09UCD1 PRELIMINARY; PRT; 30 AA.

AC 09UCD1;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE BETA-AMYLOID PROTEIN (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=94153015; PubMed=8109908;

RA Wisniewski T., Lalowski M., Levy E., Marques M.R., Frangione B.;

RT "The amino acid sequence of neuritic plaque amyloid from a familial Alzheimer's disease patient.";

RL Ann. Neurol. 35:245-246(1994).

DR HSSP; P05067; 1BA4.

SO SEQUENCE 30 AA; 3391 MW; FF4167ABD081160A CRC64;

Query Match 75.0%; Score 30; DB 4; Length 30;

Best Local Similarity 100.0%; Pred. No. 3.7e-25;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGEYVHHOKLVEFAEDVGSNGKA 30

DB 1 DAEFRHDSGEYVHHOKLVEFAEDVGSNGKA 30

RESULT 15

ID 09UCD1 PRELIMINARY; PRT; 28 AA.

AC 09UCD1;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE BETA-AMYLOID PEPTIDE (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=94045685; PubMed=8229004;

RA Vingo-Pellfrey C., Lee D., Keim P., Lieberburg I., Schenk D.B.;

RT "Characterization of beta-amyloid peptide from human cerebrospinal fluid.";

RL J. Neurochem. 61:1965-1968(1993).

DR HSSP; P05067; 1AMB.

SO SEQUENCE 28 AA; 3244 MW; DE7BD081160AFC81 CRC64;

Query Match 67.5%; Score 27; DB 4; Length 28;

Best Local Similarity 100.0%; Pred. No. 5.7e-22;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGEYVHHOKLVEFAEDVGSN 27

DB 1 DAEFRHDSGEYVHHOKLVEFAEDVGSN 27

Search completed: April 24, 2002, 09:24:25

Job time: 249 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:15:16 ; Search time 66.28 Seconds  
(without alignments)  
44.703 Million cell updates/sec

Title: US-09-689-469-3

Perfect score: 209

Sequence: 1 DAEFRHDSGYEHVHOKLVFAEDVGNKGAITGLMGVV 40

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_1101.\*  
1: /SID8/gcgdata/geneseq/geneseq/AA1980.DAT:\*  
2: /SID8/gcgdata/geneseq/geneseq/AA1981.DAT:\*  
3: /SID8/gcgdata/geneseq/geneseq/AA1982.DAT:\*  
4: /SID8/gcgdata/geneseq/geneseq/AA1983.DAT:\*  
5: /SID8/gcgdata/geneseq/geneseq/AA1984.DAT:\*  
6: /SID8/gcgdata/geneseq/geneseq/AA1985.DAT:\*  
7: /SID8/gcgdata/geneseq/geneseq/AA1986.DAT:\*  
8: /SID8/gcgdata/geneseq/geneseq/AA1987.DAT:\*  
9: /SID8/gcgdata/geneseq/geneseq/AA1988.DAT:\*  
10: /SID8/gcgdata/geneseq/geneseq/AA1989.DAT:\*  
11: /SID8/gcgdata/geneseq/geneseq/AA1990.DAT:\*  
12: /SID8/gcgdata/geneseq/geneseq/AA1991.DAT:\*  
13: /SID8/gcgdata/geneseq/geneseq/AA1992.DAT:\*  
14: /SID8/gcgdata/geneseq/geneseq/AA1993.DAT:\*  
15: /SID8/gcgdata/geneseq/geneseq/AA1994.DAT:\*  
16: /SID8/gcgdata/geneseq/geneseq/AA1995.DAT:\*  
17: /SID8/gcgdata/geneseq/geneseq/AA1996.DAT:\*  
18: /SID8/gcgdata/geneseq/geneseq/AA1997.DAT:\*  
19: /SID8/gcgdata/geneseq/geneseq/AA1998.DAT:\*  
20: /SID8/gcgdata/geneseq/geneseq/AA1999.DAT:\*  
21: /SID8/gcgdata/geneseq/geneseq/AA2000.DAT:\*  
22: /SID8/gcgdata/geneseq/geneseq/AA2001.DAT:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 209   | 100.0       | 40     | AA33191  | Beta-amyloid pepti |
| 2          | 209   | 100.0       | 40     | AA60364  | Beta-amyloid (1-40 |
| 3          | 209   | 100.0       | 40     | AAW3507  | Amyloid beta prote |
| 4          | 209   | 100.0       | 40     | AAW2335  | Amyloid beta prote |
| 5          | 209   | 100.0       | 40     | AAW4726  | Beta-amyloid pepti |
| 6          | 209   | 100.0       | 40     | AAW3939  | Beta-amyloid prote |
| 7          | 209   | 100.0       | 40     | AAW39804 | Beta-amyloid prote |
| 8          | 209   | 100.0       | 40     | AAW25135 | Human amyloid beta |
| 9          | 209   | 100.0       | 40     | AAW14099 | Human beta-amyloid |
| 10         | 209   | 100.0       | 40     | AAW9584  | Wild type aggregat |
| 11         | 209   | 100.0       | 40     | AAW92723 | Human tachykinin a |

|    |     |       |    |          |                    |
|----|-----|-------|----|----------|--------------------|
| 12 | 209 | 100.0 | 40 | AAW81473 | Synthetic amyloid  |
| 13 | 209 | 100.0 | 40 | AAE05483 | Human peptide anti |
| 14 | 209 | 100.0 | 40 | AAW84426 | Partial sequence o |
| 15 | 209 | 100.0 | 40 | AAW91780 | Amyloid beta-prote |
| 16 | 209 | 100.0 | 40 | AAW91802 | Amyloid beta-prote |
| 17 | 209 | 100.0 | 40 | AAW91813 | Amyloid beta-prote |
| 18 | 209 | 100.0 | 40 | AAW91829 | Amyloid beta-prote |
| 19 | 209 | 100.0 | 41 | AAW60365 | Beta-amyloid (1-41 |
| 20 | 209 | 100.0 | 41 | AAW25136 | Human amyloid beta |
| 21 | 209 | 100.0 | 41 | AAW11497 | Human amyloid beta |
| 22 | 209 | 100.0 | 42 | AAW20330 | Sequence of A99 (b |
| 23 | 209 | 100.0 | 42 | AAW60366 | Beta-amyloid (1-42 |
| 24 | 209 | 100.0 | 42 | AAW60368 | Beta/A4-amyloid pe |
| 25 | 209 | 100.0 | 42 | AAW94591 | Alzheimer amyloid  |
| 26 | 209 | 100.0 | 42 | AAW12828 | Beta A4 peptide.   |
| 27 | 209 | 100.0 | 42 | AAW64507 | Neurotoxic beta-am |
| 28 | 209 | 100.0 | 42 | AAW47230 | Beta-amyloid pepti |
| 29 | 209 | 100.0 | 42 | AAW42989 | Full length beta-a |
| 30 | 209 | 100.0 | 42 | AAW49691 | Human beta amyloid |
| 31 | 209 | 100.0 | 42 | AAW33407 | Human amyloidogen  |
| 32 | 209 | 100.0 | 42 | AAW25137 | Human amyloid beta |
| 33 | 209 | 100.0 | 42 | AAW08607 | Human beta-amyloid |
| 34 | 209 | 100.0 | 42 | AAW25093 | A-beta-binding pep |
| 35 | 209 | 100.0 | 42 | AAW9585  | Mutant aggregating |
| 36 | 209 | 100.0 | 42 | AAW92726 | Human tachykinin a |
| 37 | 209 | 100.0 | 42 | AAW81474 | Synthetic amyloid  |
| 38 | 209 | 100.0 | 42 | AAW6956  | Beta-amyloid 1-42  |
| 39 | 209 | 100.0 | 42 | AAW82622 | Amyloid-beta pepti |
| 40 | 209 | 100.0 | 42 | AAE05484 | Human peptide anti |
| 41 | 209 | 100.0 | 42 | AAW86134 | Human Alzheimer-be |
| 42 | 209 | 100.0 | 42 | AAW91779 | Amyloid beta-prote |
| 43 | 209 | 100.0 | 42 | AAW91812 | Amyloid beta-prote |
| 44 | 209 | 100.0 | 42 | AAW49098 | Human amyloid beta |
| 45 | 209 | 100.0 | 42 | AAW48497 | Human amyloid prot |

#### ALIGNMENTS

RESULT 1  
ID AAR33191 standard; peptide: 40 AA.  
XX  
AC AAR33191;  
XX  
DT 01-JUL-1993 (first entry)  
XX  
DE Beta-amyloid peptide.  
XX  
KW Alzheimer's disease; amyloid deposition; diagnosis; therapy.  
OS Synthetic.  
XX  
PN WO9304194-A.  
XX  
PD 04-MAR-1993.  
XX  
PF 10-AUG-1992; 92WO-US06700.  
XX  
PR 13-AUG-1991; 91US-0744767.  
XX  
PA (HARD ) HARVARD COLLEGE.  
PA (MING ) UNIV MINNESOTA.  
XX  
Maggio JE, Mantyh PW;  
WPI: 1993-094020/11.  
PT Detecting Alzheimer's disease using beta-amyloid peptide -  
PT includes quantitating amyloid deposition onto tissue samples, and  
PT using screen agents as therapeutic agents  
XX  
PS Disclosure: Page 34; 51pp; English.

XX The peptide is an internal fragment of the beta amyloid peptide (BAP)  
 CC precursor, which was produced synthetically. The peptide, when  
 CC labelled, may be used in in vitro methods for the detection of  
 CC Alzheimer's disease.  
 CC See also AAR3192.

SO Sequence 40 AA;

Query Match 100.0%; Score 209; DB 14; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-24;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAERHDGSEVHHOKLVFAEDVGNKGAITIGLVGCVV 40  
 DB 1 daefrhdsgyevhhoklvfaedvgnkga1g1mvgvv 40

# RESULT 2

AAR60364  
 ID AAR60364 standard; peptide; 40 AA.

AC AAR60364;  
 XX  
 DT 15-MAR-1995 (first entry)  
 XX  
 DE Beta-amyloid (1-40).  
 XX  
 KW Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;  
 KM anti-beta-amyloid antibody; diagnosis.  
 XX  
 OS Homo sapiens.

PN WO9417197-A.

PD 04-AUG-1994.

PF 24-JAN-1994; 94MO-JP00089.

PR 25-JAN-1993; 93JP-0010132.

PR 05-FEB-1993; 93JP-0019035.

PR 16-NOV-1993; 93JP-0286985.

PR 28-DEC-1993; 93JP-0334773.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX Kitada C, Otake A, Suzuki N;

XX WPI: 1994-264110/32.

XX

PT Antibodies recognising specific parts of beta-amyloid - can be

PT used for diagnosis of diseases implicating beta-amyloid, such as

PT Alzheimer's disease

PS disclosure; Page 82; 116pp; Japanese.

XX Antibodies which recognise specific subfragments of the beta-amyloid

XX protein are claimed. Specifically, the antibodies (which are pref.

XX monoclinal) recognise residues 1-16 and/or 1-28 from the N-terminal

XX portion of beta-amyloid or they recognise residues 25-35 or 35-43

XX from the C-terminal portion. The antibodies are useful for assaying

XX beta-amyloid and its derivatives for diagnosis of Alzheimer's

XX disease.

SO Sequence 40 AA;

Query Match 100.0%; Score 209; DB 15; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-24;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAERHDGSEVHHOKLVFAEDVGNKGAITIGLVGCVV 40

DB 1 daefrhdsgyevhhoklvfaedvgnkga1g1mvgvv 40

# RESULT 3

AAM37507  
 ID AAM37507 standard; peptide; 40 AA.

XX AAM37507;

XX 20-APR-1998 (first entry)

XX Amyloid beta protein fragment (1-40) immunogen.

XX Amyloid beta protein: A beta; immunogen; human; Alzheimer's disease;

XX amyloid precursor protein; soluble; APP; monoclonal antibody; diagnosis.

XX Synthetic.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Cleavage-site 16..17

XX EP783104-A1.

XX 09-JUL-1997.

XX 17-DEC-1996; 96EP-0120269.

XX 27-DEC-1995; 95JP-0351296.

XX (ORIT ) ORIENTAL YEAST CO LTD.

XX Fujita T, Matuo Y, Taniguchi Y;

XX WPI: 1997-343989/32.

XX

PT Assay for soluble amyloid precursor protein useful to diagnose

PT Alzheimer's disease - uses antibodies against amyloid beta-protein,

PT also new hydridoma producing antibodies

PS Example 1; Fig 2; 10pp; English.

XX A novel method has been developed of assaying for soluble amyloid

XX precursor protein (SAPP). The method uses an antibody against amyloid

XX beta-protein (A beta; produced from SAPP) or SAPP. The present sequence

XX represents amino acids 1 to 40 of amyloid beta-protein. SAPP can be

XX assayed accurately, and when including a monoclonal antibody recognising

XX the N-terminus of A beta and a monoclonal antibody recognising SAPP, the

XX assay can be used to diagnose Alzheimer's disease. Senior plaque

XX observed in the brain of Alzheimer's patients is primarily composed of

XX A beta, which is generated from SAPP. Simple and accurate assay of SAPP

XX is possible. The antibody (preferably monoclonal) preferably has an

XX antigen recognition site which is an amino acid sequence common to

XX A beta and SAPP, or specific to SAPP. The SAPP assayed for preferably

XX has part of the A beta sequence at its amino terminus and is preferably

XX solubilised through cleavage of the A beta between positions 16 (lysine)

XX and 17 (leucine) from the amino acid terminus. The preferred method

XX comprises immobilising one antibody (especially generated by (2)) on to

XX an insoluble carrier, capturing a substance to be assayed on to this

XX antibody, reacting another, labelling, antibody with the assay substance

XX and detecting the activity of the labelling substance bound to the

XX carrier.

SO Sequence 40 AA;

Query Match 100.0%; Score 209; DB 18; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-24;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAERHDGSEVHHOKLVFAEDVGNKGAITIGLVGCVV 40

DB 1 daefrhdsgyevhbkqlvffaedvgsnkgallglmwgvv 40

# RESULT 4

ID AAW23335 standard; peptide; 40 AA.

XX AAW23335;

DT 12-MAR-1998 (first entry)

DE Amyloid beta peptide 1 used to inhibit damage to cells in Alzheimer's.

XX Amyloid beta peptide; extracellular deposit; Alzheimer's disease;

KW neurite outgrowth; microglial activation; neuronal cell degeneration;

KW receptor for advanced glycosylation end product;

XX amyloid beta peptide fibril.

XX Homo sapiens.

OS WO9726913-A1.

PN 31-JUL-1997.

PD 21-JAN-1997; 97WO-US00857.

PF 26-JAN-1996; 96US-0592070.

XX (UYCO ) UNIV COLUMBIA NEW YORK.

PA Schmidt AM, Stern D, Yan SD;

PI WPI; 1997-393374/36.

DR Inhibiting damage to cells in e.g. Alzheimer's disease - using an

XX agent which inhibits interaction of an amyloid-beta peptide with a

PT receptor for advanced glycosylation end product

PS Claim 4; Page 10; 91pp; English.

XX Peptides AAW23335-36 are portions of the the amyloid beta peptide, which

CC is the principal component of extracellular deposits in Alzheimer's

CC disease. It has been shown to promote neurite outgrowth, generate

CC reactive oxygen intermediates, induce cellular oxidant stress, lead to

CC neuronal cytotoxicity, and promote microglial activation. The present

CC peptide, which comprises amino acids 1-40 of the amyloid beta peptide,

CC is used in a pharmaceutical composition. This composition comprises an

CC agent capable of inhibiting interaction of an amyloid-beta peptide with

CC a receptor for advanced glycosylation end product and a carrier. A

CC method for inhibiting interaction of amyloid beta peptide with a receptor

CC for advanced glycosylation on the surface of a cell comprises contacting

CC the cell with e.g. present peptide. Depending on the type of cell,

CC inhibiting the interaction between the amyloid beta peptide and the

CC receptor for advanced glycosylation can be used for inhibiting

CC degeneration of a neuronal cell, inhibiting formation of an amyloid beta

CC peptide fibril on a cell, inhibiting extracellular assembly of amyloid

CC beta peptide into a fibril, inhibiting aggregation of amyloid beta

CC peptide on the surface of a cell, inhibiting infiltration of a microglial

CC cell into senile plaques, and inhibiting activation of microglial cells

CC by amyloid beta peptide. The methods can be used for treating e.g.

CC diabetes, Alzheimer's Disease, senility, renal failure, hyperlipidemic

CC atherosclerosis, neuronal cytotoxicity, Down's syndrome, dementia

CC associated with head trauma, amyotrophic lateral sclerosis, multiple

CC sclerosis or neuronal degeneration.

CC Sequence 40 AA:

XX

Query Match 100.0%; Score 209; DB 18; Length 40;

Best Local Similarity 100.0%; Pred. No. 3.5e-24;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHOKLVEFAEDVGSNKGALLGLMWGVV 40

DB 1 daefrhdsgyevhbkqlvffaedvgsnkgallglmwgvv 40

# RESULT 5

ID AAW47226 standard; peptide; 40 AA.

XX AAW47226;

DT 22-MAY-1998 (first entry)

DE Beta-amyloid peptide residues 1-40.

XX Screening assay; beta-amyloid peptide; treatment;

KW amyloidosis disease; Alzheimer's disease.

XX Homo sapiens.

OS US5721106-A.

PN 24-FEB-1998.

PD 12-SEP-1994; 94US-0304585.

PF 12-SEP-1994; 94US-0304585.

PR 13-AUG-1991; 91US-0744767.

XX (HARD ) HARVARD COLLEGE.

PA (MIND ) UNIV MINNESOTA.

PI Maggio JE, Mantyh PW;

DR WPI; 1998-168404/15.

XX New in vitro screening assay for Alzheimer's disease drugs -

XX comprises assessing binding of labelled beta-amyloid peptide to silk

XX sample

PS Claim 8; Columns 29-30; 36pp; English.

XX The present sequence was used in the development of a novel in

CC vitro screening assay for agents capable of affecting the

CC deposition of beta-amyloid peptide (BAP) on tissue. The method

CC comprises contacting a silk sample with labelled BAP, optionally

CC in the presence of a test agent, detecting the amount of label

CC bound to the silk and assessing the effect of the agent on the

CC deposition of BAP. Agents that inhibit binding of BAP to silk are

CC potentially useful for treating amyloidosis diseases, especially

CC Alzheimer's disease.

XX Sequence 40 AA:

XX

Query Match 100.0%; Score 209; DB 19; Length 40;

Best Local Similarity 100.0%; Pred. No. 3.5e-24;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHOKLVEFAEDVGSNKGALLGLMWGVV 40

KW Beta-amyloid protein; Alzheimer's disease; extracellular amyloid plaque;  
 KW cerebral blood vessel; sulphated macromolecule; kuru;  
 KW conophilic maltase-cross spherical amyloid plaque;  
 KW Creutzfeldt-Jacob disease; Gertmann-Straussler syndrome.  
 OS Homo sapiens.  
 XX W09945947-A1.  
 XX 16-SEP-1999.  
 XX 12-MAR-1999: 99WO-US05438.  
 XX 13-MAR-1998: 98US-0077924.  
 XX (UNIW ) UNIV WASHINGTON.  
 XX Castillo G, Snow AD;  
 XX WPI: 1999-571666/48.  
 XX  
 PT Formation of amyloid plaques using amyloid protein and sulphated  
 PT macromolecules, for, e.g. identification of agents for treating  
 PT Alzheimer's disease -  
 XX  
 XX Claim 3: Page 87; 89pp; English.  
 PS  
 CC This sequence is 40 amino acids of the beta-amyloid protein. Alzheimer's  
 CC disease is characterised by the accumulation of a 39-43 amino acid  
 CC peptide termed the beta-amyloid peptide in the form of extracellular  
 CC amyloid plaques and as amyloid in the walls of cerebral blood vessels.  
 CC The invention relates to methods for the formation of conophilic  
 CC maltase-cross spherical amyloid plaques, which are characteristic of  
 CC Alzheimer's disease. The amyloid plaques are formed by co-incubation of  
 CC this beta-amyloid protein with sulphated macromolecules. The methods can  
 CC be used to study the formation of amyloid plaques and to identify  
 CC anti-plaque therapeutics. They can be used for diseases such as  
 CC Alzheimer's disease, Creutzfeldt-Jacob disease, Gertmann-Straussler  
 CC syndrome and kuru.  
 CC  
 XX  
 SO Sequence 40 AA;  
 Query Match 100.0%; Score 209; DB 20; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-24;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DAEFRHDSGCEVHHOKIVFFAEDVGSNKGAITGLMGVV 40  
 DB 1 daefrhdsgcevhqhkvlfafedvgsnkgailglmgvv 40  
 RESULT 7  
 AA39804  
 ID AAY39804 standard; peptide; 40 AA.  
 AC AAY39804;  
 XX  
 XX 29-NOV-1999 (first entry)  
 DE Beta-amyloid protein, Beta/A4 amyloid (1-40).  
 XX  
 XX Beta-amyloid protein; Alzheimer's disease; amyloidosis; joint swelling;  
 KW long-standing inflammation; malignancy; Familial Mediterranean Fever;  
 KW multiple myeloma; plasma cell dyscrasia; long-term haemodialysis; kuru;  
 KW carpal tunnel syndrome; multiple spontaneous fracture; radiolucency;  
 KW endocrine tumour; medullary carcinoma; Down's syndrome; scrapie;  
 KW Creutzfeldt-Jacob disease; Gertmann Straussler Syndrome;  
 KW subacute spongiform encephalopathy; therapy.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WPI: 1999-571666/48.  
 PN

XX  
 PD 28-SEP-1999.  
 XX  
 XX 05-JUN-1995: 95US-0461216.  
 XX  
 XX 23-OCT-1992: 92US-0969734.  
 XX 23-SEP-1992: 92US-0950417.  
 XX  
 XX (UNIW ) UNIV WASHINGTON.  
 XX  
 XX Snow AD;  
 XX WPI: 1999-561062/47.  
 XX  
 PT Peptides of 6-8 amino acids useful for treating or preventing  
 PT amyloidosis -  
 XX  
 XX Disclosure: Column 67-68; 83pp; English.  
 PS  
 CC This sequence represents a fragment of the beta-amyloid protein. The  
 CC invention relates to a method for treating or preventing a form of  
 CC amyloidosis, including Alzheimer's disease using this sequence. The  
 CC compositions may be useful for treating or preventing the amyloidosis  
 CC associated with long-standing inflammation, various forms of malignancy  
 CC (including B-cell type malignancies), Familial Mediterranean Fever,  
 CC multiple myeloma, plasma cell dyscrasias, long-term haemodialysis, carpal  
 CC tunnel syndrome, joint swelling, multiple spontaneous fractures,  
 CC radiolucency in the wrist and hip, endocrine tumours, medullary carcinoma  
 CC of the thyroid, diabetes, Alzheimer's disease, Down's syndrome,  
 CC Creutzfeldt-Jacob disease, Gertmann Straussler Syndrome, kuru, scrapie  
 CC and other subacute spongiform encephalopathies.  
 CC  
 XX  
 SO Sequence 40 AA;  
 Query Match 100.0%; Score 209; DB 20; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-24;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DAEFRHDSGCEVHHOKIVFFAEDVGSNKGAITGLMGVV 40  
 DB 1 daefrhdsgcevhqhkvlfafedvgsnkgailglmgvv 40  
 RESULT 8  
 AA25135  
 ID AAY25135 standard; peptide; 40 AA.  
 AC AAY25135;  
 XX  
 XX 26-AUG-1999 (first entry)  
 DE Human amyloid beta-A4 peptide 2.  
 XX  
 XX Amyloid protein; beta-A4 peptide; aggregation; screening; inhibition;  
 KW therapeutic drug; brain; Alzheimer's disease.  
 KW  
 XX Homo sapiens.  
 OS  
 XX US5919631-A.  
 XX  
 XX 06-JUL-1999.  
 PD  
 XX 17-JUL-1996: 96US-0682245.  
 XX 17-JUL-1996: 96US-0682245.  
 XX  
 XX (HMRI ) HOECHST MARION ROUSSEL, INC.  
 PA  
 XX Goyal S, Paul JW, Riedel NG, Sahasrabudhe SR;  
 PI  
 XX WPI: 1999-403957/34.  
 XX

PT Determination of degree of aggregation of a peptide, useful for  
XX identifying therapeutic drugs for treating Alzheimer's disease  
XX  
PS Disclosure; Column 5-6; 8pp; English.  
XX  
CC This invention describes a novel method for the determination of the  
CC degree of aggregation of an amyloid beta A4 peptide (I) in solution.  
CC Determination comprises: (a) incubating a sample of unaggregated  
CC (I) with Coomassie Brilliant Blue G 250 dye (II) which only binds to  
CC unaggregated (I); (b) measuring the amount of (II) bound to (I) to  
CC obtain a value (I); (c) repeating steps (a) and (b) with a second  
CC sample at a different time to obtain a second value (II); and (d)  
CC determining the difference between (I) and (II) which is inversely  
CC related to the degree of aggregation of (I). This method may be  
CC applied to a screen for compounds that inhibit aggregation of (I).  
CC These inhibitors may be used as therapeutic drugs to inhibit the  
CC formation of these aggregates in the brains of patients suffering  
CC from Alzheimer's disease.  
XX  
SQ Sequence 40 AA;  
  
Query Match 100.0%; Score 209; DB 20; Length 40;  
Best Local Similarity 100.0%; Pred. No. 3.5e-24;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 DAEFRHDSGEYVHHOKLVEFADVGSNKGAIIGLMVGAV 40  
DB 1 daefrhdsgyevhbkltvfaedvgnskgaillgmvgav 40  
  
RESULT 9  
ID AAY14099 standard; peptide; 40 AA.  
XX AAY14099;  
XX  
DT 21-JUL-1999 (first entry)  
XX  
DE Human beta-amyloid protein fragment.  
XX  
KW Beta-amyloid; human; amyloid plaque deposition; Alzheimer's disease;  
KM induction; AD; sleep; circadian activity; circadian rhythm disturbance.  
XX  
OS Homo sapiens.  
XX  
PN W09921978-A1.  
XX  
PD 06-MAY-1999.  
XX  
PF 27-OCT-1998; 98MO-US22731.  
XX  
PR 28-OCT-1997; 97US-0959148.  
XX  
PA (MIRI-) MIRIAM HOSPITAL LIFESPAN PARTNER.  
XX  
PI Majocha R, Newton JL, Tate BA;  
XX  
DR WPI; 1999-326700/27.  
XX  
PT Inducing amyloid plaque deposition in a mammal, used to screen for  
XX agents against Alzheimer's disease  
XX  
PS Claim 2; Page 30; 43pp; English.  
XX  
CC This sequence represents a fragment of the human beta-amyloid protein,  
CC and can be used in the method of the invention. The method is for  
CC inducing amyloid plaque deposition in a mammal by infusing into the brain  
CC an amyloid peptide (I) at a basic pH. Animals in which amyloid plaque  
CC deposition has been induced are models of human Alzheimer's disease (AD)  
CC and are used to screen for agents (A) that inhibit: (a) deposition of  
CC amyloid plaque; and (b) AD-associated disruptions to sleep and circadian  
CC activity. They may also be used to study the etiology of AD. Compared

CC with known methods for inducing plaque deposition, this process causes  
CC less mechanical damage; the vehicle used is less neurotoxic and at basic  
CC pH (I) is soluble enough for delivery by continuous infusion with  
CC effective delivery to brain tissue. The control peptide causes few, if  
CC any, plaques and does not stimulate an immune response. Most (I)-treated  
CC animals develop AD-type pathology (contrast transgenic models of the  
CC disease), including sleep and circadian rhythm disturbances.  
XX  
SQ Sequence 40 AA;  
  
Query Match 100.0%; Score 209; DB 20; Length 40;  
Best Local Similarity 100.0%; Pred. No. 3.5e-24;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 DAEFRHDSGEYVHHOKLVEFADVGSNKGAIIGLMVGAV 40  
DB 1 daefrhdsgyevhbkltvfaedvgnskgaillgmvgav 40  
  
RESULT 10  
ID AAM99584 standard; peptide; 40 AA.  
XX AAM99584;  
XX  
DT 22-JUN-1999 (first entry)  
XX  
DE Wild type aggregating amyloid-beta peptide.  
XX  
KW Aggregation; amyloid-beta peptide; fluorescent group; detection;  
KM diagnosis; Alzheimer's disease.  
XX  
OS Synthetic.  
XX  
PN W09908695-A1.  
XX  
PD 25-FEB-1999.  
XX  
PF 13-AUG-1998; 98MO-US16809.  
XX  
PR 14-AUG-1997; 97US-0055660.  
XX  
PA (REGC ) UNITV CALIFORNIA.  
XX  
PI Garzon-Rodriguez W, Glabe C;  
XX  
DR WPI; 1999-190112/16.  
XX  
PT New fluorescent labeled amyloid A-beta peptides  
XX  
PS Example 1; Page 21; 50pp; English.  
XX  
CC This sequence corresponds to an aggregating amyloid-beta peptide which  
CC can be covalently labelled with a fluorescent group. The detection or  
CC monitoring of an amyloid aggregate in a sample can be used to diagnose  
CC or detect a predisposition to Alzheimer's disease. The screening assays  
CC can be used to identify compounds for the treatment or amelioration of  
CC Alzheimer's disease or its symptoms. The fluorescent derivatives of the  
CC amyloid-beta peptide are also useful for exploring other aspects of the  
CC amyloid structure.  
XX  
SQ Sequence 40 AA;  
  
Query Match 100.0%; Score 209; DB 20; Length 40;  
Best Local Similarity 100.0%; Pred. No. 3.5e-24;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 DAEFRHDSGEYVHHOKLVEFADVGSNKGAIIGLMVGAV 40  
DB 1 daefrhdsgyevhbkltvfaedvgnskgaillgmvgav 40

```

RESULT 11
ID AAW92723 standard; peptide; 40 AA.
XX
XX AAW92723;
AC
XX
XX 30-APR-1999 (first entry)
DT
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #69.
XX
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
OS Homo sapiens.
XX
XX US5876948-A.
PN
XX
XX 02-MAR-1999.
PD
XX
XX 27-JUL-1991; 91US-0737371.
PF
XX
XX 29-JUL-1991; 91US-0737371.
PR
XX 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX Yankner BA;
PI
XX
XX WPI: 1999-189630/16.
DR
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX Claim 1b; Column 41-42; 28pp; English.
XX
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
XX
XX Sequence 40 AA;
SQ

```

```

Query Match 100.0%; Score 209; DB 20; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.5e-24;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 DAEFRHDSGYEVHOKLVFEADVGSNKGAIIGLMVGVV 40
    |||||||||||||||||||||||||||||||||||
DB 1 daefrhdsgyevhoklvfeadvgsnkgaiiglmvgvv 40

```

```

RESULT 12
ID AAW81473 standard; peptide; 40 AA.
XX
XX AAW81473;
AC
XX
XX 28-JAN-1999 (first entry)
DT
XX
XX Synthetic amyloid beta (Abeta) peptide 8 (residues 1-40).
DE
XX
XX Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
KW research; neurotoxicity; free-radical; glutamine synthetase.
XX
XX

```

```

OS Synthetic.
XX
XX US5840838-A.
PN
XX
XX 24-NOV-1998.
PD
XX
XX 29-FEB-1996; 96US-0609090.
PF
XX
XX 29-FEB-1996; 96US-0609090.
PR
XX
XX (KENT ) UNIV KENTUCKY RES FOUND.
XX
XX Aksekov M, Butterfield DA, Carney JM, Hensley K;
PI WPI: 1999-034120/03.
XX
XX Process for treating synthetic amyloid beta peptides - by organic
PT solvent treatment, useful for studying neurotoxicity
XX
XX Claim 5; Columns 11-12; 14pp; English.
XX
XX Sequences AAW81466 to AAW81476 represent synthetic amyloid beta (Abeta)
CC peptides. The invention provides a process for treating a synthetic
CC Abeta peptide that comprises dissolving the peptide in a deoxygenated
CC solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl
CC sulfoxide, morpholinopropanesulphonic acid, dimethylformamide and
CC acetonitrile to a concentration of 0.01-10 mg/ml, incubating the
CC solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by
CC "evaporative deposition" in 5-10 minutes. Synthetic amyloid beta
CC peptides are useful as research tools for studying neurotoxicity
CC resulting from Abeta peptide -enhanced free-radical production. The
CC treatment increases the activity of the synthetic Abeta peptides in tests
CC to determine free-radical generating capacity and glutamine synthetase
CC inactivation.
XX
XX Sequence 40 AA;
SQ

```

```

Query Match 100.0%; Score 209; DB 20; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.5e-24;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 DAEFRHDSGYEVHOKLVFEADVGSNKGAIIGLMVGVV 40
    |||||||||||||||||||||||||||||||||||
DB 1 daefrhdsgyevhoklvfeadvgsnkgaiiglmvgvv 40

```

```

RESULT 13
ID AAE05483 standard; peptide; 40 AA.
XX
XX AAE05483;
AC
XX
XX 24-SEP-2001 (first entry)
DT
XX
XX Human peptide antigen comprising beta amyloid (Abeta) 40.
XX

```

```

KW Human; heat shock protein; hsp. A beta 40; beta amyloid; hypotensive;
KW neurodegenerative disorder; vaccine; Alzheimer's disease; hypertension;
KW age-related cognitive function loss; senile dementia; Wilson's disease;
KW Parkinson's disease; amyotrophic lateral sclerosis; cerebroprotective;
KW cerebral palsy; progressive supranuclear palsy; Guam disease; ataxia;
KW Lewy body dementia; prion disease; spongiform encephalopathy; glaucoma;
KW Creutzfeldt-Jakob disease polyglutamine disease; Huntington's disease;
KW myotonic dystrophy; neuropsychiatric disorder; seizure disorder; stroke;
KW Gilles de la Tourette's syndrome; nocturnal; chronic seizure disorder;
KW brain trauma; spinal cord trauma; acquired immunodeficiency syndrome;
KW AIDS; dementia; alcoholism; autism; retinal ischaemia; ophthalmological;
KW autonomic function disorder; Friedrich's ataxia; schizophrenia; therapy;
KW vasotrophic; neuroprotective; anti-HIV; human immunodeficiency virus;
KW anticonvulsant; epilepsy; neuroleptic; immunostimulant.
XX
XX Homo sapiens.
OS

```



PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;  
 XX WPI; 2001-112059/12.

XX  
 PT Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure; Page 506; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutically active amino acid region (III) and a  
 CC reactive group (II) (e.g. succinimide and maleimide groups) attached to  
 CC a less therapeutically active amino acid region (IV), which covalently  
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity  
 CC in vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention.

XX Sequence 40 AA;

Query Match 100.0%; Score 209; DB 22; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-24;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHQQLVFAEDVGSNKGAIIGLMVGAVV 40  
 ||||||||||||||||||||||||||||||||||||  
 Db 1 daefrhdsgyevhqqklvfaedvgsnkgaliglmvgavv 40

Search completed: April 24, 2002, 09:17:36  
 Job time: 140 sec





RESULT 2  
US-08-235-400-2  
Sequence 2, Application US/08235400  
Patent No. 5352426  
GENERAL INFORMATION:  
APPLICANT: Lunn, William H.  
APPLICANT: Monn, James A.  
APPLICANT: Zimmerman, Dennis M.  
TITLE OF INVENTION: METHODS FOR TREATING A PHYSIOLOGICAL  
TITLE OF INVENTION: DISORDER ASSOCIATED WITH BETA AMYLOID PEPTIDE  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Eli Lilly and Company  
STREET: Lilly Corporate Center/1104  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: United States of America  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/235,400  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaylo, Paul J.  
REGISTRATION NUMBER: 36,808  
REFERENCE/DOCKET NUMBER: X-9507  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 276-0756  
TELEFAX: (317) 276-3861  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-235-400-2

Query Match 100.0%; Score 209; DB 1; Length 40;  
Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40  
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 3  
US-08-476-464A-2  
Sequence 2, Application US/08476464A  
Patent No. 5707821  
GENERAL INFORMATION:  
APPLICANT: RYDEL, RUSSELL E.  
APPLICANT: DAPPEN, MICHAEL S.  
TITLE OF INVENTION: THERAPEUTIC INHIBITION OF PHOSPHOLIPASE  
TITLE OF INVENTION: A2 IN A-BETA PEPTIDE-MEDIATED NEURODEGENERATIVE DISEASE  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND & TOWNSEND & CREM LLP  
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: U.S.A.  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,464A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: STORELLA, JOHN R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 15270-002300  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)326-2400  
TELEFAX: (415)576-0300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: linear  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-476-464A-2

Query Match 100.0%; Score 209; DB 1; Length 40;  
Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40  
Db 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

RESULT 4  
US-08-304-585-1  
Sequence 1, Application US/08304585  
Patent No. 5721106  
GENERAL INFORMATION:  
APPLICANT: Magglo, John E.  
APPLICANT: Mantlyh, Patrick W.  
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND  
TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mueling, Raasch, Gebhardt & Schwappach, P.A.  
STREET: P.O. Box 581415  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55458-1415  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/304,585  
FILING DATE: 12-SEP-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mueling, Ann M.  
REGISTRATION NUMBER: 33,977  
REFERENCE/DOCKET NUMBER: 110,00010120  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-305-1217  
TELEFAX: 612-305-1228  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide

US-08-304-585-1

Query Match 100.0%; Score 209; DB 1; Length 40;  
Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVV 40  
DB 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVV 40

## RESULT 5

US-08-302-808-3  
; Sequence 3, Application US/08302808  
; Patent No. 5750349  
; GENERAL INFORMATION:  
; APPLICANT: SUZUKI, No. 5750349uhltro  
; APPLICANT: ODAKA, Asano  
; APPLICANT: KITADA, Chieko  
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR  
; DERIVATIVES AND USE THEREOF  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02019  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/302, 808  
; FILING DATE: 15-SEP-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP94/00089  
; FILING DATE: 24-JAN-1994  
; APPLICATION NUMBER: 010132/1993  
; FILING DATE: 25-JAN-1993  
; APPLICATION NUMBER: 019035/1993  
; FILING DATE: 05-FEB-1993  
; APPLICATION NUMBER: 286885/1993  
; FILING DATE: 16-NOV-1993  
; APPLICATION NUMBER: 334773/1993  
; FILING DATE: 28-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DAVID, RESNICK S  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 44631  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELEX: 200291 STRE  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; US-08-302-808-3

Query Match 100.0%; Score 209; DB 1; Length 40;

Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVV 40  
DB 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVV 40

## RESULT 6

US-08-433-734-1  
; Sequence 1, Application US/08433734  
; Patent No. 5837473  
; GENERAL INFORMATION:  
; APPLICANT: Maggio, John E.  
; APPLICANT: Mantyh, Patrick W.  
; TITLE OF INVENTION: Labelled -Amyloid Peptide and Methods  
; TITLE OF INVENTION: for Use in Detecting Alzheimer's Disease  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Mueling, Raasch, Gebhardt & Schwappach, P.A.  
; STREET: P.O. Box 581415  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55458-1415  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/433,734  
; FILING DATE: 03-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mueling, Ann M.  
; REGISTRATION NUMBER: 33,977  
; REFERENCE/DOCKET NUMBER: 110,00010102  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-305-1220  
; TELEFAX: 612-305-1228  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-433-734-1

Query Match 100.0%; Score 209; DB 2; Length 40;  
Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVV 40  
DB 1 DAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGVV 40

## RESULT 7

US-08-609-090-8  
; Sequence 8, Application US/08609090  
; Patent No. 5840838  
; GENERAL INFORMATION:  
; APPLICANT: HENSLEY, Kenneth  
; APPLICANT: BUTTERFIELD, D. A.  
; APPLICANT: CARNEY, John M.  
; APPLICANT: AKSENOV, Michael  
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF  
; TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LOWE PRICE LEBLANC & BECKER

STREET: 99 Canal Center Plaza, Suite 300  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/609,090  
FILING DATE: 29-FEB-1996  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Kraus, Eric J.  
REGISTRATION NUMBER: 36,190  
REFERENCE/DOCKET NUMBER: 434-059  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-684-1111  
TELEFAX: 703-684-1124  
INFORMATION FOR SEQ. ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-609-090-8

Query Match 100.0%; Score 209; DB 2; Length 40;  
Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAERHDSGYEVHHQKLVFAEDVGNKGAIIIGLMVGCV 40  
DB 1 DAERHDSGYEVHHQKLVFAEDVGNKGAIIIGLMVGCV 40

RESULT 8  
US-07-737-371E-69  
Sequence 69, Application US/07737371E  
Patent No. 5876948  
GENERAL INFORMATION:  
APPLICANT: Yankner, Bruce A.  
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY  
NUMBER OF SEQUENCES: 77  
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/737,371E  
FILING DATE: 29-JUL-1991  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/559,172  
FILING DATE: 27-JUL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 00108/028002  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ. ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-737-371E-69

Query Match 100.0%; Score 209; DB 2; Length 40;  
Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAERHDSGYEVHHQKLVFAEDVGNKGAIIIGLMVGCV 40  
DB 1 DAERHDSGYEVHHQKLVFAEDVGNKGAIIIGLMVGCV 40

RESULT 9  
US-08-682-245A-2  
Sequence 2, Application US/08682245A  
Patent No. 5919631  
GENERAL INFORMATION:  
APPLICANT: GOYAL, SHEFALI  
APPLICANT: PAUL, JOSEPH W  
APPLICANT: RIEDEL, NORBERT G  
APPLICANT: SAHASRABUDHE, SUDHIR  
TITLE OF INVENTION: A METHOD OF DETERMINING THE DEGREE OF  
TITLE OF INVENTION: AGGREGATION OF THE B44 PEPTIDE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOECHST MARION ROUSSEL, INC.  
STREET: 2110 E. GALBRAITH RD., P.O. BOX 156300  
CITY: CINCINNATI  
STATE: OHIO  
COUNTRY: U.S.A.  
ZIP: 45215-6300  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/682,245A  
FILING DATE: 17-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/039,414  
FILING DATE: 16-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: LENTZ, NELSEN L.  
REGISTRATION NUMBER: 38,537  
REFERENCE/DOCKET NUMBER: HR-1257A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 513-948-7369  
TELEFAX: 513-948-7961 OR 4681  
TELEX: 214320  
INFORMATION FOR SEQ. ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: linear  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-682-245A-2

Query Match 100.0%; Score 209; DB 2; Length 40;  
Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40  
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 10  
US-08-986-948-3  
; Sequence 3, Application US/08986948  
; Patent No. 5955317  
; GENERAL INFORMATION:  
; APPLICANT: SUZUKI, No. 5955317uh1ro  
; APPLICANT: ODAKA, Asano  
; APPLICANT: KITADA, Chieko  
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR  
; DERIVATIVES AND USE THEREOF  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02019  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: IBM Compatible  
; SOFTWARE: FASTSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/986,948  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/302,808  
; FILING DATE: 15-SEP-1994  
; APPLICATION NUMBER: PCT/JP94/00089  
; FILING DATE: 24-JAN-1994  
; APPLICATION NUMBER: 010132/1993  
; FILING DATE: 25-JAN-1993  
; APPLICATION NUMBER: 019035/1993  
; FILING DATE: 05-FEB-1993  
; APPLICATION NUMBER: 286985/1993  
; FILING DATE: 16-NOV-1993  
; APPLICATION NUMBER: 334773/1993  
; FILING DATE: 28-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DAVID, RESNICK S  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 44631  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELEX: 200291 STRE  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; US-08-986-948-3

Query Match 100.0%; Score 209; DB 2; Length 40;  
Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 11  
US-08-461-216-1  
; Sequence 1, Application US/08461216  
; Patent No. 5958883  
; GENERAL INFORMATION:  
; APPLICANT: Snow, A.D.  
; TITLE OF INVENTION: ANIMAL MODELS OF HUMAN AMYLOIDOSES  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness  
; STREET: 1420 Fifth Avenue, Suite 2800  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101-2347  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette-5.25 inch, 1.2mb storage  
; COMPUTER: IBM PC/386 Compatible  
; OPERATING SYSTEM: MS-DOS 4.01  
; SOFTWARE: Word for Windows-t  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461,216  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/969,734  
; FILING DATE: October 23, 1992  
; APPLICATION NUMBER: 07/950,417  
; FILING DATE: September 23, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Broderick, Thomas F.  
; REGISTRATION NUMBER: 31,332  
; REFERENCE/DOCKET NUMBER: UOPW-1-6707  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 1-206-682-8100; 1-206-224-0709 (direct)  
; TELEFAX: 1-206-224-0779  
; TELEX: 4938023  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; DESCRIPTION: [SYMBOL 98 \f "Symbol"]/M4(1-40);  
; DESCRIPTION: FIGURES 23-29  
; US-08-461-216-1

Query Match 100.0%; Score 209; DB 2; Length 40;  
Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40  
DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVV 40

RESULT 12  
US-08-959-148-1  
; Sequence 1, Application US/08959148  
; Patent No. 6172277  
; GENERAL INFORMATION:  
; APPLICANT: Tate, Barbara A.  
; APPLICANT: Majocha, Ronald  
; APPLICANT: Newton, Julie L.  
; TITLE OF INVENTION: NON-TRANSGENIC ANIMAL MODEL OF ALZHEIMER'S DISEASE  
; FILE REFERENCE: 04930/022001  
; CURRENT APPLICATION NUMBER: US/08/959,148

;; CURRENT FILING DATE: 1997-10-28  
;; NUMBER OF SEQ ID NOS: 2  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 1  
;; LENGTH: 40  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-08-959-148-1

Query Match 100.0%; Score 209; DB 4; Length 40;  
Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVSNKGAIIGLMVGVV 40  
DB 1 DAEFRHDSGYEVHHQKLVFAEDVSNKGAIIGLMVGVV 40

RESULT 13  
PCT-US92-06700-1  
Sequence 1, Application PC/TUS9206700  
GENERAL INFORMATION:  
APPLICANT: Mantyh, Patrick W.  
APPLICANT: Magglo, John E.  
TITLE OF INVENTION: Labelled -Amyloid Peptide  
TITLE OF INVENTION: and Alzheimer's Disease Detection  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant & Gould  
STREET: 3100 Northwest Center  
CITY: Minneapolis  
STATE: Minnesota  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch, 720 KB  
COMPUTER: Northgate 386  
OPERATING SYSTEM: DOS 4.0  
SOFTWARE: Wordperfect 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/06700  
FILING DATE: 19920810  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kowalchuk, Alan W.  
REGISTRATION NUMBER: 31,535  
REFERENCE/DOCKET NUMBER: 600.226-WO-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (612) 332-5300  
TELEFAX: (612) 332-9081  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acid residues  
TYPE: AMINO ACID  
TOPOLOGY: Linear  
MOLECULE TYPE: Peptide  
FRAGMENT TYPE: Internal Fragment  
ORIGINAL SOURCE: Synthetically Derived  
FEATURE:  
NAME/KEY: Internal fragment of the  
NAME/KEY: amyloid peptide precursor  
LOCATION: Represents isolated internal  
LOCATION: sequence of 40 amino acid residues from  
LOCATION: the amyloid peptide precursor  
PCT-US92-06700-1

Query Match 100.0%; Score 209; DB 5; Length 40;  
Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 DAEFRHDSGYEVHHQKLVFAEDVSNKGAIIGLMVGVV 40

DB 1 DAEFRHDSGYEVHHQKLVFAEDVSNKGAIIGLMVGVV 40

RESULT 14  
US-08-302-808-4  
Sequence 4, Application US/08302808  
Patent No. 5750349  
GENERAL INFORMATION:  
APPLICANT: SUZUKI, No. 5750349uhiro  
APPLICANT: ODAKA, Asano  
APPLICANT: KITADA, Chieko  
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR  
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02019  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/302,808  
FILING DATE: 15-SEP-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP94/00089  
FILING DATE: 24-JAN-1994  
APPLICATION NUMBER: 010132/1993  
FILING DATE: 25-JAN-1993  
APPLICATION NUMBER: 019035/1993  
FILING DATE: 05-FEB-1993  
APPLICATION NUMBER: 286985/1993  
FILING DATE: 16-NOV-1993  
APPLICATION NUMBER: 334773/1993  
FILING DATE: 28-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: DAVID, RESNICK S  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 44631  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
TELEX: 200291 SPRE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 41 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
US-08-302-808-4

Query Match 100.0%; Score 209; DB 1; Length 41;  
Best Local Similarity 100.0%; Pred. No. 2.4e-25;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVSNKGAIIGLMVGVV 40  
DB 1 DAEFRHDSGYEVHHQKLVFAEDVSNKGAIIGLMVGVV 40

## RESULT 15

US-08-682-245A-3

; Sequence 3, Application US/08682245A

; Patent No. 5919631

; GENERAL INFORMATION:

; APPLICANT: GOYAL, SHEFALI

; APPLICANT: PAUL, JOSEPH W

; APPLICANT: RIEDEL, NORBERT G

; APPLICANT: SAHASRABUDHE, SUDHIR

; TITLE OF INVENTION: A METHOD OF DETERMINING THE DEGREE OF

; TITLE OF INVENTION: AGGREGATION OF THE B44 PEPTIDE

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HOECHST MARION ROUSSEL, INC.

; STREET: 2110 E. GALBRAITH RD., P.O. BOX 156300

; CITY: CINCINNATI

; STATE: OHIO

; COUNTRY: U.S.A.

; ZIP: 45215-6300

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/682,245A

; FILING DATE: 17-JUL-1996

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 60/039,414

; FILING DATE: 16-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: LENTZ, NELSEN L

; REGISTRATION NUMBER: 38,537

; REFERENCE/DOCKET NUMBER: HR-1257A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 513-948-7369

; TELEFAX: 513-948-7961 OR 4681

; TELEX: 214320

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 41 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-682-245A-3

Query Match 100.0%; Score 209; DB 2; Length 41;

Best Local Similarity 100.0%; Pred No. 2.4e-25;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIIGLMVGCV 40  
|||||  
Db 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIIGLMVGCV 40

Search completed: April 24, 2002, 09:18:15  
Job time: 174 sec

**THIS PAGE BLANK (USPTO)**



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:15:41 ; Search time 38.71 Seconds  
(without alignments)  
78.713 Million cell updates/sec

Title: US-09-689-469-3

Perfect score: 209

Sequence: 1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGAITGLMWGVV 40

Scoring table: BLOSUM62  
Gapop 10.0 , Gapect 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 209   | 100.0       | 42     | 2  | beta-amyloid prote |
| 2          | 209   | 100.0       | 57     | 2  | Alzheimer's diseas |
| 3          | 209   | 100.0       | 57     | 2  | Alzheimer's diseas |
| 4          | 209   | 100.0       | 57     | 2  | Alzheimer's diseas |
| 5          | 209   | 100.0       | 57     | 2  | Alzheimer's diseas |
| 6          | 209   | 100.0       | 57     | 2  | Alzheimer's diseas |
| 7          | 209   | 100.0       | 57     | 2  | Alzheimer's diseas |
| 8          | 209   | 100.0       | 57     | 2  | Alzheimer's diseas |
| 9          | 209   | 100.0       | 69     | 2  | Alzheimer's diseas |
| 10         | 209   | 100.0       | 77     | 1  | Alzheimer's diseas |
| 11         | 190   | 90.9        | 69     | 2  | Alzheimer's diseas |
| 12         | 190   | 90.9        | 69     | 2  | Alzheimer's diseas |
| 13         | 190   | 90.9        | 74     | 2  | Alzheimer's diseas |
| 14         | 133   | 63.6        | 33     | 2  | Alzheimer's diseas |
| 15         | 57    | 27.3        | 32     | 2  | beta-amyloid prote |
| 16         | 56.5  | 27.0        | 37     | 2  | Alzheimer's diseas |
| 17         | 55.5  | 26.6        | 67     | 2  | Alzheimer's diseas |
| 18         | 55    | 26.3        | 48     | 2  | Alzheimer's diseas |
| 19         | 55    | 26.3        | 50     | 2  | Alzheimer's diseas |
| 20         | 55    | 26.3        | 75     | 1  | Alzheimer's diseas |
| 21         | 55    | 26.3        | 30     | 2  | Alzheimer's diseas |
| 22         | 54.5  | 26.1        | 67     | 2  | Alzheimer's diseas |
| 23         | 54.5  | 26.1        | 83     | 2  | Alzheimer's diseas |
| 24         | 54    | 25.8        | 84     | 2  | Alzheimer's diseas |
| 25         | 54    | 25.8        | 75     | 1  | Alzheimer's diseas |
| 26         | 53.5  | 25.6        | 97     | 1  | Alzheimer's diseas |
| 27         | 53.5  | 25.6        | 97     | 1  | Alzheimer's diseas |
| 28         | 53    | 25.4        | 25     | 2  | Alzheimer's diseas |
| 29         | 53    | 25.4        | 42     | 2  | Alzheimer's diseas |

|    |      |      |      |   |        |                    |
|----|------|------|------|---|--------|--------------------|
| 30 | 53   | 25.4 | 60   | 2 | T02581 | nodulin-like prote |
| 31 | 53   | 25.4 | 155  | 2 | JT0959 | polyprotein - pota |
| 32 | 52.5 | 25.1 | 678  | 2 | C86495 | hypothetical prote |
| 33 | 52.5 | 25.1 | 678  | 2 | H72128 | 3-methyl-2-oxobuta |
| 34 | 52   | 24.9 | 272  | 2 | F70979 | hypothetical prote |
| 35 | 52   | 24.9 | 417  | 2 | F70132 | conserved hypothet |
| 36 | 52   | 24.9 | 297  | 2 | T18232 | conserved hypothet |
| 37 | 51.5 | 24.6 | 297  | 2 | G69525 | formylmethanofuran |
| 38 | 51.5 | 24.6 | 314  | 2 | F86805 | cation transporter |
| 39 | 51.5 | 24.6 | 1364 | 2 | T51920 | probable xanthine  |
| 40 | 51   | 24.4 | 103  | 2 | D75449 | sugr protein - Del |
| 41 | 51   | 24.4 | 494  | 2 | C70940 | probable cobq prot |
| 42 | 50.5 | 24.2 | 519  | 2 | PC1072 | nuclear inclusion  |
| 43 | 50.5 | 24.2 | 833  | 2 | T01547 | probable phosphol  |
| 44 | 50.5 | 24.2 | 1345 | 2 | S55669 | tegument protein 7 |
| 45 | 50   | 23.9 | 285  | 1 | B64105 | naphthoate synthas |

## ALIGNMENTS

RESULT 1  
PNO512  
beta-amyloid protein - guinea pig (fragment)  
C:Species: Cavia porcellus (guinea pig)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
C:Accession: PNO512  
R:Shimohigashi, Y.; Matsunoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamaya, H.; Ohno  
Biochem. Biophys. Res. Commun. 193, 624-630, 1993  
A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra  
A:Reference number: PNO512; MUID:93290653  
A:Accession: PNO512  
A:Molecule type: protein  
A:Residues: 1-42 <SH1>  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
C:Keywords: alternative splicing; amyloid

Query Match 100.0%; Score 209; DB 2; Length 42;  
Best Local Similarity 100.0%; Pred. No. 2.3e-21;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGAITGLMWGVV 40  
DB 1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGAITGLMWGVV 40

RESULT 2  
E60045  
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)  
C:Species: Ovis sp. (sheep)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: E60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045; MUID:92017079  
A:Accession: E60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56130  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 209; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 3.2e-21;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGAITGLMWGVV 40  
DB 6 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGAITGLMWGVV 45

RESULT 3  
F60045  
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999  
C:Accession: F60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; M0ID:92017079  
A:Accession: F60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56127; NID:q1895; PIDN:CA39592.1; PID:q1896  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 209; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 3.2e-21;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGGVV 40  
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGGVV 45

RESULT 4  
G60045  
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)  
C:Species: Cavia porcellus (guinea pig)  
C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: G60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; M0ID:92017079  
A:Accession: G60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56126  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 209; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 3.2e-21;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGGVV 40  
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGGVV 45

RESULT 5  
D60045  
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: D60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; M0ID:92017079  
A:Accession: D60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56124  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 209; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 3.2e-21;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGGVV 40  
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGGVV 45

RESULT 6  
A60045  
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)  
C:Species: Canis lupus familiaris (dog)  
C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: A60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045; M0ID:92017079  
A:Accession: A60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56125  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 209; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 3.2e-21;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGGVV 40  
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGGVV 45

RESULT 7  
B60045  
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)  
C:Species: Ursus maritimus (polar bear)  
C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999  
C:Accession: B60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045; M0ID:92017079  
A:Accession: B60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56128; NID:q2165; PIDN:CA39593.1; PID:q2166  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 209; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 3.2e-21;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGGVV 40  
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGNKGAIIIGLMVGGVV 45

RESULT 8  
PQ0438  
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 30-Sep-1993 #sequence\_revision 19-Oct-1995 #text\_change 19-Oct-1995  
C:Accession: PQ0438; C60045  
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.  
Biochem. Biophys. Res. Commun. 188, 905-911, 1992  
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs  
A:Reference number: PQ0438; M0ID:93075180

A:Accession: PQ0438  
 A:Molecule type: DNA  
 A:Residues: 1-82 <DAB>  
 A:Cross-references: GB:M83556; GB:M83657  
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
 Brain Res. Mol. Brain Res. 10, 299-305, 1991  
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
 A:Reference number: A60045; MUID:92017079  
 A:Accession: C60045  
 A:Molecule type: mRNA  
 A:Residues: 12-68 <JOH>  
 A:Cross-references: EMBL:X56129  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase  
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 209; DB 2; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-21;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGATIGLVGCV 40  
 DB 17 DAEFRHDSGYEVHOKLVFPAEDVGSNKGATIGLVGCV 56

RESULT 9  
 A49795  
 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque  
 C:Species: Macaca fascicularis (crab-eating macaque)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: A49795  
 R:Podlisky, M.B.; Tolian, D.R.; Selkoe, D.J.  
 Am. J. Pathol. 138, 1423-1435, 1991  
 A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a  
 A:Reference number: A49795; MUID:91273117  
 A:Accession: A49795  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-695 <POD>  
 A:Cross-references: GB:M58727; NID:9342062; PIDN:AA36629.1; PID:9342063  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase  
 C:Keywords: alternative splicing

Query Match 100.0%; Score 209; DB 1; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 5e-20;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHOKLVFPAEDVGSNKGATIGLVGCV 40  
 DB 597 DAEFRHDSGYEVHOKLVFPAEDVGSNKGATIGLVGCV 636

RESULT 10  
 ORHND4  
 Alzheimer's disease amyloid beta protein precursor [validated] - human  
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inhibi  
 N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vasculat  
 protein precursor splice form APP(770)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Jun-1987 #sequence\_revision 28-Jul-1995 #text\_change 15-Sep-2000  
 C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39453; I59562; A44  
 4668; A28583; A29302; A60805; J00388; S06121; A60355; A59011; A38384; S29076; S38252; S3  
 R:Leinarte, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey  
 Nucleic Acids Res. 17, 517-522, 1989  
 A:Title: The PEDA(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b  
 A:Reference number: S02260; MUID:89128427  
 A:Accession: S02260  
 A:Molecule type: DNA  
 A:Residues: 1-288, 'V', 365-770 <LEM1>  
 A:Cross-references: EMBL:X13466  
 A:Note: alternative splice form APP(695)  
 R:Leinarte, H.G.

submitted to the EMBL Data Library, November 1988  
 A:Reference number: S05194  
 A:Accession: S05194  
 A:Molecule type: DNA  
 A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>  
 A:Cross-references: EMBL:X13466; NID:935598; PIDN:CAA31830.1; PID:9871360  
 A:Note: alternative splice form APP(695)  
 R:La Pauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.  
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989  
 A:Title: Characterization of the 5'-end region and the first two exons of the beta-pr  
 A:Reference number: A32277; MUID:89165870  
 A:Accession: A32277  
 A:Molecule type: DNA  
 A:Residues: 1-75 <LAF>  
 A:Cross-references: GB:M24546; GB:M24547; NID:9341202; PIDN:AAAC13654.1; PID:9516074  
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.  
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989  
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simila  
 A:Reference number: A33260; MUID:89392030  
 A:Accession: A33260  
 A:Molecule type: DNA  
 A:Residues: 656-737 <JOH>  
 A:Cross-references: GB:M29270; NID:9178863; PIDN:AA51768.1; PID:9178865  
 R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B  
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990  
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid  
 A:Reference number: A35486; MUID:90321244  
 A:Accession: A35486  
 A:Molecule type: DNA  
 A:Residues: 672-710 <PRE1>  
 A:Note: 693-Gln was found in DNA isolated from HCHWA-D patients  
 R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.  
 Gene 87, 257-263, 1990  
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.  
 A:Reference number: I39451; MUID:90236318  
 A:Accession: I39452  
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
 A:Molecule type: DNA  
 A:Residues: 1-770 <YOS1>  
 A:Cross-references: GB:M3112; NID:9178613; PIDN:AA55902.1; PID:9178616  
 A:Accession: I39451  
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
 A:Molecule type: DNA  
 A:Residues: 1-530, 'QWMPVPAFPAFAKVR' <YOS2>  
 A:Cross-references: GB:M34875; NID:9178608; PIDN:AA55901.1; PID:9178615  
 R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.  
 Gene 102, 291-292, 1991  
 A:Reference number: A59020; MUID:91340168  
 A:Contents: annotation; erratum  
 A:Note: revised physical map for reference I39451  
 R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Du  
 Science 248, 1124-1126, 1990  
 A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemo  
 A:Reference number: I39453; MUID:90260663  
 A:Accession: I39453  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 656-737 <LEV>  
 A:Cross-references: GB:M37896; NID:9178618; PIDN:AA51727.1; PID:9178620  
 A:Note: a mutation with 693-Gln is presented  
 R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.  
 Science 254, 97-99, 1991  
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe  
 A:Reference number: I59562; MUID:9202253  
 A:Accession: I59562  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 689-716, 'F', 718-737 <MUR>  
 A:Cross-references: GB:S57665; NID:9236720; PIDN:AA19991.1; PID:9236721  
 R:Kamano, K.; Orr, H.T.; Payami, H.; Wajsmann, E.M.; Alonso, M.E.; Pulst, S.M.; Anders  
 atakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Mart  
 Am. J. Hum. Genet. 51, 998-1014, 1992  
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t

A:Reference number: A44017, MUID:93035397  
 A:Accession: A44017  
 A:Molecule type: DNA  
 A:Residues: 687-692, 'G', 694-718 <KAM1>  
 A:Cross-references: GB:S45135, NID:q257377, PIDN:AAB23645.1, PID:q257378  
 A:Experimental source: Familial Alzheimer disease family SB  
 A>Note: Sequence extracted from NCBI backbone (NCBIP:115374)  
 A:Accession: B44017  
 A:Molecule type: DNA  
 A:Residues: 687-718 <KAM2>  
 A:Cross-references: GB:S45136, NID:q257379, PIDN:AAB23646.1, PID:q257380  
 A:Experimental source: Familial Alzheimer disease family LIT  
 A>Note: Sequence extracted from NCBI backbone (NCBIP:115376)  
 A:Note: This sequence has a silent mutation  
 A:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.; Nature 325, 733-736, 1987  
 A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface  
 A:Reference number: A03134, MUID:87144572  
 A:Accession: A03134  
 A:Molecule type: mRNA  
 A:Residues: 1-288, 'V', 365-770 <KAN>  
 A:Cross-references: GB:Y00264, NID:q28525, PIDN:CAA68374.1, PID:q28526  
 A:Note: Alternative splice form APP(695)  
 R:Obakts, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987  
 A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular  
 A:Reference number: A29030, MUID:87231971  
 A:Accession: A29030  
 A:Molecule type: mRNA  
 A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>  
 A:Cross-references: GB:M16765, NID:q178539, PIDN:AAAS1722.1, PID:q178540  
 A:Note: The authors translated the codon GAG for residue 647 as Asp  
 R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.  
 Science 235, 877-880, 1987  
 A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid  
 A:Reference number: A47584, MUID:87120328  
 A:Accession: A47584  
 A:Molecule type: mRNA  
 A:Residues: 674-756, 'S', 758-770 <GOL>  
 A:Cross-references: GB:M15533, NID:q178706, PIDN:AAAS5540.1, PID:q178707  
 A:Experimental source: brain  
 R:Ranzl, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke  
 Science 235, 880-884, 1987  
 A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th  
 A:Reference number: A47585, MUID:87120329  
 A:Accession: A47585  
 A:Molecule type: mRNA  
 A:Residues: 674-703 <TAN1>  
 A:Cross-references: GB:M1532, NID:q177957, PIDN:AAAS1564.1, PID:q177958  
 R:Dykes, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle  
 EMBO J. 7, 949-957, 1988  
 A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec  
 A:Reference number: S02638, MUID:88296437  
 A:Accession: S02638  
 A:Molecule type: mRNA  
 A:Residues: 672-678 <DYR>  
 A:Cross-references: EMBL:X06982, NID:q28817, PIDN:CAA30042.1, PID:q929612  
 A:Experimental source: promyelocytic leukemia cell line HL60  
 A:Note: Alternative splice form APP(751)  
 R:Ponte, P.; Gonzalez-Demilly, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da  
 Nature 331, 525-527, 1988  
 A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi  
 A:Reference number: S00925, MUID:88122659  
 A:Accession: S00925  
 A:Molecule type: mRNA  
 A:Residues: 1-344, 'I', 365-770 <PO2>

A:Cross-references: GB:X06989, EMBL:Y00297, NID:q28720, PIDN:CAA30050.1, PID:q28721  
 A:Note: Alternative splice form APP(751)  
 R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.  
 Nature 331, 530-532, 1988  
 A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibi  
 A:Reference number: A38949, MUID:88122641  
 A:Accession: A38949  
 A:Molecule type: mRNA  
 A:Residues: 287-367 <KIT>  
 A:Cross-references: GB:X06981, NID:q28816, PIDN:CAA30041.1, PID:q929611  
 A:Experimental source: glioblastoma cell line  
 A:Note: Alternative splice form APP(770)  
 R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ash  
 Brain Res. Mol. Brain Res. 4, 121-131, 1988  
 A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three  
 A:Reference number: A30320  
 A:Accession: A30320  
 A>Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 284-288, 'V', 365-770 <VIT1>  
 A:Accession: B30320  
 A>Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 122-288, 'V', 365-770 <VIT2>  
 A:Accession: C30320  
 A>Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 606-770 <VIT3>  
 R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta,  
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988  
 A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease  
 A:Reference number: A31087, MUID:88124954  
 A:Accession: A31087  
 A:Molecule type: mRNA  
 A:Residues: 507-770 <ZAI>  
 A:Cross-references: GB:M18734, NID:q178572, PIDN:AAAS1726.1, PID:q178573  
 A:Note: The authors translated the codon GAA for residue 599 as Gly, ACC for residue  
 8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue  
 R:Masters, C.L.; Multhaup, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther,

Query Match 100.0%; Score 209; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-20;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRDSCGYEHKQKLVFAEDVGSNKGATIGLWGVV 40  
 Db 672 DAEFRDSCGYEHKQKLVFAEDVGSNKGATIGLWGVV 711

RESULT 11  
 A27485  
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse  
 N:Alternate names: proteinase nexin II  
 C:Species: Mus musculus (house mouse)  
 C:Date: 31-Mar-1989 #sequence,revision 31-Mar-1989 #text\_change 13-Aug-1999  
 C:Accession: A27485, S19727; I49485  
 R:Ramada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.  
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987  
 A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein pr  
 A:Reference number: A27485, MUID:88106489  
 A:Accession: A27485  
 A:Molecule type: mRNA  
 A:Residues: 1-695 <RAM>  
 A:Cross-references: GB:M18373, NID:q191568, PIDN:AAAS37139.1, PID:q309085  
 A:Experimental source: brain  
 R:de Strooper, B.; Van Leuven, F.; Van den Berghe, H.  
 Biochem. Biophys. Acta 1129, 141-143, 1991  
 A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is clos  
 A:Reference number: S19727, MUID:92096458  
 A:Accession: S19727  
 A:Molecule type: mRNA  
 A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>

A:Cross-references: EMBL:X59379  
R:izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.  
Gene 112, 189-195, 1992  
A:Title: Positive and negative regulatory elements for the expression of the Alzheimer's  
A:Reference number: I49485; MUID:92209998  
A:Accession: I49485  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-19 <RES>  
A:Cross-references: GB:D10603; NID:q220328; PIDN:BA01456.1; PID:q220329  
C:Genetics:  
A:Map position: 16c3  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase  
C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 90.9%; Score 190; DB 2; Length 695;  
Best Local Similarity 92.5%; Pred. No. 1.8e-17;  
Matches 37; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLMGVV 40  
Db 597 DAEFGHDSGEVVRHOKLVFAEDVGSNKGAIIIGLMGVV 636

## RESULT 12

S00550  
Alzheimer's disease amyloid beta protein precursor - rat  
M:Alternate names: beta-A4 amyloid protein  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 13-Aug-1999  
C:Accession: S00550; A41245; A39820; S46251  
R:Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.  
EMBO J. 7, 1365-1370, 1988  
A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain  
A:Reference number: S00550; MUID:88312583  
A:Accession: S00550  
A:Molecule type: mRNA  
A:Residues: 1-695 <SHI>  
A:Cross-references: EMBL:X07648; NID:g55616; PIDN:CA30488.1; PID:g55617  
R:Schubert, D.; Schroeder, R.; Jacordiere, M.; Salton, T.; Cole, G.  
Science 241, 223-226, 1988  
A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core  
A:Reference number: A41245; MUID:88264430  
A:Accession: A41245  
A:Molecule type: protein  
A:Residues: 18-37, 'X', '39-40', 'X', '42-44' <SCH>  
A:Note: evidence for heparan sulfate attachment  
R:Hesse, L.; Behner, D.; Masters, C.L.; Multhaup, G.  
FEBS Lett. 349, 109-116, 1994  
A:Title: The beta-A4 amyloid precursor protein binding to copper.  
A:Reference number: S46251; MUID:94320627  
A:Contents: annotation; copper binding sites  
A:Note: rat peptides were isolated but not sequenced  
R:Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Muller, D.L.  
J. Biol. Chem. 266, 8464-8469, 1991  
A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain  
A:Reference number: A39820; MUID:91217087  
A:Accession: A39820  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 18-32 <POT>  
A:Experimental source: brain  
C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is ch  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase  
C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein  
F:625-648/Domain: transmembrane #status predicted <TMM>

Query Match 90.9%; Score 190; DB 2; Length 695;  
Best Local Similarity 92.5%; Pred. No. 1.8e-17;  
Matches 37; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLMGVV 40  
Db 597 DAEFGHDSGEVVRHOKLVFAEDVGSNKGAIIIGLMGVV 636

## RESULT 13

JH0773  
Alzheimer's disease amyloid beta protein precursor - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C>Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 13-Aug-1999  
C:Accession: JH0773  
R:Okado, H.; Okamoto, H.  
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992  
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: development  
A:Reference number: JH0773; MUID:93129227  
A:Accession: JH0773  
A:Molecule type: mRNA  
A:Residues: 1-747 <OKA>  
A:Cross-references: GB:S52417; NID:q263150; PIDN:AAB24853.1; PID:q263151  
A:Experimental source: larva  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase  
C:Keywords: alternative splicing; amyloid  
F:287-337/Domain: animal kunitz-type proteinase inhibitor homology <BPI>

Query Match 90.9%; Score 190; DB 2; Length 747;  
Best Local Similarity 87.5%; Pred. No. 1.9e-17;  
Matches 35; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLMGVV 40  
Db 649 DSEVRHDTAVEVHOKLVFAEDVGSNKGAIIIGLMGVV 688

## RESULT 14

S23094  
beta-amyloid protein precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 03-May-1996  
C:Accession: S23094  
R:Kojima, S.; Omori, M.  
FEBS Lett. 304, 57-60, 1992  
A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic protein  
A:Reference number: S23094; MUID:92316198  
A:Accession: S23094  
A:Molecule type: protein  
A:Residues: 1-33 <KOJ>  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase

Query Match 63.6%; Score 133; DB 2; Length 33;  
Best Local Similarity 89.3%; Pred. No. 2.7e-11;  
Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFAEDVGSNK 28  
Db 6 DAEFGHDSGEVVRHOKLVFAEDVGSNK 33

## RESULT 15

S11435  
genome polyprotein - potato virus Y (fragment)  
N:Contains: coat protein; NIB protein  
C:Species: potato virus Y, PVY  
C>Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Nov-2000  
C:Accession: S11435; S11549; J01526  
R:Zhou, X.R.; Fang, R.X.; Wang, C.O.; Wang, K.Q.  
Nucleic Acids Res. 18, 5554, 1990  
A:Title: CDNA sequence of the 3'-coding region of PVY genome (the Chinese isolate).  
A:Reference number: S11435; MUID:91016851  
A:Accession: S11435  
A:Molecule type: mRNA  
A:Residues: 1-327 <ZHO1>

A:Cross-references: EMBL:X54058  
 R:Zhou, X.R.  
 Submitted to the EMBL Data Library, July 1990  
 A:Reference number: S11549  
 A:Accession: S11549  
 A:Molecule type: mRNA  
 A:Residues: 1-90, 'E', 92-327 <ZH02>  
 A:Cross-references: EMBL:X54058; NID:g61219; PIDN:CAA37993.1; PID:g833159  
 R:Ohshima, K.; Hataya, T.; Sano, T.; Inoue, A.K.; Shikata, E.  
 Ann. Phytopathol. Soc. Jpn. 57, 615-622, 1991  
 A:Title: Comparison of biological properties, serological characteristics and amino acid  
 A:Reference number: JC1526  
 A:Accession: JC1526  
 A:Molecule type: genomic RNA  
 A:Residues: 61-68, 'E', 71-73, 'E', 76-111, 'S', 113-201, 'E', 203-327 <OHS>  
 C:Genetics:  
 A:Start codon: GCA  
 C:Superfamily: tobacco etch virus genome polyprotein  
 C:Keywords: coat protein; polyprotein  
 F:61-327/Product: coat protein #status predicted <COP>

Query Match 27.38; Score 57; DB 2; Length 327;  
 Best Local Similarity 53.18; Pred. No. 5;  
 Matches 17; Conservative 0; Mismatches 5; Indels 10; Gaps 3;  
 QY 1 DAEPFRHDSGYEVHHQKLVFFAED---VGSNK 28  
 ||| ||||| | | | | |  
 Db 47 DDEFEFDS-YEVHHQ-----ANDTIDAVGDNK 72

Search completed: April 24, 2002, 09:19:00  
 Job time: 199 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:16:11 ; Search time 62.94 Seconds  
(without alignments)  
92.960 Million cell updates/sec

Title: US-09-689-469-3

Perfect score: 209

Sequence: 1 DAERDSDGYEHHQKLVFFAEDVGSNKGALIGLMGVGV 40

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_17:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_fodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|-------|-------------|
| 1          | 209   | 100.0         | 82     | 4     | P78438      |
| 2          | 209   | 100.0         | 82     | 4     | Q16014      |
| 3          | 209   | 100.0         | 82     | 4     | Q16019      |
| 4          | 209   | 100.0         | 82     | 4     | Q16020      |
| 5          | 209   | 100.0         | 534    | 13    | Q93296      |
| 6          | 209   | 100.0         | 569    | 13    | Q9PVL1      |
| 7          | 209   | 100.0         | 695    | 13    | Q60496      |
| 8          | 209   | 100.0         | 695    | 13    | Q9DG78      |
| 9          | 209   | 100.0         | 751    | 13    | Q9DGJ7      |
| 10         | 209   | 100.0         | 770    | 6     | Q9TUI0      |
| 11         | 199   | 95.2          | 97     | 4     | Q13778      |
| 12         | 190   | 90.9          | 79     | 11    | Q35463      |
| 13         | 190   | 90.9          | 607    | 13    | Q99K32      |
| 14         | 190   | 90.9          | 693    | 13    | Q98SG0      |
| 15         | 190   | 90.9          | 695    | 11    | P97487      |
| 16         | 190   | 90.9          | 747    | 13    | Q91963      |
| 17         | 187   | 89.5          | 695    | 13    | Q98SF9      |
| 18         | 180   | 86.1          | 699    | 13    | O57394      |
| 19         | 176   | 84.2          | 33     | 4     | Q9UC33      |

073683 tetraodon f  
093279 figu rubrip  
Q9uca9 homo sapien  
Q919e7 brachydanio  
Q9ucd1 homo sapien  
Q97917 bos taurus  
Q9ucc8 homo sapien  
Q9rps4 enterococcu  
Q9awb6 lycopersico  
O22662 arabidopsis  
Q9qgn5 potato viru  
Q9wg05 potato viru  
O81120 lotus japon  
Q9r717 agrobacteri  
Q9r694 agrobacteri  
Q9r472 agrobacteri  
O84344 chlamydia t  
Q44388 agrobacteri  
Q9pk54 chlamydia m  
Q9xgt0 gossypium h  
P93745 arabidopsis  
P93733 arabidopsis  
Q85276 potato viru  
Q9ca59 arabidopsis  
O50548 thermotoga  
O80960 arabidopsis

20 167 79.9 780 13 073683  
21 163 78.0 737 13 093279  
22 162 77.5 30 4 Q9UCA9  
23 149.5 71.5 612 13 0919E7  
24 147 70.3 28 4 Q9UCD1  
25 113 54.1 49 6 Q97917  
26 106 50.7 19 4 Q9UCC8  
27 64 30.6 328 2 Q9RPS4  
28 57.5 27.5 895 10 Q9AWB6  
29 57 27.3 195 10 O22662  
30 57 27.3 332 12 Q9QGN5  
31 57 27.3 365 12 Q9WG05  
32 57 27.3 575 10 O81120  
33 56 26.8 755 2 Q9R717  
34 56 26.8 755 2 Q9R694  
35 56 26.8 755 2 Q9R472  
36 55.5 26.6 678 2 O84344  
37 55 26.3 755 2 Q44388  
38 54.5 26.1 678 2 Q9PK54  
39 54.5 26.1 829 10 Q9XGT0  
40 54.5 26.1 832 10 P93745  
41 54.5 26.1 968 10 P93733  
42 54 25.8 292 12 Q85276  
43 53 25.4 256 10 Q9CA59  
44 53 25.4 422 2 O50548  
45 53 25.4 601 10 O80960

#### ALIGNMENTS

RESULT 1  
P78438  
ID P78438 PRELIMINARY; PRT; 82 AA.  
AC P78438;  
DT 01-MAY-1997 (TREMBLrel. 03, Created)  
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).  
GN APP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89392030; PubMed=2675837;  
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H., Little S.P.;  
RA "Alzheimer's disease amyloid peptide is encoded by two exons and shows similarity to soybean trypsin inhibitor."  
RT Biochem. Biophys. Res. Commun. 163:1248-1255(1989).  
RL [2]  
RN [2]  
RP SEQUENCE OF 19-48 FROM N.A.  
RX MEDLINE=87120329; PubMed=2949367;  
RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P., Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;  
RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near the Alzheimer locus."  
RL Science 235:880-884(1987).  
RN [3]  
RP SEQUENCE OF 32-63 FROM N.A.  
RX MEDLINE=93035397; PubMed=1415269;  
RA Kamino K., Orr H.T., Payami H., Wijsman E.M., Alonso M.E., Pulst S.M., Anderson L., O' Dahl S., Nemens E., White J.A.;  
RT "Linkage and mutational analysis of familial Alzheimer disease kindreds for the APP gene region."  
RL Am. J. Hum. Genet. 51:998-1014(1992).  
DR EMBL; M29269; AAA51768.1; JOINED.  
DR EMBL; M29269; AAA51768.1; JOINED.  
DR EMBL; M15532; AAA51564.1; -.  
DR EMBL; S45136; AAA23646.1; -.  
DR HSSP; P05067; 1BA4.

FT NON\_TER 1  
SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match 100.0%; Score 209; DB 4; Length 82;  
Best Local Similarity 100.0%; Pred. No. 2.1e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEADVGSNGKAIIGLMVGGV 40  
Db 17 DAEFRHDSGYEVHHOKLVFFAEADVGSNGKAIIGLMVGGV 56

RESULT 2  
Q16014 PRELIMINARY; PRT; 82 AA.  
AC Q16014  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)  
DE BETA-AMYLLOID PEPTIDE PRECURSOR (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93236601; PubMed=8476439;  
RA Derman R.B., Rosenzwaig R., Miller D.L.;  
RT "A system for studying the effect(s) of familial Alzheimer disease  
mutations on the processing of the beta-amyloid peptide precursor."  
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
DR EMBL; S60721; AAB26263.2; -  
DR HSP; P05067; 1BA4.  
FT NON\_TER 1  
FT NON\_TER 82  
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 100.0%; Score 209; DB 4; Length 82;  
Best Local Similarity 100.0%; Pred. No. 2.1e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEADVGSNGKAIIGLMVGGV 40  
Db 18 DAEFRHDSGYEVHHOKLVFFAEADVGSNGKAIIGLMVGGV 57

RESULT 3  
Q16019 PRELIMINARY; PRT; 82 AA.  
AC Q16019  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)  
DE BETA-AMYLLOID PEPTIDE PRECURSOR (FRAGMENT).  
OS BETA APP.  
GN Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93236601; PubMed=8476439;  
RA Derman R.B., Rosenzwaig R., Miller D.L.;  
RT "A system for studying the effect(s) of familial Alzheimer disease  
mutations on the processing of the beta-amyloid peptide precursor."  
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
DR EMBL; S61380; AAB26264.2; -  
DR HSP; P05067; 1BA4.  
FT NON\_TER 1  
FT NON\_TER 82  
SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match 100.0%; Score 209; DB 4; Length 82;  
Best Local Similarity 100.0%; Pred. No. 2.1e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEADVGSNGKAIIGLMVGGV 40  
Db 18 DAEFRHDSGYEVHHOKLVFFAEADVGSNGKAIIGLMVGGV 57

RESULT 4  
Q16020 PRELIMINARY; PRT; 82 AA.  
AC Q16020  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)  
DE BETA-AMYLLOID PEPTIDE PRECURSOR (FRAGMENT).  
GN BETA APP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93236601; PubMed=8476439;  
RA Derman R.B., Rosenzwaig R., Miller D.L.;  
RT "A system for studying the effect(s) of familial Alzheimer disease  
mutations on the processing of the beta-amyloid peptide precursor."  
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
DR EMBL; S61383; AAB26265.2; -  
DR HSP; P05067; 1BA4.  
FT NON\_TER 1  
FT NON\_TER 82  
SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match 100.0%; Score 209; DB 4; Length 82;  
Best Local Similarity 100.0%; Pred. No. 2.1e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVFFAEADVGSNGKAIIGLMVGGV 40  
Db 18 DAEFRHDSGYEVHHOKLVFFAEADVGSNGKAIIGLMVGGV 57

RESULT 5  
Q93296 PRELIMINARY; PRT; 534 AA.  
AC Q93296  
DT 01-NOV-1998 (TRENBLrel. 08, Created)  
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)  
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
DE AMYLLOID PRECURSOR PROTEIN (FRAGMENT).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Barnes N.Y., Ling L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,  
RA Milligan C.E.;  
RT "Increased production of amyloid precursor protein provides a  
substrate for Caspase 3 in dying motoneurons."  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF042098; AAC35052.1; -  
DR HSP; P05067; 1BA4.  
DR InterPro; IPR001868; A4\_APP.  
DR PRINTS; PR00203; AMYLLOIDA4.  
DR PROSITE; PS00319; A4\_EXTRA; 1.  
DR PROSITE; PS00320; A4\_INTRA; 1.



FT NON\_TER 1 1  
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E6D4C92 CRC64;

Query Match 100.0%; Score 209; DB 13; Length 534;  
Best Local Similarity 100.0%; Pred. No. 2e-19;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNGKGAIGLMVGWV 40  
|||||  
Db 436 DAEFRHDSGYEVHHOKLVFFAEDVGSNGKGAIGLMVGWV 475

RESULT 6

ID Q9PVL1 PRELIMINARY; PRT; 569 AA.  
AC Q9PVL1  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE AMYLOID PROTEIN PRECURSOR (FRAGMENT).  
GN APP.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BRAIN;  
RA Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;  
RT "What the evolution of the amyloid protein precursor supergene family  
RL Neurochem. Int. 0:0-0(2000).  
DR EMBL; AF030341; AAF12698.1; -.  
DR HSSP; P05067; IBA4.  
DR InterPro; IPR001868; A4\_APP.  
DR Pfam; PF02177; A4\_EXTRA; 1.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR SMART; SM00006; A4\_EXTRA; 1.  
DR PROSITE; PS00319; A4\_EXTRA; 1.  
DR PROSITE; PS00320; A4\_INTRA; 1.  
FT NON\_TER 1  
SQ SEQUENCE 569 AA; 64753 MW; 0AB8BB851863A19D CRC64;

Query Match 100.0%; Score 209; DB 13; Length 569;  
Best Local Similarity 100.0%; Pred. No. 2.1e-19;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNGKGAIGLMVGWV 40  
|||||  
Db 472 DAEFRHDSGYEVHHOKLVFFAEDVGSNGKGAIGLMVGWV 511

RESULT 7

ID Q60496 PRELIMINARY; PRT; 695 AA.  
AC Q60496;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BRAIN;  
RA Beck M., Mueller D., Bigl V.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO

CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
CC GIO).

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -!- SIMILARITY: TO OTHER SPECIES APP ANALOGUES.

DR EMBL; X97631; CAA66230.1; -.  
DR HSSP; P05067; IBA4.  
DR InterPro; IPR001868; A4\_APP.  
DR Pfam; PF02177; A4\_EXTRA; 1.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR SMART; SM00006; A4\_EXTRA; 1.  
DR PROSITE; PS00319; A4\_EXTRA; 1.  
DR PROSITE; PS00320; A4\_INTRA; 1.  
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 100.0%; Score 209; DB 11; Length 695;  
Best Local Similarity 100.0%; Pred. No. 2.7e-19;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNGKGAIGLMVGWV 40  
|||||  
Db 597 DAEFRHDSGYEVHHOKLVFFAEDVGSNGKGAIGLMVGWV 636

RESULT 8

ID Q9DGJ8 PRELIMINARY; PRT; 695 AA.  
AC Q9DGJ8;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sarasa M., Rodolosse A., Sorribas V.;  
RT "Cloning of full-length chicken beta-amyloid precursor protein  
RT isoforms".  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF289218; AAG00593.1; -.  
DR InterPro; IPR001868; A4\_APP.  
DR Pfam; PF02177; A4\_EXTRA; 1.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR SMART; SM00006; A4\_EXTRA; 1.  
DR PROSITE; PS00319; A4\_EXTRA; 1.  
DR PROSITE; PS00319; A4\_EXTRA; 1.  
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 100.0%; Score 209; DB 13; Length 695;  
Best Local Similarity 100.0%; Pred. No. 2.7e-19;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNGKGAIGLMVGWV 40  
|||||  
Db 597 DAEFRHDSGYEVHHOKLVFFAEDVGSNGKGAIGLMVGWV 636

RESULT 9

ID Q9DGJ7 PRELIMINARY; PRT; 751 AA.  
AC Q9DGJ7;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE BETA-AMYLOID PRECURSOR PROTEIN 751 ISOFORM.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Gallus.

```

OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolosse A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO PANCREATIC TRYPsin INHIBITOR (KUNITZ) DOMAIN.
DR EMBL: AF289219; AAG00594.1; -
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; K0; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match 100.0%; Score 209; DB 13; Length 751;
Best Local Similarity 100.0%; Pred. No. 3e-19;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
DB 653 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 692

RESULT 10
Q9TUI0 PRELIMINARY; PRT; 770 AA.
AC Q9TUI0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE AMYLOID PRECURSOR PROTEIN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid Precursor Protein 770.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO PANCREATIC TRYPsin INHIBITOR (KUNITZ) DOMAIN.
DR EMBL: AB032550; BAA84580.1; -
DR HSP: P05067; 1AAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; K0; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 770 AA; 86961 MW; 5F7A1DCB2BCC583E CRC64;

Query Match 100.0%; Score 209; DB 6; Length 770;
Best Local Similarity 100.0%; Pred. No. 3.1e-19;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
DB 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40

```

```

DB 672 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 711
|||||
RESULT 11
Q13778 PRELIMINARY; PRT; 97 AA.
AC Q13778;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE AMYLOID PROTEIN (AD-AP) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Goldgaber D., Lerman M.I., McBride O.W., Saffioti U., Gajdusek D.C.;
RT "Characterization and chromosomal localization of a cDNA encoding
RT brain amyloid of Alzheimer's disease.";
RL Science 235:877-880(1987).
DR EMBL: M15533; AAA35540.1; -.
DR HSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR PRINTS: PR00203; AMYLOIDA4.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 97 AA; 10884 MW; E528CDB448DE474E CRC64;

Query Match 95.2%; Score 199; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 5.3e-19;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EPRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
DB 1 EPRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 38
|||||

RESULT 12
O35463 PRELIMINARY; PRT; 79 AA.
AC O35463;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE ALZHEIMER'S AMYLOID BETA PROTEIN PRECURSOR (FRAGMENT).
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RA Sambamurti K., Pinnix I., Gandhi S.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF030413; AAB86608.1; -.
DR HSP: P05067; IQCM.
DR NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF5F597 CRC64;

Query Match 90.9%; Score 190; DB 11; Length 79;
Best Local Similarity 92.5%; Pred. No. 6.5e-18;
Matches 37; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
DB 21 DAEFGHDSGFVRRHOKLVFFAEDVGSNKGAIIGLMVGVV 60
|||||

```

```
RESULT 13
Q99K32
ID Q99K32 PRELIMINARY; PRT; 607 AA.
AC Q99K32;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR IMAGE:3486773) (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HIPPOCAMPUS;
RA Flood J.F., Kumar V.B., Sasser T., Word L., Morley J.E.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U84012; AAB41502.1; -.
DR EMBL; U82624; AAB40919.1; -.
DR HSSP; P05067; IQCM.
DR MGD; MGI:88059; App.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 607 AA; 68391 MW; BF802214CBA7D172 CRC64;

Query Match 90.9%; Score 190; DB 11; Length 607;
Best Local Similarity 92.5%; Pred. No. 7.5e-17;
Matches 37; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 509 DAEFGHDSGFVRRHQKLVFFAEDVGSNKGAIIGLMVGGVV 548

RESULT 14
Q98SG0
ID Q98SG0 PRELIMINARY; PRT; 693 AA.
AC Q98SG0;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN A.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hurk W.H.;
RL Thesis (2001), Department of Biological Sciences,
RL University of Nijmegen, Nijmegen, Netherlands.
DR EMBL; AJ298150; CAC37193.1; -.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 693 AA; 78568 MW; CAF1DF655C1AB653 CRC64;

Query Match 90.9%; Score 190; DB 13; Length 693;
Best Local Similarity 87.5%; Pred. No. 8.8e-17;
Matches 35; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
1:||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 595 DSEYRHTAYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 634

RESULT 15
P97487
ID P97487 PRELIMINARY; PRT; 695 AA.
AC P97487; P97942;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
```

```
DE HIPPOCAMPAL AMYLOID PROTEIN.
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SAMP8; TISSUE=HIPPOCAMPUS;
RA Flood J.F., Kumar V.B., Sasser T., Word L., Morley J.E.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U84012; AAB41502.1; -.
DR EMBL; U82624; AAB40919.1; -.
DR HSSP; P05067; IQCM.
DR MGD; MGI:88059; App.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78414 MW; 9A5FBE2ED261236E CRC64;

Query Match 90.9%; Score 190; DB 11; Length 695;
Best Local Similarity 92.5%; Pred. No. 8.9e-17;
Matches 37; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 597 DAEFGHDSGFVRRHQKLVFFAEDVGSNKGAIIGLMVGGVV 636

Search completed: April 24, 2002, 09:20:10
Job time: 239 sec
```



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:16:26 ; Search time 21.42 Seconds  
(without alignments)  
68.468 Million cell updates/sec

Title: US-09-689-469-3

Perfect score: 209

Sequence: 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID        | Description        |
|------------|-------|-------------|--------|--------------|--------------------|
| 1          | 209   | 100.0       | 57     | 1 A4_PIG     | Q29023 sus scrofa  |
| 2          | 209   | 100.0       | 57     | 1 A4_URSWA   | Q29149 ursus marit |
| 3          | 209   | 100.0       | 58     | 1 A4_CANFA   | Q28280 canis faml  |
| 4          | 209   | 100.0       | 58     | 1 A4_RABIT   | Q28748 oryctolagus |
| 5          | 209   | 100.0       | 58     | 1 A4_SHEEP   | Q28757 ovis aries  |
| 6          | 209   | 100.0       | 59     | 1 A4_BOVIN   | Q28053 bos taurus  |
| 7          | 209   | 100.0       | 751    | 1 A4_SALSC   | Q95241 salmisi sci |
| 8          | 209   | 100.0       | 770    | 1 A4_HUMAN   | P05067 homo sapien |
| 9          | 190   | 90.9        | 770    | 1 A4_MOUSE   | P12023 mus musculu |
| 10         | 190   | 90.9        | 770    | 1 A4_RAT     | P08592 rattus norv |
| 11         | 57    | 27.3        | 327    | 1 POLG_PVYCH | P21294 potat viru  |
| 12         | 56.5  | 27.0        | 378    | 1 SLG1_YEAST | P54867 saccharomyc |
| 13         | 55    | 26.3        | 488    | 1 DHAL_PSESP | P33008 pseudomonas |
| 14         | 55    | 26.3        | 503    | 1 Y226_MYCPN | P73462 mycoplasma  |
| 15         | 55    | 26.3        | 755    | 1 TR2M_AGR74 | P04029 agrobacteri |
| 16         | 55    | 26.3        | 3063   | 1 POLG_PVYN  | P18247 p genome po |
| 17         | 54    | 25.8        | 284    | 1 POLG_PVYTO | P11897 potat viru  |
| 18         | 54    | 25.8        | 755    | 1 TR2M_AGR73 | P25017 agrobacteri |
| 19         | 53.5  | 25.6        | 708    | 1 YNZB_CAREL | P45972 caenorhabdi |
| 20         | 53.5  | 25.6        | 971    | 1 Y228_BORBU | O51246 borrelia bu |
| 21         | 51.5  | 24.6        | 297    | 1 FTR_ARCFU  | O28076 archaeoglob |
| 22         | 51    | 24.4        | 494    | 1 COBQ_MYCTU | O53677 mycobacteri |
| 23         | 50    | 23.9        | 285    | 1 MENB_HAEIN | P44960 haemophilus |
| 24         | 49    | 23.4        | 568    | 1 NTRS_PSEAE | P24474 pseudomonas |
| 25         | 49    | 23.4        | 611    | 1 YCR3_YEAST | P25313 saccharomyc |
| 26         | 49    | 23.4        | 704    | 1 SSP2_BOMMO | P20613 bombyx mori |
| 27         | 49    | 23.4        | 753    | 1 PEE2_HUMAN | O14830 homo sapien |
| 28         | 49    | 23.4        | 757    | 1 PEE2_MOUSE | O35385 mus musculu |
| 29         | 49    | 23.4        | 769    | 1 ITB2_BOVIN | P32592 bos taurus  |
| 30         | 49    | 23.4        | 1080   | 1 HDC_DROME  | O9n2m8 drosophila  |
| 31         | 49    | 23.4        | 1437   | 1 MRP5_HUMAN | O15440 homo sapien |
| 32         | 48.5  | 23.2        | 160    | 1 FMDR_ECOLI | P24093 escherichia |
| 33         | 48.5  | 23.2        | 330    | 1 COAT_PEMV  | P07993 pepper mott |

|    |      |      |      |              |                    |
|----|------|------|------|--------------|--------------------|
| 34 | 48.5 | 23.2 | 393  | 1 GUN1_USTMA | P54424 ustilago ma |
| 35 | 48.5 | 23.2 | 510  | 1 YH43_YEAST | Q03218 saccharomyc |
| 36 | 48   | 23.0 | 409  | 1 RHAG_HUMAN | Q02094 homo sapien |
| 37 | 48   | 23.0 | 703  | 1 ARVB_WANSE | P14297 manduca sex |
| 38 | 48   | 23.0 | 930  | 1 DPOL_HAEIN | P43741 haemophilus |
| 39 | 47.5 | 22.7 | 251  | 1 FGEN_HUMAN | Q9gzv9 homo sapien |
| 40 | 47.5 | 22.7 | 1052 | 1 RPOC_BACAN | P77819 bacillus an |
| 41 | 47.5 | 22.7 | 1053 | 1 RPOC_BROTH | P77839 brochothrix |
| 42 | 47   | 22.5 | 119  | 1 YVAE_BACSU | O32227 bacillus su |
| 43 | 47   | 22.5 | 247  | 1 EST_BACST  | O06174 bacillus st |
| 44 | 47   | 22.5 | 478  | 1 G6PD_BORBU | O51581 borrelia bu |
| 45 | 47   | 22.5 | 560  | 1 NIRS_PSEST | P24040 pseudomonas |

ALIGNMENTS

| RESULT | 1  |                                   |
|--------|--|-----------------------------------|
| ID     | A4_PIG   | STANDARD; PRT; 57 AA.             |
| AC     | Q29023;  |                                   |
| DT     | 01-NOV-1997 (Rel. 35, Created)   |                                   |
| DT     | 01-NOV-1997 (Rel. 35, Last sequence update)                                |                                   |
| DT     | 20-AUG-2001 (Rel. 40, Last annotation update)                              |                                   |
| DE     | ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID     |                                   |
| DE     | PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).                                   |                                   |
| GN     | APP.   |                                   |
| OS     | Sus scrofa (Pig).  |                                   |
| OC     | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;          |                                   |
| OC     | Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.                   |                                   |
| OX     | NCBI_TaxID=9823;   |                                   |
| RN     | [1]  |                                   |
| RP     | SEQUENCE FROM N.A.   |                                   |
| RC     | TISSUE=Brain;  |                                   |
| RX     | MEDLINE=92017079; PubMed=1656157;  |                                   |
| RA     | Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;         |                                   |
| RT     | "Conservation of the sequence of the Alzheimer's disease amyloid           |                                   |
| RT     | peptide in dog, polar bear and five other mammals by cross-species         |                                   |
| RT     | polymerase chain reaction analysis."                                       |                                   |
| RL     | Brain Res. Mol. Brain Res. 10:299-305(1991).                               |                                   |
| CC     | FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO                    |                                   |
| CC     | INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN            |                                   |
| CC     | G(O) (BY SIMILARITY).  |                                   |
| CC     | FUNCTION: BELONGS TO THE APP FAMILY.                                       |                                   |
| CC     | THIS SWISS-PROT entry is copyright. It is produced through a collaboration |                                   |
| CC     | between the Swiss Institute of Bioinformatics and the EMBL outstation -    |                                   |
| CC     | the European Bioinformatics Institute. There are no restrictions on its    |                                   |
| CC     | use by non-profit institutions as long as its content is in no way         |                                   |
| CC     | modified and this statement is not removed. Usage by and for commercial    |                                   |
| CC     | entities requires a license agreement (See http://www.isb-sib.ch/announce/ |                                   |
| CC     | or send an email to license@isb-sib.ch).                                   |                                   |
| CC     | EMBL; X56127; CAA39592.1; -  |                                   |
| DR     | HSSP; P05067; 1AML.  |                                   |
| DR     | InterPro; IPR001868; A4_APP.   |                                   |
| DR     | PROSITE; PS00319; A4_EXTRA; PARTIAL.                                       |                                   |
| DR     | PROSITE; PS00320; A4_INTRA; PARTIAL.                                       |                                   |
| DR     | Glycoprotein; Amyloid; Neurope; Transmembrane.                             |                                   |
| FT     | NON_TER 1  |                                   |
| FT     | CHAIN 6 48   | BETA-AMYLOID PROTEIN (POTENTIAL). |
| FT     | DOMAIN <1 33   | EXTRACELLULAR (POTENTIAL).        |
| FT     | TRANSMEM 34 57   | POTENTIAL.                        |
| FT     | NON_TER 57 57  |                                   |
| SQ     | SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;                           |                                   |

Query Match 100.0%; Score 209; DB 1; Length 57;  
Best Local Similarity 100.0%; Pred No. 2.1e-21;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40

Db 6 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVV 45  
|||||

## RESULT 2

A4\_URSMA ID A4\_URSMA STANDARD; PRT; 57 AA.  
AC Q29149;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID  
DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).  
GN APP.  
OS Ursus maritimus (Polar bear) (Thalarchos maritimus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.  
OX NCBI\_TaxID=29073;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=92017079; PubMed=1656157;  
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
RT "Conservation of the sequence of the Alzheimer's disease amyloid  
RT peptide in dog, polar bear and five other mammals by cross-species  
RT polymerase chain reaction analysis.";  
RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
CC G(O) (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL; X56128; CAA39593.1; -  
DR HSSP; P05067; IAML.  
DR InterPro; IPR001868; A4\_APP.  
DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
DR PROSITE; PS00320; A4\_INTRA; PARTIAL.  
KW Glycoprotein; Amyloid; Neuron; Transmembrane.  
FT NON\_TER 1  
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).  
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 34 57 POTENTIAL.  
FT NON\_TER 57  
FT SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;  
-----

Query Match 100.0%; Score 209; DB 1; Length 57;  
Best Local Similarity 100.0%; Pred. No. 2.1e-21;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
-----

QY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVV 40

Db 6 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVV 45  
|||||

## RESULT 3

A4\_CANFA ID A4\_CANFA STANDARD; PRT; 58 AA.  
AC Q28280;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID  
DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).  
GN APP.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=92017079; PubMed=1656157;  
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
RT "Conservation of the sequence of the Alzheimer's disease amyloid  
RT peptide in dog, polar bear and five other mammals by cross-species  
RT polymerase chain reaction analysis.";  
RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
CC G(O) (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL; X56128; CAA39593.1; -  
DR HSSP; P05067; IAML.  
DR InterPro; IPR001868; A4\_APP.  
DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
DR PROSITE; PS00320; A4\_INTRA; PARTIAL.  
KW Glycoprotein; Amyloid; Neuron; Transmembrane.  
FT NON\_TER 1  
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL).  
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 34 57 POTENTIAL.  
FT NON\_TER 57  
FT SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;  
-----

GN APP.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=92017079; PubMed=1656157;  
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
RT "Conservation of the sequence of the Alzheimer's disease amyloid  
RT peptide in dog, polar bear and five other mammals by cross-species  
RT polymerase chain reaction analysis.";  
RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
CC G(O) (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.  
CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL; X56125; CAA39590.1; -  
DR HSSP; P05067; IAML.  
DR InterPro; IPR001868; A4\_APP.  
DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
DR PROSITE; PS00320; A4\_INTRA; PARTIAL.  
KW Glycoprotein; Amyloid; Neuron; Transmembrane.  
FT NON\_TER 1  
FT CHAIN 1 49 BETA-AMYLOID PROTEIN (POTENTIAL).  
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 35 58 POTENTIAL.  
FT NON\_TER 58  
FT SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;  
-----

Query Match 100.0%; Score 209; DB 1; Length 58;  
Best Local Similarity 100.0%; Pred. No. 2.1e-21;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
-----

QY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVV 40

Db 7 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVV 46  
|||||

## RESULT 4

A4\_RABIT ID A4\_RABIT STANDARD; PRT; 58 AA.  
AC Q28748;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID  
DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).  
GN APP.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=92017079; PubMed=1656157;  
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
RT "Conservation of the sequence of the Alzheimer's disease amyloid  
RT peptide in dog, polar bear and five other mammals by cross-species  
RT polymerase chain reaction analysis.";  
RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
CC G(O) (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.  
CC -----

DR EMBL; X56125; CAA39590.1; -  
DR HSSP; P05067; IAML.  
DR InterPro; IPR001868; A4\_APP.  
DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
DR PROSITE; PS00320; A4\_INTRA; PARTIAL.  
KW Glycoprotein; Amyloid; Neuron; Transmembrane.  
FT NON\_TER 1  
FT CHAIN 1 49 BETA-AMYLOID PROTEIN (POTENTIAL).  
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 35 58 POTENTIAL.  
FT NON\_TER 58  
FT SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;  
-----

Query Match 100.0%; Score 209; DB 1; Length 58;  
Best Local Similarity 100.0%; Pred. No. 2.1e-21;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
-----

QY 1 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVV 40

Db 7 DAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGVV 46  
|||||

RESULT 4  
A4\_RABIT ID A4\_RABIT STANDARD; PRT; 58 AA.  
AC Q28748;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID  
DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).  
GN APP.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=92017079; PubMed=1656157;  
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
RT "Conservation of the sequence of the Alzheimer's disease amyloid  
RT peptide in dog, polar bear and five other mammals by cross-species  
RT polymerase chain reaction analysis.";  
RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
CC G(O) (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.  
CC -----

```

RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X56129; CAA39594.1; -.
CC HSP; P05067; IAML.
CC InterPro; IPR001868; A4_APP.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
CC CHAIN 1 1 BETA-AMYLOID PROTEIN (POTENTIAL).
CC DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 34 57 POTENTIAL.
CC DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
CC NON_TER 58 58
CC SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

DR HSP; P05067; IAML.
DR InterPro; IPR001868; A4_APP.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 1 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
FT SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 209; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.1e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 45

RESULT 5
A4_SHEEP
ID A4_SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).
GN APP.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

```

```

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X56130; CAA39595.1; -.
CC HSP; P05067; IAML.
CC InterPro; IPR001868; A4_APP.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
CC CHAIN 1 1 BETA-AMYLOID PROTEIN (POTENTIAL).
CC DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 34 57 POTENTIAL.
CC DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
CC NON_TER 58 58
CC SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 209; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.1e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 40
Db 6 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVV 45

RESULT 6
A4_BOVIN
ID A4_BOVIN STANDARD; PRT; 59 AA.
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).
GN APP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X56124; CAA39589.1; -.
CC EMBL; X56126; CAA39591.1; -.
CC HSP; P05067; IAML.
CC InterPro; IPR001868; A4_APP.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.

```

```

FT NON_TER 1 1
FT CHAIN 7 49
FT DOMAIN <1 34
FT TRANSMEM 35 58
FT DOMAIN 59 >59
FT NON_TER 59 59
SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match 100.0%; Score 209; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.1e-21;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
    |||||
DB 7 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 46

RESULT 7
A4_SAISC STANDARD; PRT; 751 AA.
AC Q95241;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR [CONTAINS: BETA-
DE AMYLOID PROTEIN (BETA-APP) (A-BETA)].
GN APP.
OS Samir's sclerous (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver, and Kidney;
RX MEDLINE=96108492; PubMed=8532114;
RA Levy E., Amorim A., Frangione B., Walker L.C.;
RT "Beta-amyloid precursor protein gene in squirrel monkeys with
RT cerebral amyloid angiopathy."
RL Neurobiol. Aging 16:805-808(1995).
CC !- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O).
CC !- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC !- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC !- SIMILARITY: BELONGS TO THE APP FAMILY.
CC !- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; S81024; AAD14347.1; .
CC InterPro; IPR001868; A4_APP.
CC DR InterPro; IPR002223; Kunitz_BPTI.
CC DR Pfam; PF02177; A4_EXTRA; 1.
CC DR Pfam; PF00014; Kunitz_BPTI; 1.
CC DR PRINTS; PR00203; AMYLOIDA4.
CC DR PRINTS; PR00204; BETAAMYLOID.
CC DR PRINTS; PR00759; BASICPTASE.
CC DR SMART; SM00006; A4_EXTRA; 1.
CC DR SMART; SM00131; KU; 1.
CC DR PROSITE; PS00319; A4_EXTRA; 1.
CC DR PROSITE; PS00320; A4_INTRA; 1.
CC DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.

```

```

DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
Signal; Serine protease inhibitor.
FT SIGNAL 1 17
FT CHAIN 18 751
FT CHAIN 653 695
FT DOMAIN 18 680
FT TRANSMEM 681 704
FT DOMAIN 705 751
FT DOMAIN 287 345
FT SITE 740 743
FT ACT_SITE 301 302
FT DISULFID 291 341
FT DISULFID 300 324
FT DISULFID 316 337
FT CARBOHYD 523 523
FT CARBOHYD 552 552
SQ SEQUENCE 751 AA; 84893 MW; 6C3E431089569049 CRC64;

Query Match 100.0%; Score 209; DB 1; Length 751;
Best Local Similarity 100.0%; Pred. No. 3.1e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 40
    |||||
DB 653 DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV 692

RESULT 8
A4_HUMAN STANDARD; PRT; 770 AA.
AC P05067; P09000; Q16011;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR (PROTEASE NEXIN-II)
DE (PN-II) (APP) [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)].
GN APP OR A4 OR CVAP OR ADL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=87144572; PubMed=2881207;
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RT cell-surface receptor."
RL Nature 325:733-736(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88122639; PubMed=2893289;
RA Ponte P., Gonzalez-Bewhitt P., Schilling J., Miller J., Hsu D.,
RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine
RT proteinase inhibitors."
RL Nature 331:525-527(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89128427; PubMed=2783775;
RA Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayne R.M.,
RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
RT is encoded by 16 exons."
RL Nucleic Acids Res. 17:517-522(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97263807; PubMed=9108164;
RA Hattori M., Tsukahara F., Furuhashi Y., Tanahashi H., Hirose M.,

```



RA Saito M., Tsukuni S., Sakaki Y.;  
 RT "A novel method for making nested deletions and its application for  
 RL sequencing of a 300 kb region of human APP locus."; [5]  
 RN Nucleic Acids Res. 25:1802-1808(1997).  
 RP  
 RA SEQUENCE OF 286-345 AND 365-366 FROM N.A.  
 RX MEDLINE=88126640; PubMed=2893290;  
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,  
 RA Gusella J.F., Neve R.L.;  
 RT "Protease inhibitor domain encoded by an amyloid protein precursor  
 RL mRNA associated with Alzheimer's disease."; [6]  
 RN Nature 331:528-530(1988).  
 RP  
 RA SEQUENCE OF 287-367 FROM N.A.  
 RX MEDLINE=88126641; PubMed=2893291;  
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;  
 RT "Novel precursor of Alzheimer's disease amyloid protein shows  
 RL protease inhibitory activity."; [7]  
 RN Nature 331:530-532(1988).  
 RP  
 RA SEQUENCE OF 284-289 AND 365-770 FROM N.A.  
 RX MEDLINE=87231971; PubMed=3035574;  
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;  
 RT "Molecular cloning and characterization of a cDNA encoding the  
 RL cerebrovascular and the neuritic plaque amyloid peptides."; [8]  
 RN Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).  
 RP  
 RA SEQUENCE OF 507-770 FROM N.A.  
 RX MEDLINE=88124954; PubMed=2893379;  
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,  
 RA Marotta C.A.;  
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer  
 RL disease brain: coding and noncoding regions of the fetal precursor  
 RN mRNA are expressed in the cortex."; [9]  
 RN Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).  
 RP  
 RA SEQUENCE OF 672-681.  
 RX MEDLINE=88035004; PubMed=3312495;  
 RA Partridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,  
 RA Tourtellotte W.W., Huebner V., Shively J.E.;  
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition  
 RL and partial sequence of a 4,200-dalton peptide isolated from cortical  
 RN microvessels."; [10]  
 RN J. Neurochem. 49:1394-1401(1987).  
 RP  
 RA SEQUENCE OF 739-770 FROM N.A.  
 RX MEDLINE=90236318; PubMed=2110105;  
 RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;  
 RT "Genomic organization of the human amyloid beta-protein precursor  
 RL gene."; [11]  
 RN Gene 87:257-263(1990).  
 RP  
 RA SEQUENCE OF 1-10 FROM N.A.  
 RX TISSUE=Liver;  
 RA MEDLINE=89016647; PubMed=3140222;  
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;  
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)  
 RL encodes a 95-kDa polypeptide."; [12]  
 RN Nucleic Acids Res. 16:9351-9351(1988).  
 RP  
 RA SEQUENCE OF 18-50.  
 RX MEDLINE=87250462; PubMed=3597385;  
 RA van Nostrand W.E., Cunningham D.D.;  
 RT "Purification of protease nexin II from human fibroblasts."; [13]  
 RN J. Biol. Chem. 262:9508-9514(1987).  
 RP  
 RA IDENTITY OF APP WITH NEXIN-II.  
 RX MEDLINE=89384866; PubMed=2506449;  
 RA Oltsdorf T., Fritz L.C., Schenk D.B., Lieberburg I., Dovey H.F.,  
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Sinha S.;  
 RT "The secreted form of the Alzheimer's amyloid precursor protein with  
 RL the Kunitz domain is protease nexin-II.";

RL Nature 341:144-147(1989).  
 RP  
 RA PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.  
 RX MEDLINE=90211252; PubMed=1969731;  
 RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;  
 RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's  
 RL disease amyloid protein precursor."; [15]  
 RN Biochem. Biophys. Res. Commun. 167:716-721(1990).  
 RP  
 RA COMPLEX WITH G(O).  
 RX MEDLINE=93189965; PubMed=8446172;  
 RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,  
 RA Murayama Y., Ogata E.;  
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding  
 RL protein G(O)."; [16]  
 RN Nature 362:75-79(1993).  
 RP  
 RA X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.  
 RX MEDLINE=99215582; PubMed=10201399;  
 RA Rossjohn J., Cappai R., Feil S.C., Henry A., McKinstry W.J.,  
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,  
 RA Parker M.W.;  
 RT "Crystal structure of the N-terminal, growth factor-like domain of  
 RL Alzheimer amyloid precursor protein."; [17]  
 RN Nat. Struct. Biol. 6:327-331(1999).  
 RP  
 RA X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.  
 RX MEDLINE=91104913; PubMed=2125487;  
 RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrot C., Kossiakof A.A.;  
 RT "X-ray crystal structure of the protease inhibitor domain of  
 RL Alzheimer's amyloid beta-protein precursor."; [18]  
 RN Biochemistry 29:10018-10022(1990).  
 RP  
 RA STRUCTURE BY NMR OF 289-344.  
 RX MEDLINE=92031488; PubMed=1718421;  
 RA Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayney R.M.,  
 RA Kamark M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,  
 RA Tamburini P.P.;  
 RT "Sequential NMR resonance assignment and structure determination of  
 RL the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid  
 RN precursor protein."; [19]  
 RN Biochemistry 30:10467-10478(1991).  
 RP  
 RA STRUCTURE BY NMR OF 672-699.  
 RX MEDLINE=94281210; PubMed=7516706;  
 RA Talafous J., Marcinkowski K.J., Klopman G., Zagorski M.G.;  
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide."; [20]  
 RN Biochemistry 33:7788-7796(1994).  
 RP  
 RA STRUCTURE BY NMR OF 696-706.  
 RX MEDLINE=97128622; PubMed=8973180;  
 RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;  
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in  
 RL membrane-mimicking environment."; [21]  
 RN Biochemistry 35:16094-16104(1996).  
 RP  
 RA STRUCTURE BY NMR OF 672-711.  
 RX MEDLINE=98359783; PubMed=9693002;  
 RA Coles M., Bicknell W., Watson A.A., Craik D.J.;  
 RT "Solution structure of amyloid beta-peptide(1-40) in a water-micelle  
 RL environment. Is the membrane-spanning domain where we think it is?"; [22]  
 RN Biochemistry 37:11064-11077(1998).  
 RP  
 RA STRUCTURE BY NMR OF 672-699.  
 RX MEDLINE=20400066; PubMed=10940222;  
 RA Poulsen S.-A., Watson A.A., Craik D.J.;  
 RT "Solution structures in aqueous SDS micelles of two amyloid beta  
 RL peptides of Abeta(1-28) mutated at the alpha-secretase cleavage  
 RN site."; [23]  
 RN J. Struct. Biol. 130:142-152(2000).  
 RP  
 RA SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.  
 RX MEDLINE=88296437; PubMed=2900137;

RA Dyrks T., Weidemann A., Muthaupt G., Salbaum J.M., Lemaire H.-G.,  
 RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;  
 RT "Identification, transmembrane orientation and biogenesis of the  
 RT amyloid A4 precursor of Alzheimer's disease.";  
 RL EMBO J. 7:949-957(1988).  
 RN [24]  
 RP REVIEW.  
 RX MEDLINE=92271194; PubMed=1589757;  
 RA Kosik K.S.;  
 RT "Alzheimer's disease: a cell biological perspective.";  
 RL Science 256:780-783(1992).  
 RN [25]

Query Match 100.0%; Score 209; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-20;  
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFAEDVGSNGKAIIGLMVGGV 40  
 DB 672 DAEFRHDSGYEVHOKLVFAEDVGSNGKAIIGLMVGGV 711  
 |||||||||||||||||||||||||||||||||||||||||

RESULT 9  
 ID A4\_MOUSE STANDARD; PRT; 770 AA.  
 AC P12023;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR  
 DE (AMYLOIDOGENIC GLYCOPROTEIN) (AG).  
 GN APP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.  
 RC STRAIN-BALB/C; TISSUE-Brain;  
 RX MEDLINE=92096458; PubMed=1756177;  
 RA de Strooper B., van Leuven F., van den Berghe H.;  
 RT "The amyloid beta protein precursor or protease nexin II from mouse  
 RT is closer related to its human homolog than previously reported.";  
 RL Biochim. Biophys. Acta 1129:141-143(1991).  
 RN [2]  
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.  
 RC TISSUE-Brain;  
 RX MEDLINE=88106489; PubMed=3322280;  
 RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sasaki Y.;  
 RT "Complementary DNA for the mouse homolog of the human amyloid beta  
 RT protein precursor.";  
 RL Biochem. Biophys. Res. Commun. 149:665-671(1987).  
 RN [3]  
 RP REVISIONS.  
 RA Yamada T.;  
 RL Submitted (MAR-1988) to the EMBL/GenBank/DBSJ databases.  
 RN [4]  
 RP SEQUENCE OF 289-364 FROM N.A.  
 RC STRAIN-CD-1; TISSUE-Placenta;  
 RX MEDLINE=89345111; PubMed=2369710;  
 RA Fukuchi K., Martin G.M., Deeb S.S.;  
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein  
 RT precursor of Mus domesticus.";  
 RL Nucleic Acids Res. 17:5396-5396(1989).  
 RN [5]  
 RP SEQUENCE OF 1-19 FROM N.A.  
 RX MEDLINE=92209998; PubMed=1555768;  
 RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,  
 RA Sakai Y.;  
 RT "Positive and negative regulatory elements for the expression of the  
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";  
 RL Gene 112:189-195(1992).  
 RN [6]

RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.  
 RC TISSUE-Brain, and Kidney;  
 RX MEDLINE=89149813; PubMed=2493250;  
 RA Yamada T., Sasaki H., Dohura K., Goto I., Sasaki Y.;  
 RT "Structure and expression of the alternatively-spliced forms of mRNA  
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein  
 RT precursor.";  
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),  
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING.  
 CC -!- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS  
 CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND  
 CC LIVER.  
 CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION  
 CC WITH XII-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC  
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE  
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF  
 CC PHOSPHORYLATION (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.  
 CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; X59379; -; NOT ANNOTATED\_CDS.  
 DR EMBL; M18373; AAA37139.1; -;  
 DR EMBL; X15210; CAA33280.1; -;  
 DR EMBL; D10603; BAA01456.1; -;  
 DR EMBL; M24397; AAA39929.1; -;  
 DR PIR; A27485; A27485.  
 DR PIR; S04855; S04855.  
 DR PIR; S19727; S19727.  
 DR MGI; 88059; App.  
 DR InterPro; IPR001868; A4\_APP.  
 DR InterPro; IPR002223; Kunitz\_BPTI.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR Pfam; PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00204; BETAAMYLOID.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR SMART; SM00131; KU; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE; PS00279; BPTI\_KUNITZ\_2; 1.  
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;  
 KW Alternative splicing; Serine protease inhibitor.  
 FT SIGNAL 1 17  
 FT CHAIN 18 770  
 FT ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN  
 FT HOMOLOG.  
 FT EXTRACELLULAR (POTENTIAL).  
 FT POTENTIAL.  
 FT TRANSMEM 700 723  
 FT DOMAIN 724 770  
 FT CYTOPLASMIC (POTENTIAL).  
 FT EQUIVALENT OF BETA-AMYLOID PROTEIN.  
 FT DOMAIN 673 715  
 FT BPTI/KUNITZ INHIBITOR.  
 FT DOMAIN 287 345  
 FT CLATHRIN-BINDING (BY SIMILARITY).  
 FT SITE 759 762  
 FT BY SIMILARITY.  
 FT DISULFID 291 341  
 FT DISULFID 300 324  
 FT DISULFID 316 337  
 FT CARBOHYD 542 542  
 FT CARBOHYD 571 571  
 FT CARBOHYD 571 571  
 FT N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT E -> V (IN ISOFORM APP(695)).  
 FT VARSPLIC 289 289  
 FT VARSPLIC 290 364  
 FT VARSPLIC 346 380  
 FT MISSING (IN ISOFORM APP(751)).  
 FT MISSING (IN ISOFORM APP(751)).  
 SQ SEQUENCE 770 AA; 86752 MW; 26C50DE0890CAF7A CRC64;

```
Query Match          90.9%; Score 190; DB 1; Length 770;
Best Local Similarity 92.5%; Pred. No. 1.le-17;
Matches 37; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGVEVHHQKLVFFAEDVGSNGKAIGLMVGWV 40
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 672 DAEFGHDSGFEVRRHKLFFAEDVGSNGKAIGLMVGWV 711

RESULT 10
A4_RAT
ID A4_RAT STANDARD; PRT; 770 AA.
AC P08592;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE (ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR
  (AMYLOIDGENIC GLYCOPROTEIN) (AG).
GN APP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88312583; PubMed=2900758;
RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RT Seeburg P.H.;
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
  in rat brain suggests a role in cell contact.";
RL EMBO J. 7:1365-1370(1988).
RN [2]
RP SEQUENCE OF 289-364 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89183625; PubMed=2648331;
RA Kang J., Mueller-Hill B.;
RT "The sequence of the two extra exons in rat preA4.";
RL Nucleic Acids Res. 17:2130-2130(1989).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
  APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
  SPLICING.
CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
  WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
  RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
  NXYX MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
  PHOSPHORYLATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (see http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X07648; CAA30488.1; -
CC EMBL; X14066; CAA32229.1; -
CC PIR; S00550; S00550.
CC PIR; S03607; S03607.
CC InterPro; IPR001868; A4_APP.
CC InterPro; IPR002223; Kunitz_BPTI.
CC Pfam; PF02177; A4_EXTRA; 1.
CC Pfam; PF00014; Kunitz_BPTI; 1.
CC PRINTS; PR00014; AMYLOIDA4.
CC PRINTS; PR00203; AMYLOIDA4.
CC PRINTS; PR00204; BETAAMYLOID.
CC PRINTS; PR00759; BASICPTASE.
CC SMART; SM00006; A4_EXTRA; 1.
CC -----

DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
FT Alternative splicing; Serine protease inhibitor.
FT SIGNAL 1 17
FT CHAIN 18 770
FT ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
  HOMOLOG..
FT DOMAIN 18 699
  EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 700 723
  POTENTIAL.
FT DOMAIN 724 770
  CYTOPLASMIC (POTENTIAL).
FT DOMAIN 673 715
  EQUIVALENT OF BETA-AMYLOID PROTEIN.
FT DOMAIN 287 345
  BPTI/KUNITZ INHIBITOR.
FT SITE 759 762
  CLATHRIN-BINDING (BY SIMILARITY).
FT DISULFID 291 341
  BY SIMILARITY.
FT DISULFID 300 324
  BY SIMILARITY.
FT DISULFID 316 337
  BY SIMILARITY.
FT CARBOHYD 542 542
  N-LINKED (GLCNAC.. ) (POTENTIAL).
FT CARBOHYD 571 571
  N-LINKED (GLCNAC.. ) (POTENTIAL).
FT VARSPPLIC 289 289
  E -> V (IN ISOFORM APP(695)).
FT VARSPPLIC 290 364
  MISSING (IN ISOFORM APP(695)).
SQ SEQUENCE 770 AA; 86704 MW; C26C9D6B2D929A7 CRC64;

Query Match          90.9%; Score 190; DB 1; Length 770;
Best Local Similarity 92.5%; Pred. No. 1.le-17;
Matches 37; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGVEVHHQKLVFFAEDVGSNGKAIGLMVGWV 40
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 672 DAEFGHDSGFEVRRHKLFFAEDVGSNGKAIGLMVGWV 711

RESULT 11
POLG_PVYCH
ID POLG_PVYCH STANDARD; PRT; 327 AA.
AC P21294;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: NUCLEAR INCLUSION PROTEIN B (NI-B) (NIB)
  (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48); COAT PROTEIN (CP)]
  (FRAGMENT).
DE Potato virus Y (strain Chinese isolate) (PVY).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OC NCBI_TaxID=12218;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91016851; PubMed=2216735;
RA Zhou X.R., Fang R.X., Wang C.Q., Wang K.Q.;
RT "cDNA sequence of the 3'-coding region of PVY genome (the Chinese
  isolate).";
RL Nucleic Acids Res. 18:5554-5554(1990).
CC -!- PWM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
  POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
  PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
  INDIVIDUAL PROTEINS.
CC -!- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (see http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X54058; CAA37993.1; -
CC PIR; S11549; S11549.
CC HSSP; P05067; IAMB.
```

DR InterPro; IPR001592; Poty\_coat.  
 KW Pfam; PF00767; Poty\_Coat; 1.  
 KW Transferase; RNA-directed RNA polymerase; Coat protein; Polyprotein.  
 FT NON\_TER 1 60 NUCLEAR INCLUSION PROTEIN B.  
 FT CHAIN 61 327 COAT PROTEIN.  
 FT CHAIN 61 327 COAT PROTEIN.  
 SQ SEQUENCE 327 AA; 36868 MW; 8F8355E2DE62F2F18 CRC64;

Query Match 27.3%; Score 57; DB 1; Length 327;  
 Best Local Similarity 53.1%; Pred. No. 2.5;  
 Matches 17; Conservative 0; Mismatches 5; Indels 10; Gaps 3;

QY 1 DAEFRHDSGYEVHHQKLVFFAEDVGSNK 28  
 DB 47 DDEFEEDS-YEVHHQ-----NDTIDAVGDNK 72

## RESULT 12

ID SLG1\_YEAST STANDARD; PRT; 378 AA.  
 AC P54867;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE SLG1 PROTEIN PRECURSOR.  
 GN SLG1 OR YOR008C OR UNF378.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA de Bettignies G., Bergez-Aullo P., Barthe C., Louvet O.,  
 RA Peypouquet M.F., Morel C., Dolignon F., Crouzet M.;  
 RL Submitted (Oct-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97051599; PubMed=8896276;  
 RA Sterky F., Holmberg A., Pettersson B., Uhlen M.;  
 FT "The sequence of a 30 kb fragment on the left arm of chromosome XV  
 from Saccharomyces cerevisiae reveals 15 open reading frames, five of  
 which correspond to previously identified genes.";  
 RL Yeast 12:1091-1095(1996).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; U39481; AAA85862.1; -  
 DR EMBL; U43491; AAC49488.1; -  
 DR EMBL; 274916; CAA99196.1; -  
 DR HSSP; P05067; 1BA6.  
 DR SGD; S0005534; SLG1.  
 DR InterPro; IPR002889; WSC.  
 DR Pfam; PF01822; WSC; 1.  
 DR SMART; SM00321; WSC; 1.  
 KW Glycoprotein; Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 378 SLG1 PROTEIN.  
 FT CARBOHYD 65 65 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 354 354 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 378 AA; 39270 MW; EE164F2374CCCE3 CRC64;

Query Match 27.0%; Score 56.5; DB 1; Length 378;  
 Best Local Similarity 42.4%; Pred. No. 3.4;  
 Matches 14; Conservative 5; Mismatches 5; Indels 9; Gaps 1;

QY 8 SGYEVHHQKLVFFAEDVGSNKGAIIIGLMGVV 40  
 DB 251 SGSKTHKKK-----ANVGAIIVGVGVGVV 274

## RESULT 13

ID DHAL\_PSESP STANDARD; PRT; 488 AA.  
 AC P33008;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE PROBABLE ALDEHYDE DEHYDROGENASE (EC 1.2.1.3).  
 GN TERPE.  
 OS Pseudomonas sp.  
 OC Bacteria; Proteobacteria.  
 OX NCBI\_TaxID=306;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92332528; PubMed=1629218;  
 RA Peterson J.A., Lu J.-Y., Geisselsoder J., Graham-Lorence S.,  
 RA Carmona C., Witney F., Lorence M.C.;  
 FT "Chromatome P-450terp. Isolation and purification of the protein and  
 cloning and sequencing of its operon.";  
 RL J. Biol. Chem. 267:14193-14203(1992).  
 CC -!- FUNCTION: INVOLVED IN A ALPHA-TERPENEOL OXIDATION SYSTEM.  
 CC -!- CATALYTIC ACTIVITY: ALDEHYDE + NAD(+) + H(2)O = ACID + NADH.  
 CC -!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; M91440; AAA25995.1; -  
 DR PIR; S27652; S27652.  
 DR PIR; C42971; C42971.  
 DR HSSP; P20000; 1A4Z.  
 DR InterPro; IPR002086; Aldehyde\_dehydr.  
 DR Pfam; PF00171; aldehyd; 1.  
 DR PROSITE; PS00070; ALDEHYDE\_DEHYDR\_CYS; 1.  
 DR PROSITE; PS00687; ALDEHYDE\_DEHYDR\_GLU; 1.  
 KW Oxidoreductase; NAD.  
 FT NP\_BIND 240 245 NAD (ADP PART) (BY SIMILARITY).  
 FT ACT\_SITE 262 262 BY SIMILARITY.  
 FT ACT\_SITE 296 296 BY SIMILARITY.  
 SQ SEQUENCE 488 AA; 52156 MW; 2144AE1B173C854 CRC64;

Query Match 26.3%; Score 55; DB 1; Length 488;  
 Best Local Similarity 40.6%; Pred. No. 7;  
 Matches 13; Conservative 5; Mismatches 10; Indels 4; Gaps 1;

QY 6 HDSGYEVHHQKLVFFAEDV----GSNKGAIIIG 33  
 DB 305 HESIYAFRDLKLVAYQNVVIGDGSQGVWTMG 336

## RESULT 14

ID Y226\_MYCPN STANDARD; PRT; 503 AA.  
 AC P75462;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE HYPOTHETICAL PROTEIN MG226 HOMOLOG (F10\_ORF503).  
 GN MPN319 OR MP517.  
 OS Mycoplasma pneumoniae.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;  
 OC Mycoplasmataceae; Mycoplasma.

OX NCBI\_TaxID=2104;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 29342 / M129;  
RX MEDLINE=97105885; PubMed=8948633;  
RA Himmelreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,  
RA Herrmann R.;  
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma  
pneumoniae.";  
RL Nucleic Acids Res. 24:4420-4449(1996).  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
CC -!- SIMILARITY: TO M.GENITALIUM MG225.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: AE000051; AAB96165.1; -  
DR InterPro: IPR002293; AA\_rel\_permease\_1.  
DR InterPro: IPR002027; Amino\_acid\_permease.  
DR Pfam: PF00324; aa\_permeases; 1.  
KW Hypothetical protein; Transmembrane; Complete proteome.  
FT TRANSMEM 20 40 POTENTIAL.  
FT TRANSMEM 43 63 POTENTIAL.  
FT TRANSMEM 106 126 POTENTIAL.  
FT TRANSMEM 138 158 POTENTIAL.  
FT TRANSMEM 166 186 POTENTIAL.  
FT TRANSMEM 215 235 POTENTIAL.  
FT TRANSMEM 249 269 POTENTIAL.  
FT TRANSMEM 301 321 POTENTIAL.  
FT TRANSMEM 359 379 POTENTIAL.  
FT TRANSMEM 405 425 POTENTIAL.  
FT TRANSMEM 443 463 POTENTIAL.  
FT TRANSMEM 468 488 POTENTIAL.  
SQ SEQUENCE 503 AA; 54960 MW; 4BC1BFDE036985B2 CRC64;

Query Match 26.3%; Score 55; DB 1; Length 503;  
Best Local Similarity 64.7%; Pred. No. 7.2;  
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 24 VGSNKGAIIGLMVGVV 40  
DB 131 VKDNNGALIGLLVGVV 147

RESULT 15  
TR2M\_AGR74  
ID TR2M\_AGR74 STANDARD; PRT; 755 AA.  
AC P04029;  
DT 23-OCT-1986 (Rel. 02, Created)  
DT 23-OCT-1986 (Rel. 02, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE TRYPTOPHAN 2-MONOOXYGENASE (EC 1.13.12.3).  
GN TMS1.  
OS Agrobacterium tumefaciens.  
OG Plasmid pTiAch5, and Plasmid pTiA6NC.  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Rhizobiaceae; Rhizobium.  
OX NCBI\_TaxID=358;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC PLASMID=pTiAch5;  
RX MEDLINE=84207942; PubMed=6327292;  
RA Gielen J., de Beuckeleer M., Seurinck J., Deboeck F., de Greve H.,  
RA Lemmers M., van Montagu M., Schell J.;  
RT "The complete nucleotide sequence of the TL-DNA of the Agrobacterium  
tumefaciens plasmid pTiAch5.";  
RL EMBO J. 3:835-846(1984).

RN [2]  
RP SEQUENCE FROM N.A.  
RC PLASMID=pTiA6NC;  
RX MEDLINE=84170374; PubMed=6584906;  
RA Klee H., Montoya A., Horodyski F., Lichtenstein C., Garfinkel D.,  
RA Fuller S., Flores C., Peschon J., Nester E., Gordon M.;  
RT "Nucleotide sequence of the tms genes of the pTiA6NC octopine Ti  
plasmid: two gene products involved in plant tumorigenesis.";  
RL Proc. Natl. Acad. Sci. U.S.A. 81:1728-1732(1984).  
CC -!- CATALYTIC ACTIVITY: L-TRYPTOPHAN + O(2) -> INDOLE-3-ACETAMIDE +  
CO(2) + H(2)O.  
CC -!- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF AUXINS FROM TRYPTOPHAN.  
CC -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF ACH5.  
CC -!- SIMILARITY: SIGNIFICANT HOMOLOGY TO THE ADENINE BINDING REGION OF  
CC P-HYDROXYBENZOATE HYDROXYLASE FROM P. FLUORESCENS. IT SEEMS THAT  
CC THIS PROTEIN BINDS ADENINE EITHER AS SUBSTRATE OR COFACTOR.  
CC -!- SIMILARITY: STRONG, WITH ITS A.TUMEFACIENS PLASMID PTITM4  
CC COUNTERPART.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: K02554; AAA92550.1; -  
DR PIR: A04497; QOAG4T.  
DR InterPro: IPR002937; Amino\_Oxidase.  
DR InterPro: IPR00205; NAD\_binding.  
DR Pfam: PF01593; Amino\_Oxidase; 1.  
KW Oxidoreductase; Monooxygenase; Auxin biosynthesis; Crown gall tumor;  
KW T-DNA; Plasmid.  
FT VARIANT 718 719 NR -> IQ (IN PTIA6NC).  
FT VARIANT 721 721 P -> A (IN PTIA6NC).  
SQ SEQUENCE 755 AA; 83947 MW; 9FD2B83FEA001A4D CRC64;

Query Match 26.3%; Score 55; DB 1; Length 755;  
Best Local Similarity 41.2%; Pred. No. 11;  
Matches 14; Conservative 5; Mismatches 9; Indels 6; Gaps 1;

OY 7 DSGYEVHOKLVFFAEDVGSNGKGAIGLMVGVV 40  
DB 223 DSG-----RIGFFEDVPKPKVAVIGAGISGLV 250

Search completed: April 24, 2002, 09:20:38  
Job time: 252 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:21:50 ; Search time 66.52 Seconds  
(without alignments)  
12.249 Million cell updates/sec

Title: US-09-689-469-4  
Perfect score: 11  
Sequence: 1 GSNKGAIIGLM 11

Scoring table: OLIIGO  
Gapop 60.0 , Gapext 60.0

Searched: 522463 seqs, 74073290 residues

Word size : 0

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A.Geneseq\_1101.\*  
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query Match | Score | Length | DB ID | Description |
|------------|-------------|-------|--------|-------|-------------|
| 1          | 11          | 100.0 | 11     | 15    | AA60369     |
| 2          | 11          | 100.0 | 11     | 16    | AA87948     |
| 3          | 11          | 100.0 | 11     | 17    | AA92807     |
| 4          | 11          | 100.0 | 11     | 18    | AA23336     |
| 5          | 11          | 100.0 | 11     | 19    | AA64497     |
| 6          | 11          | 100.0 | 11     | 19    | AA47231     |
| 7          | 11          | 100.0 | 11     | 20    | AAW81470    |
| 8          | 11          | 100.0 | 11     | 21    | AA52133     |
| 9          | 11          | 100.0 | 11     | 22    | AA91775     |
| 10         | 11          | 100.0 | 11     | 22    | AA91808     |
| 11         | 11          | 100.0 | 14     | 19    | AA64498     |

|    |    |       |    |    |          |                    |
|----|----|-------|----|----|----------|--------------------|
| 12 | 11 | 100.0 | 14 | 22 | AA91782  | Amyloid beta-prote |
| 13 | 11 | 100.0 | 14 | 22 | AA91788  | Amyloid beta-prote |
| 14 | 11 | 100.0 | 14 | 22 | AA91815  | Amyloid beta-prote |
| 15 | 11 | 100.0 | 24 | 22 | AA91805  | Amyloid beta-prote |
| 16 | 11 | 100.0 | 24 | 22 | AA91832  | Amyloid beta-prote |
| 17 | 11 | 100.0 | 26 | 19 | AA47229  | Beta-amyloid pepti |
| 18 | 11 | 100.0 | 26 | 20 | AA33408  | Human amyloidogeni |
| 19 | 11 | 100.0 | 26 | 22 | AA84431  | Partial sequence o |
| 20 | 11 | 100.0 | 27 | 20 | AA33409  | Human amyloidogeni |
| 21 | 11 | 100.0 | 32 | 22 | AA84430  | Partial sequence o |
| 22 | 11 | 100.0 | 35 | 17 | AA02336  | Beta-amyloid pepti |
| 23 | 11 | 100.0 | 35 | 19 | AA47228  | Beta-amyloid pepti |
| 24 | 11 | 100.0 | 35 | 20 | AA89356  | Beta-amyloid pepti |
| 25 | 11 | 100.0 | 35 | 20 | AA89357  | Beta-amyloid pepti |
| 26 | 11 | 100.0 | 35 | 20 | AA89360  | Beta-amyloid pepti |
| 27 | 11 | 100.0 | 35 | 20 | AA89361  | Beta-amyloid pepti |
| 28 | 11 | 100.0 | 35 | 22 | AA91803  | Amyloid beta-prote |
| 29 | 11 | 100.0 | 35 | 22 | AA91830  | Amyloid beta-prote |
| 30 | 11 | 100.0 | 36 | 20 | AA81471  | Synthetic amyloid  |
| 31 | 11 | 100.0 | 38 | 15 | AA60362  | Beta-amyloid (1-38 |
| 32 | 11 | 100.0 | 38 | 20 | AA92722  | Human tachykinin a |
| 33 | 11 | 100.0 | 38 | 22 | AA91799  | Amyloid beta-prote |
| 34 | 11 | 100.0 | 38 | 22 | AA91826  | Amyloid beta-prote |
| 35 | 11 | 100.0 | 39 | 15 | AA60363  | Beta-amyloid (1-39 |
| 36 | 11 | 100.0 | 39 | 20 | AA25134  | Human amyloid beta |
| 37 | 11 | 100.0 | 39 | 20 | AA81472  | Synthetic amyloid  |
| 38 | 11 | 100.0 | 39 | 21 | AA52132  | Human Receptor to  |
| 39 | 11 | 100.0 | 40 | 14 | AA33191  | Beta-amyloid pepti |
| 40 | 11 | 100.0 | 40 | 15 | AA60364  | Beta-amyloid (1-40 |
| 41 | 11 | 100.0 | 40 | 18 | AA37507  | Amyloid beta prote |
| 42 | 11 | 100.0 | 40 | 18 | AA23335  | Amyloid beta pepti |
| 43 | 11 | 100.0 | 40 | 19 | AA47232  | Beta-amyloid pepti |
| 44 | 11 | 100.0 | 40 | 19 | AA47226  | Beta-amyloid pepti |
| 45 | 11 | 100.0 | 40 | 22 | AAE05483 | Human peptide anti |

ALIGNMENTS

RESULT 1  
AA60369  
ID AAR60369 standard; peptide; 11 AA.  
XX  
AC AAR60369;  
XX  
DT 15-MAR-1995 (first entry)  
XX  
DE Beta-amyloid (25-35).  
XX  
KW Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;  
anti-beta-amyloid antibody; diagnosis; immunogen; antigen; epitope.  
XX  
OS Homo sapiens.  
XX  
PN WO9417197-A.  
XX  
PD 04-AUG-1994.  
XX  
PF 24-JAN-1994; 94WO-JP00089.  
XX  
PR 25-JAN-1993; 93JP-0010132.  
PR 05-FEB-1993; 93JP-0019035.  
PR 16-NOV-1993; 93JP-0286985.  
PR 28-DEC-1993; 93JP-0334773.  
XX  
(TAKE ) TAKEDA CHEM IND LTD.  
XX  
PI Kitada C, Odaka A, Suzuki N;  
XX  
DR WPI; 1994-264110/32.  
XX  
PT Antibodies recognising specific parts of beta-amyloid - can be  
used for diagnosis of diseases implicating beta-amyloid, such as

PT Alzheimer's disease

PS Claim 2; Page 84; 116pp; Japanese.

XX Antibodies which recognise specific subfragments of the beta-amyloid protein are claimed. Specifically, the antibodies (which are pref. monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal portion of beta-amyloid or they recognise residues 25-35 or 35-43 from the C-terminal portion. The antibodies are useful for assaying beta-amyloid and its derivatives for diagnosis of Alzheimer's disease.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 15; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.9e-06;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11

Db 1 gsnkgailglm 11

RESULT 2

AAR87948

ID AAR87948 standard; peptide; 11 AA.

XX AAR87948;

XX DT 05-MAR-1996 (first entry)

XX DE beta-amyloid (25-35) peptide.

XX KW Alzheimer's disease; beta-amyloid; plaque; glycosaminoglycan;

XX KW proteoglycan; A-beta.

XX OS Synthetic.

XX PN WO9506477-A1.

XX PD 09-MAR-1995.

XX PF 29-AUG-1994; 94WO-US09853.

XX PR 31-AUG-1993; 93US-0114942.

XX PA (GLIA-) GLIATECH INC.

XX PI Brunden KR, Frederickson RCA, Gupta-Bansal R, Richtercook NJ;

XX DR WPI; 1995-115259/15.

XX PT Treating Alzheimer's disease by using cpds. that inhibit beta

XX PT amyloid binding - to glycosaminoglycan(s)

XX PS Claim 49; Page 64; 88pp; English.

XX CC The invention relates to new chemical compounds which are peptides of formulae XXNX (I), XXNX2 (II) and XXNX2X3 (III), and peptides comprising the sequences (I), (II) or (III) and containing not greater than 8 amino acid residues. In the formulae, X is any amino acid with a cationic side chain, N and Z are neutral amino acids, and two of X1, X2 and X3 are amino acids with an anionic side chain and the third is an amino acid with an anionic or neutral side chain. Also new is the peptide Gly-Ser-Asn-Lys-Gly-Ala-Ile-Ile-Gly-Leu-Met. The present sequence is the latter undecapeptide which represents amino acids 25-35 of the beta-amyloid peptide A-beta.

XX CC The peptides inhibit the binding of glycosaminoglycans and/or proteoglycans to A-beta peptide and hence can be used for preventing the formation of amyloid plaques and for treating Alzheimer's disease.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 16; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.9e-06;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11

Db 1 gsnkgailglm 11

RESULT 3

AAR92807

ID AAR92807 standard; peptide; 11 AA.

XX AAR92807;

XX DT 18-OCT-1996 (first entry)

XX DE Human beta-amyloid 25-35.

XX KW PB145; PB446; PB96; beta-amyloid; treatment; Alzheimer's disease;

XX KW Down's syndrome; inhibition; neurotoxicity; beta-amyloid 25-35.

XX OS Homo sapiens.

XX PN WO9607425-A1.

XX PD 14-MAR-1996.

XX PF 07-SEP-1995; 95WO-US10989.

XX PR 09-SEP-1994; 94US-0306872.

XX PA (UNIW ) UNIV WASHINGTON.

XX PI Perlmutter DH;

XX DR WPI; 1996-171392/17.

XX PT Inhibitor peptide(s) for blocking the serpin-enzyme complex receptor - used for inhibiting amyloid-beta protein neurotoxicity in e.g. Alzheimer's disease

XX PS Claim 5; Page 18; 31pp; English.

XX CC The peptides PB145, PB446 and PB96 can be used to inhibit the neurotoxicity of the present peptide, beta-amyloid 25-35, and are therefore useful in the treatment of Alzheimer's disease and Down's syndrome.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 17; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.9e-06;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11

Db 1 gsnkgailglm 11

RESULT 4

AAW23336

ID AAW23336 standard; peptide; 11 AA.

XX AAW23336;

XX DT 12-MAR-1998 (first entry)

XX DE Amyloid beta peptide 2 used to inhibit damage to cells in Alzheimer's.

XX



KW Amyloid beta peptide; extracellular deposit; Alzheimer's disease;  
 KW nuerite outgrowth; microglial activation; neuronal cell degeneration;  
 KW receptor for advanced glycosylation end product;  
 KW amyloid beta peptide fibril.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9726913-A1.  
 XX  
 PD 31-JUL-1997.  
 XX  
 XX  
 PF 21-JAN-1997; 97WO-US00857.  
 XX  
 PR 26-JAN-1996; 96US-0592070.  
 XX  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 PA  
 PI Schmidt AM, Stern D, Yan SD;  
 DR WPI; 1997-393374/36.  
 XX  
 XX Inhibiting damage to cells in e.g. Alzheimer's disease - using an  
 PT agent which inhibits interaction of an amyloid-beta peptide with a  
 PT receptor for advanced glycosylation end product  
 XX  
 PS Claim 5; Page 10; 91pp; English.  
 XX  
 XX Peptides AAW23335-36 are portions of the the amyloid beta peptide, which  
 CC is the principal component of extracellular deposits in Alzheimer's  
 CC disease. It has been shown to promote nuerite outgrowth, generate  
 CC reactive oxygen intermediates, induce cellular oxidant stress, lead to  
 CC neuronal cytotoxicity, and promote microglial activation. The present  
 CC peptide, which comprises amino acids 25-35 of the amyloid beta peptide,  
 CC is used in a pharmaceutical composition. This composition comprises an  
 CC agent capable of inhibiting interaction of an amyloid-beta peptide with  
 CC a receptor for advanced glycosylation end product and a carrier. A  
 CC method for inhibiting interaction of amyloid beta peptide with a receptor  
 CC for advanced glycosylation on the surface of a cell comprises contacting  
 CC the cell with e.g. present peptide. Depending on the type of cell,  
 CC inhibiting the interaction between the amyloid beta peptide and the  
 CC receptor for advanced glycosylation can be used for inhibiting  
 CC degeneration of a neuronal cell, inhibiting formation of an amyloid beta  
 CC peptide fibril on a cell, inhibiting extracellular assembly of amyloid  
 CC beta peptide into a fibril, inhibiting aggregation of amyloid beta  
 CC peptide on the surface of a cell, inhibiting infiltration of a microglial  
 CC cell into senile plaques, and inhibiting activation of microglial cells  
 CC by amyloid beta peptide. The methods can be used for treating e.g.  
 CC diabetes, Alzheimer's disease, senility, renal failure, hyperlipidemic  
 CC atherosclerosis, neuronal cytotoxicity, Down's syndrome, dementia  
 CC associated with head trauma, amyotrophic lateral sclerosis, multiple  
 CC sclerosis or neuronal degeneration.  
 XX  
 SQ Sequence 11 AA;  
 Query Match 100.0%; Score 11; DB 18; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GSNKGAIIGLM 11  
 DB 1 gsnkgaiiglm 11  
 RESULT 5  
 AAW64497  
 ID AAW64497 standard; peptide; 11 AA.  
 XX  
 AC AAW64497;  
 XX  
 XX 20-OCT-1998 (first entry)  
 DT  
 DE Neurotoxic beta-amyloid peptide decoy peptide #10.

XX  
 KW Beta-amyloid peptide; beta-AP; neuropeptide; neurotoxin; calcium influx;  
 KW aggregate; Alzheimers disease; decoy; treatment.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9830229-A1.  
 XX  
 PD 16-JUL-1998.  
 XX  
 XX  
 PF 09-JAN-1998; 98WO-US00653.  
 XX  
 PR 29-OCT-1997; 97US-0960188.  
 PR 10-JAN-1997; 97US-0035847.  
 XX  
 XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
 PA  
 PI Blanchard BJ, Ingram VM;  
 DR WPI; 1998-398795/34.  
 XX  
 XX Inhibition of aggregation of, e.g. beta-amyloid peptide - by  
 PT administering decoy peptide or other calcium-influx inhibitor,  
 PT useful for, e.g. treating Alzheimer's disease  
 XX  
 PS Example 4; Page 42; 68pp; English.  
 XX  
 XX AAW64488-W64517 are decoy peptides that bind to a neurotoxic  
 CC beta-amyloid peptide (beta-AP) and reduces the ability of beta-AP's to  
 CC form aggregates that increase calcium influx into neuronal cells. Such  
 CC peptides can be used in the treatment of diseases associated with  
 CC neurotoxic aggregates of beta-AP specifically Alzheimer's disease. The  
 CC peptides are administered at 0.001-1000 (especially 0.2-20) mg/kg, by  
 CC injection and orally, or from slow-release implants.  
 XX  
 SQ Sequence 11 AA;  
 Query Match 100.0%; Score 11; DB 19; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GSNKGAIIGLM 11  
 DB 1 gsnkgaiiglm 11  
 RESULT 6  
 AAW47231  
 ID AAW47231 standard; peptide; 11 AA.  
 XX  
 AC AAW47231;  
 XX  
 XX 22-MAY-1998 (first entry)  
 DT  
 DE Beta-amyloid peptide residues 25-35.  
 XX  
 XX Screening assay; beta-amyloid peptide; treatment;  
 KW amyloidosis disease; Alzheimer's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5721106-A.  
 XX  
 PD 24-FEB-1998.  
 XX  
 XX 12-SEP-1994; 94US-0304585.  
 PF  
 XX 12-SEP-1994; 94US-0304585.  
 PR  
 PR 13-AUG-1991; 91US-0744767.  
 XX  
 XX (HARD ) HARVARD COLLEGE.  
 PA (MINU ) UNIV MINNESOTA.

XX Maggio JE, Mantyh PW;  
 PI WPI; 1998-168404/15.  
 DR  
 XX New in vitro screening assay for Alzheimer's disease drugs -  
 PT comprises assessing binding of labelled beta-amyloid peptide to silk  
 PT sample  
 XX  
 XX Example 1; Columns 29-30; 36pp; English.  
 PS  
 XX The present sequence was used in the development of a novel in  
 CC vitro screening assay for agents capable of affecting the  
 CC deposition of beta-amyloid peptide (BAP) on tissue. The method  
 CC comprises contacting a silk sample with labelled BAP, optionally  
 CC in the presence of a test agent, detecting the amount of label  
 CC bound to the silk and assessing the effect of the agent on the  
 CC deposition of BAP. Agents that inhibit binding of BAP to silk are  
 CC potentially useful for treating amyloidosis diseases, especially  
 CC Alzheimer's disease.  
 XX  
 XX Sequence 11 AA;  
 SQ

Query Match 100.0%; Score 11; DB 19; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11  
 DB 1 gsnkgaiiglm 11  
 |||||

RESULT 7  
 AAW81470  
 ID AAW81470 standard; peptide; 11 AA.  
 XX  
 AC AAW81470;  
 XX  
 DT 28-JAN-1999 (first entry)  
 XX  
 DE Synthetic amyloid beta (Abeta) peptide 5 (residues 25-35).  
 XX  
 KW Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;  
 KW research; neurotoxicity; free-radical; glutamine synthetase.  
 XX  
 OS Synthetic.  
 XX  
 PN US5840838-A.  
 XX  
 PD 24-NOV-1998.  
 XX  
 PF 29-FEB-1996; 96US-0609090.  
 XX  
 PR 29-FEB-1996; 96US-0609090.  
 XX  
 PA (KENT ) UNIV KENTUCKY RES FOUND.  
 XX  
 PI Aksenov M, Butterfield DA, Carney JM, Hensley K;  
 XX WPI; 1999-034120/03.  
 DR  
 XX Process for treating synthetic amyloid beta peptides - by organic  
 PT solvent treatment, useful for studying neurotoxicity  
 PT  
 PS Claim 5; Columns 9-10; 14pp; English.  
 XX  
 XX Sequences AAW81466 to AAW81476 represent synthetic amyloid beta (Abeta)  
 CC peptides. The invention provides a process for treating a synthetic  
 CC Abeta peptide that comprises dissolving the peptide in a deoxygenated  
 CC solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl  
 CC sulphoxide, morpholinopropanesulphonic acid, dimethylformamide and  
 CC acetonitrile to a concentration of 0.01-10 mg/ml, incubating the

CC solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by  
 CC 'evaporative deposition', in 5-10 minutes. Synthetic amyloid beta  
 CC peptides are useful as research tools for studying neurotoxicity  
 CC resulting from Abeta peptide -enhanced free-radical production. The  
 CC treatment increases the activity of the synthetic Abeta peptides in tests  
 CC to determine free-radical generating capacity and glutamine synthetase  
 CC inactivation.  
 XX  
 XX Sequence 11 AA;  
 SQ

Query Match 100.0%; Score 11; DB 20; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11  
 DB 1 gsnkgaiiglm 11  
 |||||

RESULT 8  
 AAY52133  
 ID AAY52133 standard; peptide; 11 AA.  
 XX  
 AC AAY52133;  
 XX  
 DT 28-JAN-2000 (first entry)  
 XX  
 DE Human Receptor to AGE (RAGE) amino acid sequence fragment #2.  
 XX  
 KW Soluble receptor for advanced glycation endproducts; RAGE; tumour;  
 KW invasion; metastasis; amphoterin; neuron; inhibit; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9954485-A1.  
 XX  
 PD 28-OCT-1999.  
 XX  
 PF 16-APR-1999; 99WO-US08427.  
 XX  
 PR 17-APR-1998; 98US-0062365.  
 XX  
 PA (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX  
 PI Schmidt AM, Stern D;  
 XX WPI; 2000-013260/01.  
 DR  
 XX Inhibiting tumour invasion or spreading by administration of soluble  
 PT receptor for advanced glycation endproducts -  
 XX  
 PS Claim 28; Page 62; 88pp; English.  
 XX  
 XX This is the amino acid sequence of a fragment of the human soluble  
 CC Receptor for Advanced Glycation Endproducts (RAGE). RAGE interacts with  
 CC a range of physiologically and pathophysiologically relevant ligands  
 CC when considering tumour invasion. In normal developing neurons RAGE  
 CC colocalizes with amphoterin which is a matrix associated polypeptide.  
 CC The expression of both RAGE and amphoterin decreases after birth, but  
 CC both have increased expression in tumours. RAGE polypeptides  
 CC AAY52132-Y52135 are used in the invention in a method for inhibiting  
 CC tumour invasion and metastasis. The method involves inhibiting tumour  
 CC invasion and metastasis via administration of a therapeutically effective  
 CC amount of the pharmaceutical composition containing a RAGE polypeptide.  
 CC The invention also relates to a method for evaluating the ability of an  
 CC agent to inhibit tumour invasion in a local cellular environment. RAGE  
 CC can be administered to a patient in a pharmaceutically acceptable  
 CC carrier.  
 XX  
 XX Sequence 11 AA;  
 SQ

Query Match 100.0%; Score 11; DB 21; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.9e-06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11  
DB 1 gsnkgaiiglm 11

RESULT 9  
AAB91775  
ID AAB91775 standard; Peptide; 11 AA.

XX AC AAB91775;

XX DT 22-JUN-2001 (first entry)

DE Amyloid beta-protein fragment peptide SEQ ID NO:951.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;  
KW blood component; modification; succinimidyl; maleimido group; amino;  
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX OS Homo sapiens.

OS Synthetic.

XX PN WO200069900-A2.

XX PD 23-NOV-2000.

XX PF 17-MAY-2000; 2000WO-US13576.

XX PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

DR WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents  
PT peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure: Page 504; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)  
CC comprising a therapeutically active amino acid region (III) and a  
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to  
CC a less therapeutically active amino acid region (IV), which covalently  
CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
CC factors and neurotransmitters, to protect them from peptidase activity  
CC in vivo for the treatment of various disorders. Endogenous therapeutic  
CC peptides are not suitable as drug candidates as they require frequent  
CC administration due to rapid degradation by peptidases in the body.  
CC Modifying and attaching therapeutic peptides to albumin prevents or  
CC reduces the action of peptidases to increase length of activity (half  
CC life) and specificity as bonding to large molecules decreases  
CC intracellular uptake and interference with physiological processes.  
CC AAB90829 to AAB92441 represent peptides which can be used in the  
CC exemplification of the present invention.

XX Sequence 11 AA;

Query Match 100.0%; Score 11; DB 22; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.9e-06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11  
DB 1 gsnkgaiiglm 11

RESULT 10  
AAB91808

ID AAB91808 standard; Peptide; 11 AA.

XX AC AAB91808;

XX DT 22-JUN-2001 (first entry)

DE Amyloid beta-protein fragment peptide SEQ ID NO:984.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;  
KW blood component; modification; succinimidyl; maleimido group; amino;  
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX OS Homo sapiens.

OS Synthetic.

XX PN WO200069900-A2.

XX PD 23-NOV-2000.

XX PF 17-MAY-2000; 2000WO-US13576.

XX PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

DR WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents  
PT peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure: Page 516; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)  
CC comprising a therapeutically active amino acid region (III) and a  
CC reactive group (II) (e.g. succinimidyl and maleimido groups) covalently  
CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
CC factors and neurotransmitters, to protect them from peptidase activity  
CC in vivo for the treatment of various disorders. Endogenous therapeutic  
CC peptides are not suitable as drug candidates as they require frequent  
CC administration due to rapid degradation by peptidases in the body.  
CC Modifying and attaching therapeutic peptides to albumin prevents or  
CC reduces the action of peptidases to increase length of activity (half  
CC life) and specificity as bonding to large molecules decreases  
CC intracellular uptake and interference with physiological processes.  
CC AAB90829 to AAB92441 represent peptides which can be used in the  
CC exemplification of the present invention.

XX Sequence 11 AA;

Query Match 100.0%; Score 11; DB 22; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.9e-06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11  
DB 1 gsnkgaiiglm 11

```

RESULT 11
AAW64498
ID AAW64498 standard; peptide; 14 AA.
XX
AC AAW64498;
XX
DT 20-OCT-1998 (first entry)
XX
DE Neurotoxic beta-amyloid peptide decoy peptide #11.
XX
KW Beta-amyloid peptide; beta-AP; neuropeptide; neurotoxin; calcium influx;
KW aggregate; Alzheimers disease; decoy; treatment.
XX
OS Synthetic.
XX
PN WO9830229-A1.
XX
PD 16-JUL-1998.
XX
PF 09-JAN-1998; 98WO-US00653.
XX
PR 29-OCT-1997; 97US-0960188.
PR 10-JAN-1997; 97US-0035847.
XX
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
PI Blanchard BJ, Ingram VM;
XX
DR WPI; 1998-398795/34.
XX
PT Inhibition of aggregation of, e.g. beta-amyloid peptide - by
PT administering decoy peptide or other calcium-influx inhibitor,
PT useful for, e.g. treating Alzheimer's disease
XX
PS Example 4; Page 43; 68pp; English.
XX
CC AAW64488-W64517 are decoy peptides that bind to a neurotoxic
CC beta-amyloid peptide (beta-AP) and reduces the ability of beta-AP's to
CC form aggregates that increase calcium influx into neuronal cells. Such
CC peptides can be used in the treatment of diseases associated with
CC neurotoxic aggregates of beta-AP specifically Alzheimer's disease. The
CC peptides are administered at 0.001-1000 (especially 0.2-20) mg/kg, by
CC injection and orally, or from slow-release implants.
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 11; DB 19; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
Db | | | | | | | | | |
4 gsnkgailglm 14

RESULT 12
AAB91782
ID AAB91782 standard; Peptide; 14 AA.
XX
AC AAB91782;
XX
DT 22-JUN-2001 (first entry)
XX
DE Amyloid beta-protein fragment peptide SEQ ID NO:958.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.

```

```

XX WO200069900-A2.
PN
XX 23-NOV-2000.
PD
XX
XX PF 17-MAY-2000; 2000WO-US13576.
XX
XX PR 17-MAY-1999; 99US-0134406.
XX PR 10-SEP-1999; 99US-0153406.
XX PR 15-OCT-1999; 99US-0159783.
XX
XX (CONJ-) CONJUCHEM INC.
XX
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX WPI; 2001-112059/12.
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
XX peptidase degradation, useful for increasing length of in vivo activity
PT
PT
XX
XX Disclosure; Page 507; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 11; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11
Db | | | | | | | | | |
4 gsnkgailglm 14

RESULT 13
AAB91788
ID AAB91788 standard; Peptide; 14 AA.
XX
AC AAB91788;
XX
XX 22-JUN-2001 (first entry)
DT
XX
XX Amyloid beta-protein fragment peptide SEQ ID NO:964.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
XX 23-NOV-2000.
PD

```



XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;  
PI WPI; 2001-112059/12.  
XX  
DR  
XX  
PT Modifying and attaching therapeutic peptides to albumin prevents  
PT peptidase degradation, useful for increasing length of in vivo activity  
PT  
XX  
PS Disclosure; Page 515; 733pp; English.  
XX  
CC The present invention describes a modified therapeutic peptide (I)  
CC comprising a therapeutically active amino acid region (III) and a  
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to  
CC a less therapeutically active amino acid region (IV), which covalently  
CC bonds with amino/hydroxy/thiol groups on blood components to form a  
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
CC factors and neurotransmitters, to protect them from peptidase activity  
CC in vivo for the treatment of various disorders. Endogenous therapeutic  
CC peptides are not suitable as drug candidates as they require frequent  
CC administration due to rapid degradation by peptidases in the body.  
CC Modifying and attaching therapeutic peptides to albumin prevents or  
CC reduces the action of peptidases to increase length of activity (half  
CC life) and specificity as bonding to large molecules decreases  
CC intracellular uptake and interference with physiological processes.  
CC AAB90829 to AAB92441 represent peptides which can be used in the  
CC exemplification of the present invention.  
XX  
SQ Sequence 24 AA;

Query Match 100.0%; Score 11; DB 22; Length 24;  
Best Local Similarity 100.0%; Pred. No. 7.4e-06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GSNKGAIIGLM 11  
Db 9 gsnkgailglm 19  
|||||

Search completed: April 24, 2002, 09:21:50  
Job time: 249 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:22:29 ; Search time 32.21 Seconds  
(without alignments)  
7.685 Million cell updates/sec

Title: US-09-689-469-4  
Perfect score: 11  
Sequence: 1 GSNKGAIIGLM 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 21252 seqs, 22503292 residues

Word size : 0

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pap.\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pap.\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pap.\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pap.\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pap.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | ID | Description       |
|------------|-------|-------|--------|----|-------------------|
| 1          | 11    | 100.0 | 11     | 1  | US-07-744-767A-3  |
| 2          | 11    | 100.0 | 11     | 1  | US-08-306-872-2   |
| 3          | 11    | 100.0 | 11     | 1  | US-08-346-849-5   |
| 4          | 11    | 100.0 | 11     | 1  | US-08-304-585-3   |
| 5          | 11    | 100.0 | 11     | 1  | US-08-302-808-8   |
| 6          | 11    | 100.0 | 11     | 2  | US-08-433-734-3   |
| 7          | 11    | 100.0 | 11     | 2  | US-08-609-090-5   |
| 8          | 11    | 100.0 | 11     | 2  | US-08-986-948-8   |
| 9          | 11    | 100.0 | 11     | 4  | US-08-293-284-5   |
| 10         | 11    | 100.0 | 11     | 4  | US-09-005-215-10  |
| 11         | 11    | 100.0 | 11     | 5  | PCT-US95-10989-2  |
| 12         | 11    | 100.0 | 14     | 4  | US-09-005-215-11  |
| 13         | 11    | 100.0 | 26     | 1  | US-08-304-585-7   |
| 14         | 11    | 100.0 | 34     | 2  | US-08-475-579A-4  |
| 15         | 11    | 100.0 | 35     | 1  | US-08-304-585-6   |
| 16         | 11    | 100.0 | 35     | 2  | US-08-612-785B-16 |
| 17         | 11    | 100.0 | 35     | 2  | US-08-612-785B-36 |
| 18         | 11    | 100.0 | 35     | 2  | US-08-612-785B-39 |
| 19         | 11    | 100.0 | 35     | 2  | US-08-612-785B-40 |
| 20         | 11    | 100.0 | 36     | 2  | US-08-609-090-6   |
| 21         | 11    | 100.0 | 38     | 1  | US-08-302-808-1   |
| 22         | 11    | 100.0 | 38     | 2  | US-07-737-371E-68 |
| 23         | 11    | 100.0 | 38     | 2  | US-08-986-948-1   |
| 24         | 11    | 100.0 | 39     | 1  | US-08-304-585-5   |
| 25         | 11    | 100.0 | 39     | 1  | US-08-302-808-2   |
| 26         | 11    | 100.0 | 39     | 2  | US-08-609-090-7   |
| 27         | 11    | 100.0 | 39     | 2  | US-08-682-245A-1  |

|    |    |       |    |   |                   |                    |
|----|----|-------|----|---|-------------------|--------------------|
| 28 | 11 | 100.0 | 39 | 2 | US-08-986-948-2   | Sequence 2, Appli  |
| 29 | 11 | 100.0 | 40 | 1 | US-07-744-767A-1  | Sequence 1, Appli  |
| 30 | 11 | 100.0 | 40 | 1 | US-08-235-400-2   | Sequence 2, Appli  |
| 31 | 11 | 100.0 | 40 | 1 | US-08-476-464A-2  | Sequence 2, Appli  |
| 32 | 11 | 100.0 | 40 | 1 | US-08-304-585-1   | Sequence 1, Appli  |
| 33 | 11 | 100.0 | 40 | 1 | US-08-304-585-8   | Sequence 8, Appli  |
| 34 | 11 | 100.0 | 40 | 1 | US-08-302-808-3   | Sequence 3, Appli  |
| 35 | 11 | 100.0 | 40 | 2 | US-08-433-734-1   | Sequence 1, Appli  |
| 36 | 11 | 100.0 | 40 | 2 | US-08-609-090-8   | Sequence 8, Appli  |
| 37 | 11 | 100.0 | 40 | 2 | US-07-737-371E-69 | Sequence 69, Appli |
| 38 | 11 | 100.0 | 40 | 2 | US-08-682-245A-2  | Sequence 2, Appli  |
| 39 | 11 | 100.0 | 40 | 2 | US-08-986-948-3   | Sequence 3, Appli  |
| 40 | 11 | 100.0 | 40 | 2 | US-08-461-216-1   | Sequence 1, Appli  |
| 41 | 11 | 100.0 | 40 | 4 | US-08-959-148-1   | Sequence 1, Appli  |
| 42 | 11 | 100.0 | 40 | 5 | PCT-US92-06700-1  | Sequence 1, Appli  |
| 43 | 11 | 100.0 | 41 | 1 | US-07-819-361-1   | Sequence 1, Appli  |
| 44 | 11 | 100.0 | 41 | 1 | US-08-302-808-4   | Sequence 4, Appli  |
| 45 | 11 | 100.0 | 41 | 2 | US-08-682-245A-3  | Sequence 3, Appli  |

ALIGNMENTS

RESULT 1  
US-07-744-767A-3  
; Sequence 3, Application US/07744767A  
; Patent No. 5434050  
; GENERAL INFORMATION:  
; APPLICANT: Magglio, John E.  
; APPLICANT: Magglio, John E.  
; TITLE OF INVENTION: Labelled -Amyloid Peptide and Methods  
; TITLE OF INVENTION: for Use in Detecting Alzheimer's Disease  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Schwegman, Lundberg & Woessner, P.A.  
; STREET: 3500 IDS Center  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/744,767A  
; FILING DATE: 13-AUG-1991  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Muetting, Ann M.  
; REGISTRATION NUMBER: 33,977  
; REFERENCE/DOCKET NUMBER: 600,226-US-01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-339-0331  
; TELEFAX: 612-339-3061  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-07-744-767A-3

Query Match 100.0%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GSNKGAIIGLM 11  
DB 1 GSNKGAIIGLM 11

RESULT 2  
US-08-872-2  
; Sequence 2, Application US/08306872  
; Patent No. 5514653  
; GENERAL INFORMATION:  
; APPLICANT: Perlmuter, David H.  
; TITLE OF INVENTION: Method of Blocking the SEC Receptor  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scott J. Meyer, Monsanto/Searle, A3SG  
; STREET: 800 N. Lindbergh Blvd.  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63167  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/306,872  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyer, Scott J.  
; REGISTRATION NUMBER: 25,275  
; REFERENCE/DOCKET NUMBER: WU-2833  
; TELEPHONE: (314)694-3117  
; TELEFAX: (314)694-5435  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-306-872-2

Query Match 100.0%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.le-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11  
Db 1 GSNKGAIIGLM 11

RESULT 3  
US-08-346-849-5  
; Sequence 5, Application US/08346849  
; Patent No. 5670483  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Shuguang  
; APPLICANT: Lockshin, Curtis  
; APPLICANT: Rich, Alexander  
; APPLICANT: Holmes, Todd  
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY  
; SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES  
; THEREFOR  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02173-4799  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/346,849  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/973,326  
; FILING DATE: 28 DECEMBER 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brook, David E.  
; REGISTRATION NUMBER: 22,592  
; REFERENCE/DOCKET NUMBER: MIT-6008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-346-849-5

Query Match 100.0%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.le-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11  
Db 1 GSNKGAIIGLM 11

RESULT 4  
US-08-304-585-3  
; Sequence 3, Application US/08304585  
; Patent No. 5721106  
; GENERAL INFORMATION:  
; APPLICANT: Maggio, John E.  
; APPLICANT: Mantyn, Patrick W.  
; TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND  
; METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.  
; STREET: P.O. Box 581415  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55458-1415  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/304,585  
; FILING DATE: 12-SEP-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Muetting, Ann M.  
; REGISTRATION NUMBER: 33,977  
; REFERENCE/DOCKET NUMBER: 110.00010120  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-305-1217  
; TELEFAX: 612-305-1228  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant



MOLECULE TYPE: peptide  
US-08-304-585-3

Query Match 100.0%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11  
DB 1 GSNKGAIIGLM 11

## RESULT 5

US-08-302-808-8  
; Sequence 8, Application US/08302808  
; Patent No. 5750349  
; GENERAL INFORMATION:  
; APPLICANT: SUZUKI, No. 5750349uhiro  
; APPLICANT: ODAKA, Asano  
; APPLICANT: KITADA, Chieko  
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR  
; DERIVATIVES AND USE THEREOF  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02019  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/302.808  
; FILING DATE: 15-SEP-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP94/00089  
; FILING DATE: 24-JAN-1994  
; APPLICATION NUMBER: 010132/1993  
; FILING DATE: 25-JAN-1993  
; APPLICATION NUMBER: 019035/1993  
; FILING DATE: 05-FEB-1993  
; APPLICATION NUMBER: 286985/1993  
; FILING DATE: 16-NOV-1993  
; APPLICATION NUMBER: 334773/1993  
; FILING DATE: 28-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DAVID, RESNICK S  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 44631  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELEX: 200291 STRE  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
US-08-302-808-8

Query Match 100.0%; Score 11; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11  
DB 1 GSNKGAIIGLM 11

## RESULT 6

US-08-433-734-3  
; Sequence 3, Application US/08433734  
; Patent No. 5837473  
; GENERAL INFORMATION:  
; APPLICANT: Maggio, John E.  
; APPLICANT: Mantyh, Patrick W.  
; TITLE OF INVENTION: Labelled -Amyloid Peptide and Methods  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.  
; STREET: P.O. Box 581415  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55458-1415  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/433,734  
; FILING DATE: 03-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Muetting, Ann M.  
; REGISTRATION NUMBER: 33,977  
; REFERENCE/DOCKET NUMBER: 110.00010102  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-305-1220  
; TELEFAX: 612-305-1228  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-433-734-3

Query Match 100.0%; Score 11; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11  
DB 1 GSNKGAIIGLM 11

## RESULT 7

US-08-609-090-5  
; Sequence 5, Application US/08609090  
; Patent No. 5840838  
; GENERAL INFORMATION:  
; APPLICANT: HENSLEY, Kenneth  
; APPLICANT: BUTTERFIELD, D. A.  
; APPLICANT: CARNEY, John M.  
; APPLICANT: AKSENOV, Michael  
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
US-08-609-090-5

ADDRESSEE: LOWE PRICE LEBLANC & BECKER  
 STREET: 99 Canal Center Plaza, Suite 300  
 CITY: Alexandria  
 STATE: Virginia  
 COUNTRY: USA  
 ZIP: 22314  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/609,090  
 FILING DATE: 29-FEB-1996  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kraus, Eric J.  
 REGISTRATION NUMBER: 36,190  
 REFERENCE/DOCKET NUMBER: 434-059  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-684-1111  
 TELEFAX: 703-684-1124  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 11 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-609-090-5

Query Match 100.0%; Score 11; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIGLM 11  
 |||||  
 DB 1 GSNKGAIGLM 11

RESULT 8  
 US-08-986-948-8  
 Sequence 8, Application US/08986948  
 Patent No. 5955317  
 GENERAL INFORMATION:  
 APPLICANT: SUZUKI, No. 5955317uhiro  
 APPLICANT: ODAKA, Asano  
 APPLICANT: KITADA, Chieko  
 TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR  
 DERIVATIVES AND USE THEREOF  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
 STREET: 130 WATER STREET  
 CITY: BOSTON  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02019  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/986,948  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/302,808  
 FILING DATE: 15-SEP-1994  
 APPLICATION NUMBER: PCT/JP94/00089  
 FILING DATE: 24-JAN-1994

APPLICATION NUMBER: 010132/1993  
 FILING DATE: 25-JAN-1993  
 APPLICATION NUMBER: 019035/1993  
 FILING DATE: 05-FEB-1993  
 APPLICATION NUMBER: 286985/1993  
 FILING DATE: 16-NOV-1993  
 APPLICATION NUMBER: 334773/1993  
 FILING DATE: 28-DEC-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: DAVID, RESNICK S  
 REGISTRATION NUMBER: 34,235  
 REFERENCE/DOCKET NUMBER: 44631  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-523-3400  
 TELEFAX: 617-523-6440  
 TELEX: 200291 STRE  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 11 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N-terminal  
 ORIGINAL SOURCE:  
 US-08-986-948-8

Query Match 100.0%; Score 11; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIGLM 11  
 |||||  
 DB 1 GSNKGAIGLM 11

RESULT 9  
 US-08-293-284A-5  
 Sequence 5, Application US/08293284A  
 Patent No. 5955343  
 GENERAL INFORMATION:  
 APPLICANT: Holmes, Todd  
 APPLICANT: Zhang, Shuguang  
 APPLICANT: Rich, Alexander  
 APPLICANT: Dipersio, C. Michael  
 APPLICANT: Lockshin, Curtis  
 TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY  
 SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES  
 THEREFOR  
 NUMBER OF SEQUENCES: 64  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
 STREET: Two Militia Drive  
 CITY: Lexington  
 STATE: Massachusetts  
 COUNTRY: U.S.A.  
 ZIP: 02173-4799  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/293,284A  
 FILING DATE: 22-AUG-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/973,326  
 FILING DATE: 28-DEC-1992  
 ATTORNEY/AGENT INFORMATION:

NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: MIT-6008A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-293-284A-5

Query Match 100.0%; Score 11; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11  
|||||  
Db 1 GSNKGAIIGLM 11

RESULT 10  
US-09-005-215-10  
; Sequence 10, Application US/09005215  
; Patent No. 6172043  
; GENERAL INFORMATION:  
; APPLICANT: Ingram, Vernon M.  
; APPLICANT: Blanchard, Barbara J.  
; TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S  
; TITLE OF INVENTION: DISEASE CAUSED BY -AMYLOID PEPTIDES  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
; STREET: 600 ATLANTIC AVENUE  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/005,215  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/035,847  
; FILING DATE: 10-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/960,188  
; FILING DATE: 29-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gates, Edward R.  
; REGISTRATION NUMBER: 31,616  
; REFERENCE/DOCKET INFORMATION:  
; TELEPHONE: 617-720-3500  
; TELEFAX: 617-720-2441  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
US-09-005-215-10

Query Match 100.0%; Score 11; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11  
|||||  
Db 1 GSNKGAIIGLM 11

RESULT 11  
PCT-US95-10989-2  
; Sequence 2, Application PC/TUS9510989  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Method of Blocking the SEC Receptor  
; NUMBER OF SEQUENCES: 8  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/10989  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/306,872  
; FILING DATE: 09-SEP-1994  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
PCT-US95-10989-2

Query Match 100.0%; Score 11; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11  
|||||  
Db 1 GSNKGAIIGLM 11

RESULT 12  
US-09-005-215-11  
; Sequence 11, Application US/09005215  
; Patent No. 6172043  
; GENERAL INFORMATION:  
; APPLICANT: Ingram, Vernon M.  
; APPLICANT: Blanchard, Barbara J.  
; TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S  
; TITLE OF INVENTION: DISEASE CAUSED BY -AMYLOID PEPTIDES  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
; STREET: 600 ATLANTIC AVENUE  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/005,215  
; FILING DATE:  
; CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/035,847  
FILING DATE: 10-JAN-1997  
PRIOR APPLICATION NUMBER: 08/960,188  
FILING DATE: 29-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Gates, Edward R.  
REGISTRATION NUMBER: 31,616  
REFERENCE/DOCKET NUMBER: M0656/7035  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
US-09-005-215-11

Query Match 100.0%; Score 11; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11  
DB 4 GSNKGAIIGLM 14

RESULT 13  
US-08-304-585-7  
Sequence 7, Application US/08304585  
Patent No. 5721106  
GENERAL INFORMATION:  
APPLICANT: Maggio, John E.  
APPLICANT: Mantyh, Patrick W.  
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND  
METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.  
STREET: P.O. Box 581415  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55458-1415  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/304,585  
FILING DATE: 12-SEP-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Muetting, Ann M.  
REGISTRATION NUMBER: 33,977  
REFERENCE/DOCKET NUMBER: 110.00010120  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-305-1217  
TELEFAX: 612-305-1228  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide

US-08-304-585-7

Query Match 100.0%; Score 11; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11  
DB 16 GSNKGAIIGLM 26

RESULT 14  
US-08-475-579A-4  
Sequence 4, Application US/08475579A  
Patent No. 5854215  
GENERAL INFORMATION:  
APPLICANT: Mark A. Findels et al.  
TITLE OF INVENTION: Modulators of [SYMBOL 98 \f "symbol"]-Amyloid Peptide Aggre  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,579A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/404,831  
FILING DATE: 14-MAR-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kara, Catherine J.  
REGISTRATION NUMBER: P41,106  
REFERENCE/DOCKET NUMBER: PPI-002CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-475-579A-4

Query Match 100.0%; Score 11; DB 2; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11  
DB 19 GSNKGAIIGLM 29

RESULT 15  
US-08-304-585-6  
Sequence 6, Application US/08304585  
Patent No. 5721106  
GENERAL INFORMATION:  
APPLICANT: Maggio, John E.  
APPLICANT: Mantyh, Patrick W.

;; TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND  
;; TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE  
;; NUMBER OF SEQUENCES: 12  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Mueiting, Raasch, Gebhardt & Schwappach, P.A.  
;; STREET: P.O. Box 581415  
;; CITY: Minneapolis  
;; STATE: MN  
;; COUNTRY: USA  
;; ZIP: 55458-1415  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentln Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/304,585  
;; FILING DATE: 12-SEP-1994  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mueiting, And M.  
;; REGISTRATION NUMBER: 33,977  
;; REFERENCE/DOCKET NUMBER: 110.00010120  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 612-305-1217  
;; TELEFAX: 612-305-1228  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 35 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: not relevant  
;; TOPOLOGY: not relevant  
;; MOLECULE TYPE: peptide  
;;  
US-08-304-585-6

Query Match 100.0%; Score 11; DB 1; Length 35;  
Best Local Similarity 100.0%; Pred.No. 2.5e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11  
|||||  
Db 25 GSNKGAIIGLM 35

Search completed: April 24, 2002, 09:22:29  
Job time: 248 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:23:15 ; Search time 38.65 Seconds  
(without alignments)  
21.680 Million cell updates/sec

Title: US-09-689-469-4

Perfect score: 11

Sequence: 1 GSNKGAIITGLM 11

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries.

Database :

1: PIR68:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 11    | 100.0       | 42     | 2     | PN0512      |
| 2          | 11    | 100.0       | 57     | 2     | E60045      |
| 3          | 11    | 100.0       | 57     | 2     | F60045      |
| 4          | 11    | 100.0       | 57     | 2     | G60045      |
| 5          | 11    | 100.0       | 57     | 2     | D60045      |
| 6          | 11    | 100.0       | 57     | 2     | A60045      |
| 7          | 11    | 100.0       | 57     | 2     | B60045      |
| 8          | 11    | 100.0       | 82     | 2     | P00438      |
| 9          | 11    | 100.0       | 695    | 1     | A49795      |
| 10         | 11    | 100.0       | 695    | 2     | A27485      |
| 11         | 11    | 100.0       | 695    | 2     | S00550      |
| 12         | 11    | 100.0       | 747    | 2     | JH0773      |
| 13         | 11    | 100.0       | 770    | 1     | ORH044      |
| 14         | 7     | 63.6        | 247    | 2     | B83880      |
| 15         | 6     | 54.5        | 130    | 2     | S63533      |
| 16         | 6     | 54.5        | 176    | 2     | B83837      |
| 17         | 6     | 54.5        | 184    | 1     | A30128      |
| 18         | 6     | 54.5        | 192    | 2     | T22142      |
| 19         | 6     | 54.5        | 205    | 2     | F72422      |
| 20         | 6     | 54.5        | 205    | 2     | G82358      |
| 21         | 6     | 54.5        | 219    | 2     | I52644      |
| 22         | 6     | 54.5        | 230    | 2     | B82456      |
| 23         | 6     | 54.5        | 234    | 2     | E70982      |
| 24         | 6     | 54.5        | 266    | 2     | T10609      |
| 25         | 6     | 54.5        | 290    | 2     | E86284      |
| 26         | 6     | 54.5        | 292    | 1     | A39871      |
| 27         | 6     | 54.5        | 297    | 1     | S31484      |
| 28         | 6     | 54.5        | 297    | 1     | S31486      |
| 29         | 6     | 54.5        | 297    | 1     | JN0773      |

|    |   |      |     |   |        |                    |
|----|---|------|-----|---|--------|--------------------|
| 30 | 6 | 54.5 | 297 | 2 | JC4500 | basic calponin - h |
| 31 | 6 | 54.5 | 297 | 2 | G02142 | smooth muscle cell |
| 32 | 6 | 54.5 | 327 | 2 | F82214 | galactoside ABC tr |
| 33 | 6 | 54.5 | 339 | 2 | S32624 | INDC1 protein - f  |
| 34 | 6 | 54.5 | 358 | 2 | T02903 | hypothetical prote |
| 35 | 6 | 54.5 | 382 | 2 | G85234 | hypothetical prote |
| 36 | 6 | 54.5 | 428 | 1 | A42971 | cytochrome P450ter |
| 37 | 6 | 54.5 | 442 | 1 | S36204 | probable beta-keto |
| 38 | 6 | 54.5 | 449 | 2 | T44643 | galactosyl transfe |
| 39 | 6 | 54.5 | 450 | 2 | E70590 | 3-phosphoshikimate |
| 40 | 6 | 54.5 | 462 | 2 | T34365 | hypothetical prote |
| 41 | 6 | 54.5 | 468 | 2 | T10595 | hypothetical prote |
| 42 | 6 | 54.5 | 512 | 2 | S28663 | cytochrome-c oxida |
| 43 | 6 | 54.5 | 541 | 1 | MMBYH2 | glucose transport  |
| 44 | 6 | 54.5 | 546 | 2 | S48313 | hexose transport p |
| 45 | 6 | 54.5 | 636 | 2 | C83724 | PTS system, beta-9 |

#### ALIGNMENTS

RESULT 1  
PN0512  
beta-amyloid protein - guinea pig (fragment)  
C:Species: Cavia porcellus (guinea pig)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
C:Accession: PN0512  
R:Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno  
Biochem. Biophys. Res. Commun. 193, 624-630, 1993  
A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra  
A:Reference number: PN0512; MWID:93290653  
A:Accession: PN0512  
A:Molecule type: protein  
A:Residues: 1-42 <SH1>  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
C:Keywords: alternative splicing; amyloid

Query Match 100.0%; Score 11; DB 2; Length 42;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIITGLM 11  
|||||  
DB 25 GSNKGAIITGLM 35

RESULT 2  
E60045  
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)  
C:Species: Ovis sp. (sheep)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045; MWID:92017079  
A:Accession: E60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56130  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 11; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 3.2e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIITGLM 11  
|||||  
DB 30 GSNKGAIITGLM 40

## RESULT 3

F60045

Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C&gt;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999

C:Accession: F60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A&gt;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; MID:92017079

A:Accession: F60045

A:Molecule type: mRNA

A:Residues: 1-57 &lt;JOH&gt;

A:Cross-references: EMBL:X56127; NID:q1895; PIDN:CA39592.1; PID:q1896

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

## Query Match

Best Local Similarity 100.0%; Score 11; DB 2; Length 57;  
Pred. No. 3.2e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11  
|||||

Db 30 GSNKGATIGLM 40

## RESULT 4

G60045

Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)

C:Species: Cavia porcellus (guinea pig)

C&gt;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995

C:Accession: G60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A&gt;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; MID:92017079

A:Accession: G60045

A:Molecule type: mRNA

A:Residues: 1-57 &lt;JOH&gt;

A:Cross-references: EMBL:X56126

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

## Query Match

Best Local Similarity 100.0%; Score 11; DB 2; Length 57;  
Pred. No. 3.2e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11  
|||||

Db 30 GSNKGATIGLM 40

## RESULT 5

D60045

Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C&gt;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995

C:Accession: D60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A&gt;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; MID:92017079

A:Accession: D60045

A:Molecule type: mRNA

A:Residues: 1-57 &lt;JOH&gt;

A:Cross-references: EMBL:X56124

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

## Query Match

Best Local Similarity 100.0%; Score 11; DB 2; Length 57;  
Pred. No. 3.2e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11  
|||||

Db 30 GSNKGATIGLM 40

## RESULT 6

A60045

Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)

C:Species: Canis lupus familiaris (dog)

C&gt;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995

C:Accession: A60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A&gt;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; MID:92017079

A:Accession: A60045

A:Molecule type: mRNA

A:Residues: 1-57 &lt;JOH&gt;

A:Cross-references: EMBL:X56125

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

## Query Match

Best Local Similarity 100.0%; Score 11; DB 2; Length 57;  
Pred. No. 3.2e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11  
|||||

Db 30 GSNKGATIGLM 40

## RESULT 7

B60045

Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)

C:Species: Ursus maritimus (polar bear)

C&gt;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999

C:Accession: B60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A&gt;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; MID:92017079

A:Accession: B60045

A:Molecule type: mRNA

A:Residues: 1-57 &lt;JOH&gt;

A:Cross-references: EMBL:X56128; NID:q2165; PIDN:CA39593.1; PID:q2166

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

## Query Match

Best Local Similarity 100.0%; Score 11; DB 2; Length 57;  
Pred. No. 3.2e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11  
|||||

Db 30 GSNKGATIGLM 40

## RESULT 8

PQ0438

Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C&gt;Date: 30-Sep-1993 #sequence\_revision 19-Oct-1995 #text\_change 19-Oct-1995

C:Accession: PQ0438; C60045

R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.

Biochem. Biophys. Res. Commun. 188, 905-911, 1992

A&gt;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs

A:Reference number: PQ0438; MID:93075180



A:Accession: P00438  
A:Molecule type: DNA  
A:Residues: 1-82 <DAY>  
A:Cross-references: GB:M83558; GB:M83657  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; MUID:92017079  
A:Accession: C60045  
A:Molecule type: mRNA  
A:Residues: 12-68 <JOH>  
A:Cross-references: EMBL:X56129  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 11; DB 2; Length 82;  
Best Local Similarity 100.0%; Pred. No. 4.2e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIIGLM 11  
|||||  
Db 41 GSNKGAIIIGLM 51

RESULT 9  
A49795  
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque  
C:Species: Macaca fascicularis (crab-eating macaque)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A49795  
R:Podlinsky, M.B.; Tolan, D.R.; Selkoe, D.J.  
Am. J. Pathol. 138, 1423-1435, 1991  
A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a  
A:Reference number: A49795; MUID:91273117  
A:Status: preliminary  
A:Accession: A49795  
A:Molecule type: mRNA  
A:Residues: 1-695 <POD>  
A:Cross-references: GB:M58727; NID:9342062; PIDN:AAA36829.1; PID:9342063  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase  
C:Keywords: alternative splicing

Query Match 100.0%; Score 11; DB 1; Length 695;  
Best Local Similarity 100.0%; Pred. No. 0.00022;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIIGLM 11  
|||||  
Db 621 GSNKGAIIIGLM 631

RESULT 10  
A27485  
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse  
N:Alternate names: proteinase nexin II  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 13-Aug-1999  
C:Accession: A27485; S19727; I49485  
R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.  
Biochem. Biophys. Res. Commun. 149, 665-671, 1987  
A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precu  
A:Reference number: A27485; MUID:88106489  
A:Accession: A27485  
A:Molecule type: mRNA  
A:Residues: 1-695 <YAM>  
A:Cross-references: GB:M18373; NID:9191568; PIDN:AAA37139.1; PID:9309085  
A:Experimental source: brain  
R:de Strooper, B.; van Leuven, F.; van den Berghe, H.  
Biochim. Biophys. Acta 1129, 141-143, 1991  
A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer  
A:Reference number: S19727; MUID:92096458

A:Accession: S19727  
A:Molecule type: mRNA  
A:Residues: 1-210 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>  
A:Cross-references: EMBL:X59379  
R:izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.  
Gene 112, 189-195, 1992  
A:Title: Positive and negative regulatory elements for the expression of the Alzheimer  
A:Reference number: I49485; MUID:92209998  
A:Accession: I49485  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-19 <RES>  
A:Cross-references: GB:D10603; NID:9220328; PIDN:BA01456.1; PID:9220329  
C:Genetics:  
A:Map position: 16c3  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase  
C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 100.0%; Score 11; DB 2; Length 695;  
Best Local Similarity 100.0%; Pred. No. 0.00022;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIIGLM 11  
|||||  
Db 621 GSNKGAIIIGLM 631

RESULT 11  
S00550  
Alzheimer's disease amyloid beta protein precursor - rat  
N:Alternate names: beta-A4 amyloid protein  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 13-Aug-1999  
C:Accession: S00550; A41245; A39820; S46251  
R:Shivers, B.D.; Halblach, C.; Muthaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.  
EMBO J. 7, 1365-1370, 1988  
A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat br  
A:Reference number: S00550; MUID:88312583  
A:Accession: S00550  
A:Molecule type: mRNA  
A:Residues: 1-695 <SHI>  
A:Cross-references: EMBL:X07648; NID:955616; PIDN:CA0488.1; PID:955617  
R:Schubert, D.; Schroeder, R.; Lacorbiere, M.; Saltch, T.; Cole, G.  
Science 241, 223-226, 1988  
A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan co  
A:Reference number: A41245; MUID:88264430  
A:Accession: A41245  
A:Molecule type: protein  
A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>  
A:Note: evidence for heparan sulfate attachment  
R:Hesse, L.; Behner, D.; Masters, C.L.; Multhaup, G.  
FEBS Lett. 349, 109-116, 1994  
A:Title: The beta-A4 amyloid precursor protein binding to copper.  
A:Reference number: S46251; MUID:94320627  
A:Contents: annotation; copper binding sites  
A:Note: rat peptides were isolated but not sequenced  
R:Potempa, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.  
J. Biol. Chem. 266, 8464-8469, 1991  
A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat b  
A:Reference number: A39820; MUID:91217087  
A:Accession: A39820  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 18-32 <POT>  
A:Experimental source: brain  
C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase  
C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein  
F:625-648/Domain: Transmembrane #status predicted <TMM>

Query Match 100.0%; Score 11; DB 2; Length 695;

Best Local Similarity 100.0%; Pred. No. 0.00022;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11  
DB 621 GSNKGATIGLM 631

RESULT 12  
JH0773  
Alzheimer's disease amyloid beta protein precursor - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C>Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 13-Aug-1999  
C:Accession: JH0773  
R:Okado, H.; Okamoto, H.  
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992  
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental  
A:Reference number: JH0773; M0ID:93129227  
A:Accession: JH0773  
A:Molecule type: mRNA  
A:Residues: 1-747 <OKA>  
A:Cross-references: GB:S52417; NID:q263150; PIDN:AAB24853.1; PID:q263151  
A:Experimental source: larva  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing; amyloid  
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 100.0%; Score 11; DB 2; Length 747;  
Best Local Similarity 100.0%; Pred. No. 0.00023;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11  
DB 673 GSNKGATIGLM 683

RESULT 13  
ORH04  
Alzheimer's disease amyloid beta protein precursor [validated] - human  
N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor X1a inhibi  
N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular  
protein precursor splice form APP(770)  
C:Species: Homo sapiens (man)  
C>Date: 30-Jun-1987 #sequence\_revision 28-Jul-1995 #text\_change 15-Sep-2000  
C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44  
4688; A28583; A29302; A60805; J10038; S06121; A60355; A5011; A38384; S29076; S38252; S3  
R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey  
Nucleic Acids Res. 17, 517-522, 1989  
A:Title: The preA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b  
A:Reference number: S02260; M0ID:89128427  
A:Accession: S02260  
A:Molecule type: DNA  
A:Residues: 1-288, 'V', 365-770 <LEM1>  
A:Cross-references: EMBL:X13466  
A:Note: alternative splice form APP(695)  
R:Lemaire, H.G.  
Submitted to the EMBL Data Library, November 1988  
A:Reference number: S05194  
A:Accession: S05194  
A:Molecule type: DNA  
A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>  
A:Cross-references: EMBL:X13466; NID:q35598; PIDN:CAA31830.1; PID:q871360  
A:Note: alternative splice form APP(695)  
R:Jia Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.  
Biochem. Biophys. Res. Commun. 159, 297-304, 1989  
A:Title: Characterization of the 5'-end region and the first two exons of the beta-prote  
A:Reference number: A32277; M0ID:89165870  
A:Accession: A32277  
A:Molecule type: DNA  
A:Residues: 1-75 <LAF>  
A:Cross-references: GB:M24546; GB:M24547; NID:q341202; PIDN:AAC13654.1; PID:q516074  
R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.

Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989  
A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simila  
A:Reference number: A33260; M0ID:89392030  
A:Accession: A33260  
A:Molecule type: DNA  
A:Residues: 656-737 <JOH>  
A:Cross-references: GB:M29270; NID:q178863; PIDN:AAA51768.1; PID:q178865  
R:Prelli, F.; Levy, E.; Van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B  
Biochem. Biophys. Res. Commun. 170, 301-307, 1990  
A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid  
A:Reference number: A35486; M0ID:90321244  
A:Accession: A35486  
A:Molecule type: DNA  
A:Residues: 672-710 <PRE1>  
A:Note: 693-gln was found in DNA isolated from HCHWA-D patients  
R:Yoshikai, S.I.; Sasaki, H.; Don-ura, K.; Furuya, H.; Sasaki, Y.  
Gene 87, 257-263, 1990  
A:Title: Genomic organization of the human amyloid beta-protein precursor gene.  
A:Reference number: I39451; M0ID:90236318  
A:Accession: I39452  
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
A:Molecule type: DNA  
A:Residues: 1-770 <IOS1>  
A:Cross-references: GB:M33112; NID:q178613; PIDN:AAB59502.1; PID:q178616  
A:Accession: I39451  
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
A:Molecule type: DNA  
A:Residues: 1-530, 'QWMPVYPAFWFAKVGK' <YOS2>  
A:Cross-references: GB:M34875; NID:q178608; PIDN:AAB59501.1; PID:q178615  
R:Yoshikai, S.I.; Sasaki, H.; Don-ura, K.; Furuya, H.; Sasaki, Y.  
Gene 102, 291-292, 1991  
A:Reference number: A59020; M0ID:91340168  
A:Accession: I39453  
A:Contents: annotation; extratum  
A:Note: revised physical map for reference I39451  
R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Du  
Science 248, 1124-1126, 1990  
A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemo  
A:Reference number: I39453; M0ID:90260663  
A:Accession: I39453  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 656-737 <LEV>  
A:Cross-references: GB:M37896; NID:q178618; PIDN:AAA51727.1; PID:q178620  
A:Note: a mutation with 693-gln is presented  
R:Wurrell, J.; Farlow, M.; Chetti, B.; Benson, M.D.  
Science 254, 97-99, 1991  
A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe  
A:Reference number: I59562; M0ID:92022553  
A:Accession: I59562  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 689-716, 'F', 718-737 <MUR>  
A:Cross-references: GB:S57665; NID:q236720; PIDN:AAB19991.1; PID:q236721  
R:Kamino, K.; Orr, H.T.; Payant, H.; Wilsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anders  
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Mart  
Am. J. Hum. Genet. 51, 998-1014, 1992  
A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t  
A:Reference number: A44017; M0ID:93055397  
A:Accession: A44017  
A:Molecule type: DNA  
A:Residues: 687-692, 'G', 694-718 <KAM1>  
A:Cross-references: GB:S45135; NID:q257377; PIDN:AAB23645.1; PID:q257378  
A:Experimental source: familial Alzheimer disease family SB  
A:Note: sequence extracted from NCBI backbone (NCBIRP:115374)  
A:Accession: B44017  
A:Molecule type: DNA  
A:Residues: 687-718 <KAM2>  
A:Cross-references: GB:S45136; NID:q257379; PIDN:AAB23646.1; PID:q257380  
A:Experimental source: familial Alzheimer disease family LIT  
A:Note: sequence extracted from NCBI backbone (NCBIRP:115376)  
R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.  
Nature 325, 733-736, 1987

A>Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface  
 A:Reference number: A03134; MUID:87144572  
 A:Accession: A03134  
 A:Molecule type: mRNA  
 A:Residues: 1-288, 'V', 365-770 <KAN>  
 A:Cross-References: GB:Y00264; NID:928525; PIDN:CAA6374.1; PID:928526  
 A:Note: alternative splice form APP(695)  
 R:Robkiss, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987  
 A>Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular  
 A:Reference number: A29030; MUID:87231971  
 A:Accession: A29030  
 A:Molecule type: mRNA  
 A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>  
 A:Cross-References: GB:M16765; NID:9178539; PIDN:AAA51722.1; PID:9178540  
 A:Note: the authors translated the codon GAG for residue 647 as Asp  
 R:Goldhaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.  
 Science 235, 877-880, 1987  
 A>Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid  
 A:Reference number: A47584; MUID:87120328  
 A:Accession: A47584  
 A:Molecule type: mRNA  
 A:Residues: 674-756, 'S', 758-770 <GOL>  
 A:Cross-References: GB:M15533; NID:9178706; PIDN:AAA5540.1; PID:9178707  
 A:Experimental source: brain  
 R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke  
 Science 235, 880-884, 1987  
 A>Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th  
 A:Reference number: A47585; MUID:87120329  
 A:Accession: A47585  
 A:Molecule type: mRNA  
 A:Residues: 674-703 <TRAN1>  
 A:Cross-References: GB:M15532; NID:9177957; PIDN:AAA51564.1; PID:9177958  
 R:Dykes, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Moelle  
 EMBO J. 7, 949-957, 1988  
 A>Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec  
 A:Reference number: S02638; MUID:88296437  
 A:Accession: S02638  
 A:Molecule type: mRNA  
 A:Residues: 672-678 <DYR>  
 R:Tanzi, R.E.; McClatchey, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve  
 Nature 331, 528-530, 1988  
 A>Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat  
 A:Reference number: S00707; MUID:88122640  
 A:Accession: S00707  
 A:Molecule type: mRNA  
 A:Residues: 286-344, 'I', 365-366 <TAN2>  
 A:Cross-References: EMBL:X06982; NID:928817; PIDN:CAA30042.1; PID:9292612  
 A:Experimental source: promyelocytic leukemia cell line HL60  
 A:Note: alternative splice form APP(751)  
 R:Ponte, P.; Gonzalez-Demilte, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; De  
 Nature 331, 525-527, 1988  
 A>Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit  
 A:Reference number: S00925; MUID:88122639  
 A:Accession: S00925  
 A:Molecule type: mRNA  
 A:Residues: 1-344, 'I', 365-770 <PO2>  
 A:Cross-References: GB:X06989; EMBL:Y00297; NID:928720; PIDN:CAA30050.1; PID:928721  
 A:Note: alternative splice form APP(751)  
 R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.  
 Nature 331, 530-532, 1988  
 A>Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor  
 A:Reference number: A38949; MUID:88122641  
 A:Accession: A38949  
 A:Molecule type: mRNA  
 A:Residues: 287-367 <KIT>  
 A:Cross-References: NID:928816; PIDN:CAA30041.1; PID:9292611  
 A:Experimental source: glioblastoma cell line  
 A:Note: alternative splice form APP(770)  
 R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton  
 Brain Res. Mol. Brain Res. 4, 121-131, 1988  
 A>Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three p  
 A:Reference number: A30320

A:Accession: A30320  
 A>Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 284-288, 'V', 365-770 <VIT1>  
 A:Accession: B30320  
 A>Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 122-288, 'V', 365-770 <VIT2>  
 A:Accession: C30320  
 A>Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 606-770 <VIT3>  
 R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta,  
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988  
 A>Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease  
 A:Reference number: A31087; MUID:88124954  
 A:Accession: A31087  
 A:Molecule type: mRNA  
 A:Residues: 507-770 <ZAI>  
 A:Cross-References: GB:M18734; NID:9178572; PIDN:AAA51726.1; PID:9178573  
 A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue  
 8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue  
 A:Note: the cited Genbank accession number, J03594, is not in release 101.0  
 R:Masters, C.L.; Multhaup, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther,  
 Query Match 100.0%; Score 11; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 0.00024;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GSNKGATIGLM 11  
 |||||  
 Db 696 GSNKGATIGLM 706  
 RESULT 14  
 B3880  
 3-oxoacyl-(acyl-carrier protein) reductase BH1842 [imported] - Bacillus halodurans (s  
 C:Species: Bacillus halodurans  
 C>Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 31-Dec-2000  
 C:Accession: B83880  
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H  
 Nucleic Acids Res. 28, 4317-4331, 2000  
 A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a  
 A:Reference number: A83650; MUID:20263314  
 A:Accession: B83880  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-247 <STO>  
 A:Cross-References: GB:AP001513; GB:BA000004; NID:910174345; PIDN:BA805561.1; GSPDB:G  
 A:Experimental source: strain C-125  
 C:Genetics:  
 A:Gene: BH1842  
 C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
 Query Match 63.6%; Score 7; DB 2; Length 247;  
 Best Local Similarity 100.0%; Pred. No. 1.6;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 KGATIGL 10  
 |||||  
 Db 159 KGATIGL 165  
 RESULT 15  
 S63533  
 profilin basic isoform - Entamoeba histolytica  
 C:Species: Entamoeba histolytica  
 C>Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 26-Aug-1999  
 C:Accession: S63533; S63474  
 R:Binder, M.; Ortnier, S.; Erben, H.; Scheiner, O.; Wiedermann, G.; Valenta, R.; Duch  
 Eur. J. Biochem. 233, 976-981, 1995  
 A>Title: The basic isoform of profilin in pathogenic Entamoeba histolytica: cDNA clon

A:Reference number: S63474; MUID:96085166  
A:Accession: S63533  
A:Molecule type: mRNA  
A:Residues: 1-130 <BIN>  
A:Cross-references: EMBL:X90911; NID:g1070154; PID:g1070155  
A:Accession: S63474  
A:Molecule type: protein  
A:Residues: 74-84;86-94 <BIW>  
C:Superfamily: profilin  
C:Keywords: actin binding

Query Match 54.5%; Score 6; DB 2; Length 130;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 GATIGL 10  
|||||  
DB 20 GATIGL 25

Search completed: April 24, 2002, 09:23:16  
Job time: 245 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:24:53 ; Search time 21.46 Seconds

(without alignments)  
18.794 Million cell updates/sec

Title: US-09-689-469-4  
Perfect score: 11  
Sequence: 1 GSNKGATIGLM 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 100059 seqs, 36664827 residues

Word size: 0

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID         | Description        |
|------------|-------|-------------|--------|------------|--------------------|
| 1          | 11    | 100.0       | 57     | A4_PIG     | Q29023 sus scrofa  |
| 2          | 11    | 100.0       | 57     | A4_URSWA   | Q29149 ursus marit |
| 3          | 11    | 100.0       | 58     | A4_CANFA   | Q28280 canis fam1  |
| 4          | 11    | 100.0       | 58     | A4_RABIT   | Q28748 oryctolagus |
| 5          | 11    | 100.0       | 58     | A4_SHEEP   | Q28757 ovis aries  |
| 6          | 11    | 100.0       | 59     | A4_BOVIN   | Q28053 bos taurus  |
| 7          | 11    | 100.0       | 751    | A4_SAISC   | Q95241 salmirl sci |
| 8          | 11    | 100.0       | 770    | A4_HUMAN   | P05067 homo sapien |
| 9          | 11    | 100.0       | 770    | A4_MOUSE   | P12023 mus musculu |
| 10         | 11    | 100.0       | 770    | A4_RAT     | P08592 rattus norv |
| 11         | 100.0 | 770         | 1      | PROF_ENTHT | P49330 entamoeba h |
| 12         | 6     | 54.5        | 130    | MP20_DROME | P14318 drosophila  |
| 13         | 6     | 54.5        | 184    | NP25_MOUSE | Q91498 mus musculu |
| 14         | 6     | 54.5        | 199    | NP25_RAT   | Q91498 mus musculu |
| 15         | 6     | 54.5        | 219    | NP25_MOUSE | Q91498 mus musculu |
| 16         | 6     | 54.5        | 262    | FLGG_RHIME | Q52946 rhizobium m |
| 17         | 6     | 54.5        | 282    | NP25_HUMAN | Q91498 mus musculu |
| 18         | 6     | 54.5        | 287    | LEP4_LEGPN | Q68433 legionella  |
| 19         | 6     | 54.5        | 297    | CLP1_HUMAN | P26332 gallus gall |
| 20         | 6     | 54.5        | 297    | CLP1_MOUSE | P51911 homo sapien |
| 21         | 6     | 54.5        | 297    | CLP1_MOUSE | Q08091 sus scrofa  |
| 22         | 6     | 54.5        | 297    | CLP1_MOUSE | Q08092 sus scrofa  |
| 23         | 6     | 54.5        | 321    | EUM1_EURMA | P25780 euroglyphus |
| 24         | 6     | 54.5        | 339    | IC11_TRIHA | P34055 trichoderma |
| 25         | 6     | 54.5        | 391    | CPSD_STRAG | P34055 trichoderma |
| 26         | 6     | 54.5        | 428    | CPYL_PSESP | P34055 trichoderma |
| 27         | 6     | 54.5        | 429    | ARO4_CORGL | Q92470 corynebacte |
| 28         | 6     | 54.5        | 442    | CEM1_YEAST | P39525 saccharomyc |
| 29         | 6     | 54.5        | 450    | ARO4_MYCTU | P22487 mycobacteri |
| 30         | 6     | 54.5        | 476    | COX1_PLAFA | Q02766 plasmodium  |
| 31         | 6     | 54.5        | 541    | HXT2_YEAST | P23585 saccharomyc |
| 32         | 6     | 54.5        | 543    | SGLT_VIBPA | P61699 vibrio para |
| 33         | 6     | 54.5        | 546    | HXT0_YEAST | P43581 saccharomyc |

|    |   |      |     |   |            |                    |
|----|---|------|-----|---|------------|--------------------|
| 34 | 6 | 54.5 | 661 | 1 | RDGC_DROME | P40421 drosophila  |
| 35 | 6 | 54.5 | 764 | 1 | SYER_HELPU | 092f8 helicobacte  |
| 36 | 6 | 54.5 | 813 | 1 | GYRA_TREPA | 083051 treponema p |
| 37 | 6 | 54.5 | 837 | 1 | NCM2_MOUSE | Q35136 mus musculu |
| 38 | 5 | 45.5 | 47  | 1 | RK2_WHEAT  | P11534 triticum ae |
| 39 | 5 | 45.5 | 50  | 1 | VG38_BPM15 | 005248 mycobacteri |
| 40 | 5 | 45.5 | 60  | 1 | YH05_VACCV | P17356 vaccinia v1 |
| 41 | 5 | 45.5 | 89  | 1 | RS16_MYCGE | P47684 mycoplasma  |
| 42 | 5 | 45.5 | 114 | 1 | PFDE_SCHPO | 014450 schizosacch |
| 43 | 5 | 45.5 | 125 | 1 | RSBE_ARCFU | 028130 archaeglob  |
| 44 | 5 | 45.5 | 126 | 1 | RL26_SCHPO | P78946 schizosacch |
| 45 | 5 | 45.5 | 127 | 1 | RSBE_PYRHO | 058830 pyrococcus  |

## ALIGNMENTS

| RESULT | 1  | STANDARD                                | PRT | 57 AA.                            |
|--------|--|---|-----|-----------------------------------|
| AC     | A4_PIG   |   |     |                                   |
| AC     | Q29023;  |   |     |                                   |
| DT     | 01-NOV-1997 (Rel. 35, Created)   |   |     |                                   |
| DT     | 01-NOV-1997 (Rel. 35, Last sequence update)  |   |     |                                   |
| DT     | 20-AUG-2001 (Rel. 40, Last annotation update)  |   |     |                                   |
| DE     | ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).  |   |     |                                   |
| GN     | APP.   |   |     |                                   |
| OS     | Sus scrofa (Pig).  |   |     |                                   |
| OC     | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |   |     |                                   |
| OC     | Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  |   |     |                                   |
| OX     | NCBI_TaxID=9823;   |   |     |                                   |
| RP     | SEQUENCE FROM N.A.   |   |     |                                   |
| RC     | TIS00E-Brain;  |   |     |                                   |
| RX     | MEDLINE=92017079; PubMed=1656157;  |   |     |                                   |
| RA     | Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;   |   |     |                                   |
| RT     | "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis."   |   |     |                                   |
| RL     | Brain Res. Mol. Brain Res. 10:299-305(1991).   |   |     |                                   |
| CC     | - FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO G(O) (BY SIMILARITY).  |   |     |                                   |
| CC     | - INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).  |   |     |                                   |
| CC     | - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.   |   |     |                                   |
| CC     | - SIMILARITY: BELONGS TO THE APP FAMILY.   |   |     |                                   |
| CC     | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ). |   |     |                                   |
| CC     | EMBL: X56127; CA39592.1; -   |   |     |                                   |
| DR     | HSSP: P05067; IAML.  |   |     |                                   |
| DR     | InterPro: IPR001868; A4_APP.   |   |     |                                   |
| DR     | PROSITE: PS00319; A4_EXTRA; PARTIAL.   |   |     |                                   |
| DR     | PROSITE: PS00320; A4_INTRA; PARTIAL.   |   |     |                                   |
| KW     | Glycoprotein; Amyloid; Neurone; Transmembrane.   |   |     |                                   |
| FT     | NON_TER  | 1                                       |     |                                   |
| FT     | CHAIN  | 6                                       | 48  | BETA-AMYLOID PROTEIN (POTENTIAL). |
| FT     | DOMAIN   | <1                                      | 33  | EXTRACELLULAR (POTENTIAL).        |
| FT     | TRANSMEM   | 34                                      | 57  | POTENTIAL.                        |
| FT     | NON_TER  | 57                                      |     |                                   |
| SO     | SEQUENCE   | 57 AA; 6172 MW; 84209D88EBA82DFA CRC64; |     |                                   |

Query Match 100.0%; Score 11; DB 1; Length 57;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 11; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GSNKGATIGLM 11

Db 30 GSNKGAIIGLM 40

RESULT 2

AC\_URSMA STANDARD: PRT: 57 AA.

ID A4\_URSMA

AC Q29149;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, last sequence update)

DT 30-MAY-2000 (Rel. 39, last annotation update)

DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID

PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).

GN APP.

OS Ursus maritimus (Polar bear) (Thalassos maritimus).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.

NCBI\_TaxID=29073;

OX NCBI\_TaxID=29073;

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=92017079; Pubmed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid

peptide in dog, polar bear and five other mammals by cross-species

polymers chain reaction analysis."

RT Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -1 FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO

INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN

G(C) (BY SIMILARITY).

CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1 SIMILARITY: BELONGS TO THE APP FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation

at the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial

entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC

DR EMBL: X56128; CAA39590.1; -.

DR HSP: P05067; IAML.

DR InterPro: IPR001868; A4\_APP.

DR PROSITE: PS00319; A4\_EXTRA; PARTIAL.

DR PROSITE: PS00320; A4\_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON\_TER 1 1

FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).

FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 34 57 POTENTIAL.

FT NON\_TER 57 57

FT SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

SO

QY 1 GSNKGAIIGLM 11

Db 30 GSNKGAIIGLM 40

Query Match 100.0%; Score 11; DB 1; Length 57;

Best local Similarity 100.0%; Pred. No. 1.3e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3

ID A4\_CANFA STANDARD: PRT: 58 AA.

AC Q28280;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, last sequence update)

DT 30-MAY-2000 (Rel. 39, last annotation update)

DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID

PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).

GN APP.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

NCBI\_TaxID=9615;

OX NCBI\_TaxID=9615;

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RX MEDLINE=92017079; Pubmed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid

peptide in dog, polar bear and five other mammals by cross-species

polymers chain reaction analysis."

RT Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -1 FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO

INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN

G(C) (BY SIMILARITY).

CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1 SIMILARITY: BELONGS TO THE APP FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation

at the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial

entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC

DR EMBL: X56125; CAA39590.1; -.

DR HSP: P05067; IAML.

DR InterPro: IPR001868; A4\_APP.

DR PROSITE: PS00319; A4\_EXTRA; PARTIAL.

DR PROSITE: PS00320; A4\_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON\_TER 1 1

FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).

FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 35 58 POTENTIAL.

FT NON\_TER 58 58

FT SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;

SO

QY 1 GSNKGAIIGLM 11

Db 31 GSNKGAIIGLM 41

Query Match 100.0%; Score 11; DB 1; Length 58;

Best local Similarity 100.0%; Pred. No. 1.3e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4

ID A4\_RABIT STANDARD: PRT: 58 AA.

AC Q28748;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, last sequence update)

DT 20-AUG-2001 (Rel. 40, last annotation update)

DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID

PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).

GN APP.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

NCBI\_TaxID=9986;

OX NCBI\_TaxID=9986;

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=92017079; Pubmed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid

peptide in dog, polar bear and five other mammals by cross-species

```

RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X56129; CAA39594.1; -.
DR HSSP: P05067; IAML.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

```

```

Query Match      100.0%; Score 11; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 GSNKGAIITGLM 11
   |||||||
Db 30 GSNKGAIITGLM 40

```

```

RESULT 5
A4_SHEEP          STANDARD;          PRT;          58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----

```

```

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X56130; CAA39595.1; -.
DR HSSP: P05067; IAML.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

```

```

Query Match      100.0%; Score 11; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 GSNKGAIITGLM 11
   |||||||
Db 30 GSNKGAIITGLM 40

```

```

RESULT 6
A4_BOVIN          STANDARD;          PRT;          59 AA.
ID A4_BOVIN
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X56124; CAA39589.1; -.
DR EMBL: X56126; CAA39591.1; -.
DR HSSP: P05067; IAML.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.

```

```

FT  NON_TER      1      1      BETA-AMYLOID PROTEIN (POTENTIAL).
FT  CHAIN         7      49      EXTRACELLULAR (POTENTIAL).
FT  DOMAIN        <1      34      POTENTIAL.
FT  TRANSMEM      35      58      CYTOPLASMIC (POTENTIAL).
FT  DOMAIN        59      >59
FT  NON_TER      59      59
SQ  SEQUENCE      59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match      100.0%; Score 11; DB 1; Length 59;
Best Local Similarity 100.0%; Pred No. 1.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 GSNKGATIGLM 11
    |||
Db  31 GSNKGATIGLM 41

RESULT 7
A4_SAISC STANDARD; PRT; 751 AA.
AC 095241;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR [CONTAINS: BETA-
DE AMYLOID PROTEIN (BETA-APP) (A-BETA)].
GN APP.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver, and Kidney;
RX MEDLINE=96108492; PubMed=8532114;
RA Levy E., Amornil A., Frangione B., Walker L.C.;
RT "beta-amyloid precursor protein gene in squirrel monkeys with
RL cerebral amyloid angiopathy.";
RT Neurobiol. Aging 16:805-808(1995).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
CC EMBL: S81024; AAD14347.1; -
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PRO0203; AMYLOIDA4.
DR PRINTS: PRO0204; BETAAMYLOID.
DR PRINTS: PRO0759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.

```

```

DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
KW Signal; Serine protease inhibitor.
FT SIGNAL        1      17
FT CHAIN         18      751
FT DOMAIN        653      695      A4 PROTEIN.
FT TRANSMEM      18      680      BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN        681      704      EXTRACELLULAR (POTENTIAL).
FT TRANSMEM      705      751      POTENTIAL.
FT DOMAIN        287      345      CYTOPLASMIC (POTENTIAL).
FT SITE          740      743      BPTI/KUNITZ INHIBITOR.
FT ACT_SITE      301      302      CLATHRIN-BINDING (BY SIMILARITY).
FT DISULFID      291      341      REACTIVE BOND.
FT DISULFID      300      324      BY SIMILARITY.
FT DISULFID      316      337      BY SIMILARITY.
FT CARBOHYD      523      523      N-LINKED (GLCNAC... ) (PROBABLE).
FT CARBOHYD      552      552      N-LINKED (GLCNAC... ) (PROBABLE).
SQ  SEQUENCE      751 AA; 84893 MW; 6C3E431089569049 CRC64;

Query Match      100.0%; Score 11; DB 1; Length 751;
Best Local Similarity 100.0%; Pred No. 9.7e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 GSNKGATIGLM 11
    |||
Db  677 GSNKGATIGLM 687

RESULT 8
A4_HUMAN STANDARD; PRT; 770 AA.
AC P05067; P09000; 016011;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR (PROTEASE NEXIN-II)
DE (PN-II) (APP) [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)].
GN APP OR A4 OR CVAP OR ADL.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=87144572; PubMed=2881207;
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RT cell-surface receptor.";
RT Nature 325:733-736(1987).
RL Nature 325:733-736(1987).
RN
RN SEQUENCE FROM N.A.
RP MEDLINE=88122639; PubMed=2893289;
RX Ponte P., Gonzalez-Dewhilt P., Schilling J., Miller J., Hsu D.,
RX Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RX Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine
RT proteinase inhibitors.";
RT Nature 331:525-527(1988).
RL Nature 331:525-527(1988).
RN
RN SEQUENCE FROM N.A.
RX MEDLINE=89128427; PubMed=2783775;
RA Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA Unterbeck A.G., Beyreuther K., Mueller-Hill B.;
RT "The preA4(695) precursor protein of Alzheimer's disease A4 amyloid
RT is encoded by 16 exons.";
RL Nucleic Acids Res. 17:517-522(1989).
RN
RN SEQUENCE FROM N.A.
RP MEDLINE=97263807; PubMed=9108164;
RX Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,

```



RA Saito M., Tsukuni S., Sakaki Y.;  
 RT "A novel method for making nested deletions and its application for  
 RT sequencing of a 300 kb region of human APP locus."; *Nucleic Acids Res.* 25:1802-1808(1997).  
 RL [15]  
 RN SEQUENCE OF 286-345 AND 365-366 FROM N.A.  
 RX MEDLINE=88122640; PubMed=2893290;  
 RA Tanzi R.E., McClatchey A.I., Lampertl E.D., Villa-Komaroff L.,  
 RA Gusella J.F., Neve R.L.;  
 RT "Protease inhibitor domain encoded by an amyloid protein precursor  
 RT mRNA associated with Alzheimer's disease."; *Nature* 331:528-530(1988).  
 RL [6]  
 RN SEQUENCE OF 287-367 FROM N.A.  
 RX MEDLINE=88122641; PubMed=2893291;  
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;  
 RT "Novel precursor of Alzheimer's disease amyloid protein shows  
 RT protease inhibitory activity."; *Nature* 331:530-533(1988).  
 RL [17]  
 RN SEQUENCE OF 284-289 AND 365-370 FROM N.A.  
 RX MEDLINE=87231971; PubMed=3035574;  
 RA Kobayashi N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;  
 RT "Molecular cloning and characterization of a cDNA encoding the  
 RT cerebrovascular and the neuritic plaque amyloid peptides."; *Proc. Natl. Acad. Sci. U.S.A.* 84:4190-4194(1987).  
 RL [8]  
 RN SEQUENCE OF 507-770 FROM N.A.  
 RX MEDLINE=88124954; PubMed=2893379;  
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,  
 RA Marotta C.A.;  
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer  
 RT disease brain: coding and noncoding regions of the fetal precursor  
 RT mRNA are expressed in the cortex."; *Proc. Natl. Acad. Sci. U.S.A.* 85:929-933(1988).  
 RL [9]  
 RN SEQUENCE OF 672-681.  
 RX MEDLINE=88035004; PubMed=3312495;  
 RA Partridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,  
 RA Tountellotte W.W., Huebner V., Shively J.E.;  
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition  
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical  
 RT microvessels."; *J. Neurochem.* 49:1394-1401(1987).  
 RL [10]  
 RN SEQUENCE OF 739-770 FROM N.A.  
 RX MEDLINE=90236318; PubMed=2110105;  
 RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;  
 RT "Genomic organization of the human amyloid beta-protein precursor  
 RT gene."; *Gene* 87:257-263(1990).  
 RL [11]  
 RN SEQUENCE OF 1-10 FROM N.A.  
 RP TISSUE=Liver;  
 RC "Purification of protease nexin II from human fibroblasts."; *J. Biol. Chem.* 262:8508-8514(1987).  
 RL [13]  
 RN IDENTITY OF APP WITH NEXIN-II.  
 RP MEDLINE=89384866; PubMed=2506449;  
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,  
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,  
 RA Sinha S.;  
 RT "The secreted form of the Alzheimer's amyloid precursor protein with  
 RT the Kunitz domain is protease nexin-II."; *Nature* 341:144-147(1989).  
 RL [14]  
 RN PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.  
 RP MEDLINE=90211252; PubMed=1969731;  
 RX Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;  
 RA "Protease-specificity of Kunitz inhibitor domain of Alzheimer's  
 RT disease amyloid protein precursor."; *Biochem. Biophys. Res. Commun.* 167:716-721(1990).  
 RL [15]  
 RN COMPLEX WITH G(O).  
 RX MEDLINE=9318965; PubMed=8446172;  
 RA Nishimoto I., Okamoto T., Matsura Y., Takahashi S., Okamoto T.,  
 RA Murayama Y., Ogata E.;  
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding  
 RT protein G(O)."; *Nature* 362:75-79(1993).  
 RL [16]  
 RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.  
 RP MEDLINE=9215582; PubMed=10201399;  
 RX Rosjohn J., Cappai R., Fell S.C., Henry A., McKinstry W.J.,  
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,  
 RA Parker M.W.;  
 RT "Crystal structure of the N-terminal, growth factor-like domain of  
 RT Alzheimer amyloid precursor protein."; *Nat. Struct. Biol.* 6:327-331(1999).  
 RL [17]  
 RN X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.  
 RX MEDLINE=91104913; PubMed=2125487;  
 RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrodt C., Kossiakof A.A.;  
 RT "X-ray crystal structure of the protease inhibitor domain of  
 RT Alzheimer's amyloid beta-protein precursor."; *Biochemistry* 29:10018-10022(1990).  
 RL [18]  
 RN STRUCTURE BY NMR OF 289-344.  
 RP MEDLINE=92031488; PubMed=1718421;  
 RX Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayley R.M.,  
 RA Kamack M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,  
 RA Tamburini P.P.;  
 RT "Sequential NMR resonance assignment and structure determination of  
 RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid  
 RT precursor protein."; *Biochemistry* 30:10467-10478(1991).  
 RL [19]  
 RN STRUCTURE BY NMR OF 672-699.  
 RX MEDLINE=94281210; PubMed=7516706;  
 RA Talaous J., Marchlewski K.J., Klopman G., Zagorski M.G.;  
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide."; *Biochemistry* 33:7788-7796(1994).  
 RL [20]  
 RN STRUCTURE BY NMR OF 696-706.  
 RX MEDLINE=97128622; PubMed=8973180;  
 RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;  
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in  
 RT membrane-mimicking environment."; *Biochemistry* 35:16094-16104(1996).  
 RL [21]  
 RN STRUCTURE BY NMR OF 672-711.  
 RP MEDLINE=98359783; PubMed=9693002;  
 RX Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;  
 RA "Solution structure of amyloid beta-peptide(1-40) in a water-miscible  
 RT environment. Is the membrane-spanning domain where we think it is?"; *Biochemistry* 37:11064-11077(1998).  
 RL [22]  
 RN STRUCTURE BY NMR OF 672-699.  
 RP MEDLINE=20400066; PubMed=10940222;  
 RX Poulsen S.-A., Watson A.A., Craik D.J.;  
 RA "Solution structures in aqueous SDS micelles of two amyloid beta  
 RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage  
 RT site."; *J. Struct. Biol.* 130:142-152(2000).  
 RL [23]  
 RN SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.  
 RP MEDLINE=88296437; PubMed=2900137;

```

RA Dykx T, Weidemann A., Muthaupt G., Salbaum J.M., Lemaire H.-G.,
RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.:
RA "Identification, transmembrane orientation and biogenesis of the
RA amyloid A4 precursor of Alzheimer's disease.",
RA EMBO J. 7:949-957(1988).
RL [24]
RN REVIEW.
RP MEDLINE=92271194; PubMed=1589757;
RX Kosik K.S.;
RT "Alzheimer's disease: a cell biological perspective.",
RL Science 256:780-783(1992).
RN [25]

Query Match 100.0%; Score 11; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. NO. 9.9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKAIGILM 11
DB 696 GSNKAIGILM 706

RESULT 9
ID A4_MOUSE STANDARD: PRT; 770 AA.
AC P12023:
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR
DE (AMYLOIDOGENIC GLYCOPROTEIN) (AG).
GN App.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-269 AND 365-770 FROM N.A.
RC STRAIN=BA/B.C.; TISSUE=Brain;
RC MEDLINE=92096458; PubMed=1756177;
RA de Strooper B., van Leuven F., van den Bergh H.;
RT "The amyloid beta protein precursor or protease nexin II from mouse
RL Biochim. Biophys. Acta 1129:141-143(1991).
RN [2]
RP SEQUENCE OF 1-269 AND 365-770 FROM N.A.
RC TISSUE=Brain;
RC MEDLINE=88106489; PubMed=3322280;
RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
RT "Complementary DNA for the mouse homolog of the human amyloid beta
RL protein precursor.",
RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
RN [3]
RP REVISIONS.
RA Yamada T.;
RL submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 289-364 FROM N.A.
RC STRAIN=CD-1; TISSUE=Placenta;
RC MEDLINE=89345111; PubMed=2569710;
RA Fukuchi K., Martin G.M., Deeb S.S.;
RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
RL precursor of Mus domestica."
RL Nucleic Acids Res. 17:5396-5396(1989).
RN [5]
RP SEQUENCE OF 1-19 FROM N.A.
RC MEDLINE=92209998; PubMed=1555768;
RA Izumi R., Yamada T., Yoshikai S.T., Sasaki H., Hattori M.,
RA Sakai Y.;
RT "Positive and negative regulatory elements for the expression of the
RL Alzheimer's disease amyloid precursor-encoding gene in mouse.",
RL Gene 112:189-195(1992).
RN [6]

```

|    |  |
|----|--|
| CC | SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.   |
| RC | TISSUE=Brain, and Kidney;  |
| RX | MEDLINE=69149813; PubMed=2493250.  |
| RA | Yamada T., Sakaki H., Dohura K., Goto I., Sakaki Y.,   |
| RT | "Structure and expression of the alternatively-spliced forms of mRNa<br>for the mouse homolog of Alzheimer's disease amyloid beta protein<br>precursor."   |
| RL | Biochem. Biophys. Res. Commun. 158:906-912(1989).  |
| CC | -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.   |
| CC | -I- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695),<br>APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE<br>SPLICING.  |
| CC | -I- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS<br>WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND<br>LIVER.   |
| CC | -I- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION<br>WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC<br>RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE<br>NEXT MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF<br>PHOSPHORYLATION (BY SIMILARITY)   |
| CC | -I- SIMILARITY: BELONGS TO THE APP FAMILY.   |
| CC | -I- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.   |
| CC | -----  |
| CC | This SWISS-PROT entry is copyright. It is produced through a collaboration<br>between the Swiss Institute of Bioinformatics and the EMBL Outstation -<br>the European Bioinformatics Institute. There are no restrictions on its<br>use by non-profit institutions as long as its content is in no way<br>modified and this statement is not removed. Usage by and for commercial<br>entities requires a license agreement (See <a href="http://www.isb.ch/announce/">http://www.isb.ch/announce/</a><br>or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ). |
| CC | -----  |
| DR | EMBL; X59379; -- NOT_ANNOTATED_CDS.  |
| DR | EMBL; M18373; AAA37139.1; --   |
| DR | EMBL; X15210; CA33280.1; --  |
| DR | EMBL; D10603; BAA01456.1; --   |
| DR | EMBL; M24397; AAA39929.1; --   |
| DR | PIR; A27485; A27485.   |
| DR | PIR; S04855; S04855.   |
| DR | PIR; S19727; S19727.   |
| DR | MGI; MGI:88059; App.   |
| DR | InterPro; IPRO01868; A4_APP.   |
| DR | InterPro; IPRO02223; Kunitz_BPTI.  |
| DR | Pfam; PF00177; A4_EXTRA; 1.  |
| DR | Pfam; PF00014; Kunitz_BPTI; 1.   |
| DR | PRINTS; PR00203; AMYLOIDA4.  |
| DR | PRINTS; PR00204; BETAAMYLOID.  |
| DR | PRINTS; PR00759; BASICPTASE.   |
| DR | SMART; SM00006; A4_EXTRA; 1.<br>SMART; SM00131; KU; 1.   |
| DR | PROSITE; PS00319; A4_EXTRA; 1.   |
| DR | PROSITE; PS00320; A4_INTRA; 1.   |
| DR | PROSITE; PS00280; BPTI_KUNITZ_1; 1.  |
| DR | PROSITE; PS00279; BPTI_KUNITZ_2; 1.  |
| KW | Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;<br>Alternative splicing; Serine protease inhibitor.<br>By SIMILARITY.   |
| FT | SIGNAL 1 17  |
| FT | CHAIN 18 770   |
| FT | -----  |
| FT | DOMAIN 18 699  |
| FT | TRANSMEM 700 723   |
| FT | DOMAIN 724 770   |
| FT | DOMAIN 673 715   |
| FT | DOMAIN 287 345   |
| FT | SITE 759 762   |
| FT | DISULFID 291 341   |
| FT | DISULFID 300 324   |
| FT | DISULFID 316 337   |
| FT | CARBOHYD 542 542   |
| FT | CARBOHYD 571 571   |
| FT | VARSPLIC 289 289   |
| FT | VARSPLIC 290 364   |
| FT | VARSPLIC 346 380   |
| FO | SEQUENCE 770 AA; 86752 MW; 26C50DE0890CAFA7A CXC64;  |

Query Match 100.0%; Score 11; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
 |||||  
 DB 696 GSNKGATIGLM 706

RESULT 10  
 A4\_RAT STANDARD: PRT: 770 AA.  
 ID A4\_RAT  
 AC P08592;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR  
 DE (AMYLOIDOGENIC GLYCOPROTEIN) (AG).  
 GN APP  
 OS Rattus norvegicus (rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxId=10116;  
 RN [1]  
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.  
 RC TISSUE=Brain;  
 RA MEDLINE=8812583; PubMed=2900758;  
 RA Shivers B.D., Hildich C., Multhaup G., Salbaum J.M., Beyreuther K.,  
 RA Seeburg P.H.;  
 RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern  
 RT in rat brain suggests a role in cell contact.";  
 RL EMBO J. 7:1365-1370(1988).  
 RN [2]  
 RP SEQUENCE OF 289-364 FROM N.A.  
 RC TISSUE=Liver;  
 RA MEDLINE=89183625; PubMed=2648331;  
 RA Kang J., Mueller-Hill B.;  
 RT "The sequence of the two extra exons in rat pre4.";  
 RL Nucleic Acids Res. 17:2130-2130(1989).  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: APP(395), APP(563), APP(695),  
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING.  
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION  
 CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC  
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE  
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF  
 CC PHOSPHORYLATION (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 BP1/KUNITZ INHIBITOR DOMAIN.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: X07648; CAA30488.1; -;  
 CC EMBL: X14066; CAA32229.1; -;  
 CC PIR: S00550; S00550.  
 CC PIR: S03607; S03607.  
 CC InterPro: IPR001868; A4\_APP.  
 CC InterPro: IPR002223; Kunitz\_BP1.  
 CC Pfam: PF02177; A4\_EXTRA; 1.  
 CC Pfam: PF00014; Kunitz\_BP1; 1.  
 CC PRINTS: PR00203; AMYLOIDA4  
 CC PRINTS: PR00204; BETAAMYLOID.  
 CC PRINTS: PR00759; BASICPTASE.  
 CC SMART: SM00006; A4\_EXTRA; 1.

DR SMART: SM00131; KU; 1.  
 DR PROSITE: PS00319; A4\_EXTRA; 1.  
 DR PROSITE: PS00320; A4\_INTRA; 1.  
 DR PROSITE: PS00280; BP1\_KUNITZ\_1; 1.  
 DR PROSITE: PS0279; BP1\_KUNITZ\_2; 1.  
 DR Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;  
 KW Alternative splicing; Serine protease inhibitor.  
 FT SIGNAL 1 17  
 FT CHAIN 18 770  
 FT FT  
 FT FT  
 FT DOMAIN 18 699  
 FT TRANSMEM 700 723  
 FT DOMAIN 724 770  
 FT DOMAIN 673 715  
 FT DOMAIN 287 345  
 FT SITE 759 762  
 FT DISULFID 291 341  
 FT DISULFID 300 324  
 FT DISULFID 316 337  
 FT CARBOHYD 542 542  
 FT CARBOHYD 571 571  
 FT CARBOHYD 289 289  
 FT VARSPLIC 290 364  
 FT SEQUENCE 770 AA; 86704 MW; C26C9DBB2D929A7 CRC64;

Query Match 100.0%; Score 11; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
 |||||  
 DB 696 GSNKGATIGLM 706

RESULT 11  
 ID PROF\_ENTHI STANDARD: PRT: 130 AA.  
 AC P49230;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE PROFILIN.  
 OS Entamoeba histolytica.  
 OC Eukaryota; Entamoebidae; Entamoeba.  
 OX NCBI\_TaxId=5759;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 74-84 AND 86-94.  
 RC STRAIN=SEL-3;  
 RA MEDLINE=96085166; PubMed=8521867;  
 RA Binder M., Orther S., Erben H., Scheiner O., Wiedermann G.,  
 RA Valenta R., Duchene M.;  
 RT "The basic isoform of profilin in pathogenic Entamoeba histolytica.  
 RT cDNA cloning, heterologous expression, and actin-binding  
 RT properties.";  
 RL Eur. J. Biochem. 233:976-981(1995).  
 CC -1- FUNCTION: BINDS TO ACTIN AND AFFECTS THE STRUCTURE OF THE  
 CC CYTOSKELETON. AT HIGH CONCENTRATIONS, PROFILIN PREVENTS THE  
 CC POLYMERIZATION OF ACTIN, WHEREAS IT ENHANCES IT AT LOW  
 CC CONCENTRATIONS. BY BINDING TO PIP2, IT INHIBITS THE FORMATION OF  
 CC IP3 AND DG.  
 CC -1- SUBUNIT: OCCURS IN MANY KINDS OF CELLS AS A COMPLEX WITH MONOMERIC  
 CC ACTIN IN A 1:1 RATIO.  
 CC -1- SIMILARITY: BELONGS TO THE PROFILIN FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----



CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: AB031291; BAA83499.1; -  
 DR MGD: MG1:1926784; NP25.  
 DR InterPro: IPR003247; CH\_type.  
 DR InterPro: IPR001715; Calponin\_hom.  
 DR InterPro: IPR000557; Calponin\_repeat.  
 DR Pfam: PF0402; calponin; 1.  
 DR PRINTS: PR00888; SM22CALPONIN.  
 DR PRINTS: PR00890; TRNGSELIN.  
 DR PRODOM: PD001527; CH\_type; 1.  
 DR SMART: SM00033; CH; 1.  
 DR PROSITE: PS01052; CALPONIN; 1.  
 DR PROSITE: PS50021; CH; 1.  
 DR DOMAIN 24 136 CH.  
 FT REPEAT 174 199 CALPONIN-LIKE 26 AA MOTIF.  
 SQ SEQUENCE 199 AA; 22471 MW; 53802F6F94958202 CRC64;

Query Match  
 Best Local Similarity 54.5%; Score 6; DB 1; Length 199;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGA 6  
 DB 179 GSNKGA 184

RESULT 14  
 NP25\_RAT  
 ID NP25\_RAT STANDARD; PRT; 219 AA.  
 AC P37805; Q09025;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE NEURONAL PROTEIN NP25.  
 GN NP25.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;  
 RX MEDLINE=94285742; PubMed=8015377;  
 RA Ren W.-Z., Ng G.Y.K., Wang R.-X., Wu P.H., O'Dowd B.F., Osmond D.H.,  
 RA George S.R., Lew C.-C.;  
 RT The identification of NP25: a novel protein that is differentially  
 RT expressed by neuronal subpopulations.  
 RL Brain Res. Mol. Brain Res. 22:173-185(1994).  
 CC -1- TISSUE SPECIFICITY: ABUNDANT AND UBQUITOUS EXPRESSION IN NEURONS.  
 CC -1- SIMILARITY: BELONGS TO THE CALPONIN FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: M84725; AAC42095.1; -  
 DR InterPro: IPR003247; CH\_type.  
 DR InterPro: IPR001715; Calponin\_hom.  
 DR InterPro: IPR000557; Calponin\_repeat.  
 DR InterPro: IPR003096; SM22\_calponin.  
 DR Pfam: PF00402; calponin; 1.

DR Pfam: PF00307; CH; 1.  
 DR PRINTS: PR00888; SM22CALPONIN.  
 DR PRINTS: PR00890; TRNGSELIN.  
 DR PRODOM: PD001527; CH\_type; 1.  
 DR SMART: SM00033; CH; 1.  
 DR PROSITE: PS01052; CALPONIN; 1.  
 DR PROSITE: PS50021; CH; 1.  
 DR DOMAIN 24 136 CH.  
 FT REPEAT 174 199 CALPONIN-LIKE 26 AA MOTIF.  
 SQ SEQUENCE 219 AA; 24712 MW; 7A743BA6851DDDC7 CRC64;

Query Match  
 Best Local Similarity 54.5%; Score 6; DB 1; Length 219;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGA 6  
 DB 179 GSNKGA 184

RESULT 15  
 FLAG\_RHIME  
 ID FLAG\_RHIME STANDARD; PRT; 262 AA.  
 AC O52946;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE FLAGELLAR BASAL-BODY ROD PROTEIN FLAG (DISTAL ROD PROTEIN).  
 GN FLAG.  
 OS Rhizobium meliloti (Sinorhizobium meliloti).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Sinorhizobium.  
 OX NCBI\_TaxID=382;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RUI1/001;  
 RA Platzer J., Schmitt R.;  
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBUNIT: THE BASAL BODY CONSTITUTES A MAJOR PORTION OF THE  
 CC FLAGELLAR ORGANELLE AND CONSISTS OF FOUR RINGS (L,P,S, AND M)  
 CC MOUNTED ON A CENTRAL ROD. THE ROD CONSISTS OF ABOUT 26 SUBUNITS OF  
 CC FLAG IN THE DISTAL PORTION, AND FLAG, FLAG AND FLAG ARE THOUGHT TO  
 CC BUILD UP THE PROXIMAL PORTION OF THE ROD WITH ABOUT 6 SUBUNITS  
 CC EACH (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE FLAGELLA BASAL BODY ROD PROTEINS  
 CC FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: L49337; AAB0413.1; -  
 DR InterPro: IPR001444; Flag\_bb\_rod.  
 DR Pfam: PF00460; Flag\_bb\_rod; 1.  
 DR PROSITE: PS00588; FLAGELLA\_BB\_ROD; 1.  
 KW Flagella.  
 SQ SEQUENCE 262 AA; 28062 MW; 738B0B953BAE293C CRC64;

Query Match  
 Best Local Similarity 54.5%; Score 6; DB 1; Length 262;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 GATIGL 10  
 DB 65 GATIGL 70

Wed Apr 24 09:48:05 2002

us-09-689-469-4.oli.rsp

Page 10

Search completed: April 24, 2002, 09:24:54  
Job time: 247 sec

---

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:17:36 ; Search time 66.28 Seconds  
(without alignments)  
12.293 Million cell updates/sec

Title: US-09-689-469-4

Perfect score: 54

Sequence: 1 GSNKGALIGLM 11

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq\_1101.\*  
1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:\*  
2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:\*  
3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:\*  
4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:\*  
5: /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:\*  
6: /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:\*  
7: /SIDS8/gcgdata/geneseq/geneseqp/AA1986.DAT:\*  
8: /SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:\*  
9: /SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT:\*  
10: /SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT:\*  
11: /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:\*  
12: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:\*  
13: /SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:\*  
14: /SIDS8/gcgdata/geneseq/geneseqp/AA1993.DAT:\*  
15: /SIDS8/gcgdata/geneseq/geneseqp/AA1994.DAT:\*  
16: /SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:\*  
17: /SIDS8/gcgdata/geneseq/geneseqp/AA1996.DAT:\*  
18: /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:\*  
19: /SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT:\*  
20: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:\*  
21: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:\*  
22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 54    | 100.0       | 11     | 15    | AA60369     |
| 2          | 54    | 100.0       | 11     | 16    | AA60369     |
| 3          | 54    | 100.0       | 11     | 17    | AA60369     |
| 4          | 54    | 100.0       | 11     | 18    | AA60369     |
| 5          | 54    | 100.0       | 11     | 19    | AA60369     |
| 6          | 54    | 100.0       | 11     | 19    | AA60369     |
| 7          | 54    | 100.0       | 11     | 20    | AA60369     |
| 8          | 54    | 100.0       | 11     | 21    | AA60369     |
| 9          | 54    | 100.0       | 11     | 22    | AA60369     |
| 10         | 54    | 100.0       | 11     | 22    | AA60369     |
| 11         | 54    | 100.0       | 14     | 19    | AA60369     |

#### ALIGNMENTS

|    |    |       |    |    |         |                    |
|----|----|-------|----|----|---------|--------------------|
| 12 | 54 | 100.0 | 14 | 22 | AA60369 | Amyloid beta-prote |
| 13 | 54 | 100.0 | 14 | 22 | AA60369 | Amyloid beta-prote |
| 14 | 54 | 100.0 | 14 | 22 | AA60369 | Amyloid beta-prote |
| 15 | 54 | 100.0 | 14 | 22 | AA60369 | Amyloid beta-prote |
| 16 | 54 | 100.0 | 24 | 22 | AA60369 | Amyloid beta-prote |
| 17 | 54 | 100.0 | 24 | 22 | AA60369 | Amyloid beta-prote |
| 18 | 54 | 100.0 | 26 | 20 | AA60369 | Human amyloidogeni |
| 19 | 54 | 100.0 | 26 | 20 | AA60369 | Human amyloidogeni |
| 20 | 54 | 100.0 | 27 | 20 | AA60369 | Human amyloidogeni |
| 21 | 54 | 100.0 | 32 | 22 | AA60369 | Partial sequence o |
| 22 | 54 | 100.0 | 35 | 19 | AA60369 | Beta-amyloid pepti |
| 23 | 54 | 100.0 | 35 | 19 | AA60369 | Beta-amyloid pepti |
| 24 | 54 | 100.0 | 35 | 20 | AA60369 | Beta-amyloid pepti |
| 25 | 54 | 100.0 | 35 | 20 | AA60369 | Beta-amyloid pepti |
| 26 | 54 | 100.0 | 35 | 20 | AA60369 | Beta-amyloid pepti |
| 27 | 54 | 100.0 | 35 | 20 | AA60369 | Beta-amyloid pepti |
| 28 | 54 | 100.0 | 35 | 22 | AA60369 | Amyloid beta-prote |
| 29 | 54 | 100.0 | 35 | 22 | AA60369 | Amyloid beta-prote |
| 30 | 54 | 100.0 | 36 | 20 | AA60369 | Synthetic amyloid  |
| 31 | 54 | 100.0 | 38 | 15 | AA60369 | Beta-amyloid (1-38 |
| 32 | 54 | 100.0 | 38 | 20 | AA60369 | Human tachykinin a |
| 33 | 54 | 100.0 | 38 | 22 | AA60369 | Amyloid beta-prote |
| 34 | 54 | 100.0 | 38 | 22 | AA60369 | Amyloid beta-prote |
| 35 | 54 | 100.0 | 39 | 15 | AA60369 | Beta-amyloid (1-40 |
| 36 | 54 | 100.0 | 39 | 20 | AA60369 | Amyloid beta prote |
| 37 | 54 | 100.0 | 39 | 20 | AA60369 | Amyloid beta pepti |
| 38 | 54 | 100.0 | 39 | 21 | AA60369 | Beta-amyloid pepti |
| 39 | 54 | 100.0 | 40 | 14 | AA60369 | Human Receptor to  |
| 40 | 54 | 100.0 | 40 | 15 | AA60369 | Beta-amyloid (1-40 |
| 41 | 54 | 100.0 | 40 | 18 | AA60369 | Amyloid beta prote |
| 42 | 54 | 100.0 | 40 | 18 | AA60369 | Amyloid beta pepti |
| 43 | 54 | 100.0 | 40 | 19 | AA60369 | Beta-amyloid pepti |
| 44 | 54 | 100.0 | 40 | 19 | AA60369 | Beta-amyloid pepti |
| 45 | 54 | 100.0 | 40 | 22 | AA60369 | Human peptide anti |

|          |   |                           |
|----------|---|---------------------------|
| RESULT 1 | AA60369   | standard; peptide; 11 AA. |
| ID       | AA60369   |                           |
| XX       | AA60369   |                           |
| AC       | AA60369   |                           |
| XX       | AA60369   |                           |
| DT       | 15-MAR-1995   | (first entry)             |
| XX       | Beta-amyloid (25-35).   |                           |
| DE       | Beta-amyloid (25-35).   |                           |
| XX       |   |                           |
| KW       | Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;  |                           |
| KW       | anti-beta-amyloid antibody; diagnosis; immunogen; antigen; epitope.   |                           |
| OS       | Homo sapiens.   |                           |
| XX       |   |                           |
| PN       | WO9417197-A.  |                           |
| XX       | 04-AUG-1994.  |                           |
| PD       |   |                           |
| XX       |   |                           |
| PF       | 24-JAN-1994;  | 94WO-JP00089.             |
| XX       |   |                           |
| PR       | 25-JAN-1993;  | 93JP-0010132.             |
| PR       | 05-FEB-1993;  | 93JP-0019035.             |
| PR       | 16-NOV-1993;  | 93JP-0286985.             |
| XX       | 28-DEC-1993;  | 93JP-0334773.             |
| PA       | (TAKE ) TAKEDA CHEM IND LTD.  |                           |
| XX       |   |                           |
| PI       | Kitada C, Odaka A, Suzuki N;  |                           |
| XX       |   |                           |
| DR       | WPI; 1994-264110/32.  |                           |
| XX       |   |                           |
| PT       | Antibodies recognising specific parts of beta-amyloid - can be used for diagnosis of diseases implicating beta-amyloid, such as |                           |

PT Alzheimer's disease  
 XX  
 PS Claim 2; Page 84; 116pp; Japanese.  
 XX  
 CC Antibodies which recognise specific subfragments of the beta-amyloid  
 CC protein are claimed. Specifically, the antibodies (which are pref.  
 CC monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal  
 CC portion of beta-amyloid or they recognise residues 25-35 or 35-43  
 CC from the C-terminal portion. The antibodies are useful for assaying  
 CC beta-amyloid and its derivatives for diagnosis of Alzheimer's  
 CC disease.  
 XX  
 SQ Sequence 11 AA;  
 Query Match 100.0%; Score 54; DB 15; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.00034;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GSNKGAIIIGLM 11  
 1 gsnkgalliglm 11  
 DB  
 RESULT 2  
 AAR87948  
 ID AAR87948 standard; peptide; 11 AA.  
 XX  
 AC AAR87948;  
 XX  
 DT 05-MAR-1996 (first entry)  
 XX  
 DE beta-amyloid (25-35) peptide.  
 XX  
 KW Alzheimer's disease; beta-amyloid; plaque; glycosaminoglycan;  
 KW proteoglycan; A-beta.  
 KM  
 XX  
 OS Synthetic.  
 XX  
 PN WO9506477-A1.  
 XX  
 PD 09-MAR-1995.  
 XX  
 PF 29-AUG-1994; 94WO-US09853.  
 XX  
 PR 31-AUG-1993; 93US-0114942.  
 XX  
 PA (GLIA-) GLIATECH INC.  
 XX  
 PI Brunden KR, Frederickson RCA, Gupta-Bansal R, Richtercook NJ;  
 XX  
 DR WPI; 1995-115259/15.  
 XX  
 PT Treating Alzheimer's disease by using cps. that inhibit beta  
 PT amyloid binding - to glycosaminoglycan(s)  
 XX  
 PS Claim 49; Page 64; 88pp; English.  
 XX  
 CC The invention relates to new chemical compounds which are peptides of  
 CC formulae XXNX (I), XXNX2 (II) and X1NX2X3 (III), and peptides comprising  
 CC the sequences (I), (II) or (III) or containing not greater than 8 amino  
 CC acid residues. In the formulae, X is any amino acid with a cationic side  
 CC chain, N and Z are neutral amino acids, and two of X1, X2 and X3 are  
 CC amino acids with an anionic side chain and the third is an amino acid  
 CC with an anionic or neutral side chain. Also new is the peptide  
 CC Gly-Ser-Asn-Lys-Gly-Ala-Ile-Ile-Gly-Leu-Met. The present sequence is  
 CC the latter undecapeptide which represents amino acids 25-35 of the  
 CC beta-amyloid peptide A-beta.  
 CC The peptides inhibit the binding of glycosaminoglycans and/or proteo-  
 CC glycans to A-beta peptide and hence can be used for preventing the  
 CC formation of amyloid plaques and for treating Alzheimer's disease.  
 XX  
 SQ Sequence 11 AA;

Query Match 100.0%; Score 54; DB 16; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.00034;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GSNKGAIIIGLM 11  
 1 gsnkgalliglm 11  
 DB  
 RESULT 3  
 AAR92807  
 ID AAR92807 standard; peptide; 11 AA.  
 XX  
 AC AAR92807;  
 XX  
 DT 18-OCT-1996 (first entry)  
 XX  
 DE Human beta-amyloid 25-35.  
 XX  
 KW PB145; PB446; PB96; beta-amyloid; treatment; Alzheimer's disease;  
 KW Down's syndrome; inhibition; neurotoxicity; beta-amyloid 25-35.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9607425-A1.  
 XX  
 PD 14-MAR-1996.  
 XX  
 PF 07-SEP-1995; 95WO-US10989.  
 XX  
 PR 09-SEP-1994; 94US-0306872.  
 XX  
 PA (UNITW) UNIV WASHINGTON.  
 XX  
 PI Perlmutter DH;  
 XX  
 DR WPI; 1996-171392/17.  
 XX  
 PT Inhibitor peptide(s) for blocking the serpin-enzyme complex receptor  
 PT - used for inhibiting amyloid-beta protein neurotoxicity in e.g.  
 PT Alzheimer's disease  
 XX  
 PS Claim 5; Page 18; 31pp; English.  
 XX  
 CC The peptides PB145, PB446 and PB96 can be used to inhibit the  
 CC neurotoxicity of the present peptide, beta-amyloid 25-35, and are  
 CC therefore useful in the treatment of Alzheimer's disease and Down's  
 CC syndrome.  
 XX  
 SQ Sequence 11 AA;  
 Query Match 100.0%; Score 54; DB 17; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.00034;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GSNKGAIIIGLM 11  
 1 gsnkgalliglm 11  
 DB  
 RESULT 4  
 AAW23336  
 ID AAW23336 standard; peptide; 11 AA.  
 XX  
 AC AAW23336;  
 XX  
 DT 12-MAR-1998 (first entry)  
 XX  
 DE Amyloid beta peptide 2 used to inhibit damage to cells in Alzheimer's.  
 XX



KW Amyloid beta peptide; extracellular deposit; Alzheimer's disease;  
KW neurite outgrowth; microglial activation; neuronal cell degeneration;  
KW receptor for advanced glycosylation end product;  
KW amyloid beta peptide fibril.  
XX  
OS Homo sapiens.  
XX  
PN WO9726913-A1.  
XX  
PD 31-JUL-1997.  
XX  
PF 21-JAN-1997; 97WO-US00857.  
XX  
PR 26-JAN-1996; 96US-0592070.  
XX  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
PI Schmidt AM, Stern D, Yan SD;  
XX  
DR WPI; 1997-393374/36.  
XX  
PT Inhibiting damage to cells in e.g. Alzheimer's disease - using an  
PT agent which inhibits interaction of an amyloid-beta peptide with a  
PT receptor for advanced glycosylation end product  
XX  
PS Claim 5; Page 10; 91pp; English.  
XX  
CC Peptides AAW2335-36 are portions of the the amyloid beta peptide, which  
CC is the principal component of extracellular deposits in Alzheimer's  
CC disease. It has been shown to promote neurite outgrowth, generate  
CC reactive oxygen intermediates, induce cellular oxidant stress, lead to  
CC neuronal cytotoxicity, and promote microglial activation. The present  
CC peptide, which comprises amino acids 25-35 of the amyloid beta peptide,  
CC is used in a pharmaceutical composition. This composition comprises an  
CC agent capable of inhibiting interaction of an amyloid-beta peptide with  
CC a receptor for advanced glycosylation end product and a carrier. A  
CC method for inhibiting interaction of amyloid beta peptide with a receptor  
CC for advanced glycosylation on the surface of a cell comprises contacting  
CC the cell with e.g. present peptide. Depending on the type of cell,  
CC inhibiting the interaction between the amyloid beta peptide and the  
CC receptor for advanced glycosylation can be used for inhibiting the  
CC degeneration of a neuronal cell, inhibiting formation of an amyloid beta  
CC peptide fibril on a cell, inhibiting extracellular assembly of amyloid  
CC beta peptide into a fibril, inhibiting aggregation of amyloid beta  
CC peptide on the surface of a cell, inhibiting infiltration of a microglial  
CC cell into senile plaques, and inhibiting activation of microglial cells  
CC by amyloid beta peptide. The methods can be used for treating e.g.  
CC diabetes, Alzheimer's Disease, senility, renal failure, hyperlipidemic  
CC atherosclerosis, neuronal cytotoxicity, Down's syndrome, dementia  
CC associated with head trauma, amyotrophic lateral sclerosis, multiple  
CC sclerosis or neuronal degeneration.  
XX  
SQ Sequence 11 AA;  
  
Query Match 100.0%; Score 54; DB 18; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00034;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 GSNKGAIIIGLM 11  
DB 1 gsnkgaiiglm 11  
  
RESULT 5  
AAW64497  
ID AAW64497 standard; peptide; 11 AA.  
XX  
AC AAW64497;  
XX  
DT 20-OCT-1998 (first entry)  
XX  
DE Neurotoxic beta-amyloid peptide decoy peptide #10.

XX  
KW Beta-amyloid peptide; beta-AP; neuropeptide; neurotoxin; calcium influx;  
KW aggregate; Alzheimers disease; decoy; treatment.  
XX  
OS Synthetic.  
XX  
PN WO9830229-A1.  
XX  
PD 16-JUL-1998.  
XX  
PF 09-JAN-1998; 98WO-US00653.  
XX  
PR 29-OCT-1997; 97US-0960188.  
XX  
PR 10-JAN-1997; 97US-0035847.  
XX  
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
XX  
PI Blanchard BJ, Ingram VM;  
XX  
DR WPI; 1998-398795/34.  
XX  
PT Inhibition of aggregation of, e.g. beta-amyloid peptide - by  
PT administering decoy peptide or other calcium-influx inhibitor,  
PT useful for, e.g. treating Alzheimer's disease  
XX  
PS Example 4; Page 42; 68pp; English.  
XX  
CC AAW64488-w64517 are decoy peptides that bind to a neurotoxic  
CC beta-amyloid peptide (beta-AP) and reduces the ability of beta-AP's to  
CC form aggregates that increase calcium influx into neuronal cells. Such  
CC peptides can be used in the treatment of diseases associated with  
CC neurotoxic aggregates of beta-AP specifically Alzheimer's disease. The  
CC peptides are administered at 0.001-1000 (especially 0.2-20) mg/kg, by  
CC injection and orally, or from slow-release implants.  
XX  
SQ Sequence 11 AA;  
  
Query Match 100.0%; Score 54; DB 19; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00034;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 GSNKGAIIIGLM 11  
DB 1 gsnkgaiiglm 11  
  
RESULT 6  
AAW47231  
ID AAW47231 standard; peptide; 11 AA.  
XX  
AC AAW47231;  
XX  
DT 22-MAY-1998 (first entry)  
XX  
DE Beta-amyloid peptide residues 25-35.  
XX  
KW Screening assay; beta-amyloid peptide; treatment;  
KW amyloidosis disease; Alzheimer's disease.  
XX  
OS Homo sapiens.  
XX  
PN US5721106-A.  
XX  
PD 24-FEB-1998.  
XX  
PF 12-SEP-1994; 94US-0304585.  
XX  
PR 12-SEP-1994; 94US-0304585.  
XX  
PR 13-AUG-1991; 91US-0744767.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PA (MINU ) UNIV MINNESOTA.

CC acetone nitrile to a concentration of 0.01-10 mg/ml, incubating the

| Sequence | 11 AA |
|----------|-------|
| 5Q       |       |

Query Match 100.0%; Score 54; DB 21; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.00034;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11  
 |||||  
 Db 1 gsnkgaiiglm 11

## RESULT 9

AAB91775  
 ID AAB91775 standard; Peptide; 11 AA.

AC AAB91775;

DT 22-JUN-2001 (first entry)

DE Amyloid beta-protein fragment peptide SEQ ID NO:951.

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 blood component; modification; succinimidyl; maleimido group; amino;  
 hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.  
 OS Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

PT WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity  
 PT  
 PS Disclosure; Page 504; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutically active amino acid region (III) and a  
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to  
 CC a less therapeutically active amino acid region (IV), which covalently  
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity  
 CC in vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention.

CC Sequence 11 AA;

QY Query Match 100.0%; Score 54; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.00034;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11  
 |||||  
 Db 1 gsnkgaiiglm 11

## RESULT 10

AAB91808  
 ID AAB91808 standard; Peptide; 11 AA.

AC AAB91808;

DT 22-JUN-2001 (first entry)

DE Amyloid beta-protein fragment peptide SEQ ID NO:984.

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 blood component; modification; succinimidyl; maleimido group; amino;  
 hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.  
 OS Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

PT WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity  
 PT  
 PS Disclosure; Page 516; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutically active amino acid region (III) and a  
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to  
 CC a less therapeutically active amino acid region (IV), which covalently  
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity  
 CC in vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention.

CC Sequence 11 AA;

QY Query Match 100.0%; Score 54; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.00034;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11  
 AAM64498 standard; peptide; 14 AA.  
 ID AAM64498  
 XX  
 AC AAM64498;  
 XX  
 DT 20-OCT-1998 (first entry)  
 XX  
 DE Neurotoxic beta-amyloid peptide decoy peptide #11.  
 XX  
 KW Beta-amyloid peptide; beta-AP; neuropeptide; neurotoxin; calcium influx;  
 aggregate; Alzheimers disease; decoy; treatment.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9830229-A1.  
 XX  
 PD 16-JUL-1998.  
 XX  
 PF 09-JAN-1998; 98MO-US00653.  
 XX  
 PR 29-OCT-1997; 97US-0960188.  
 PR 10-JAN-1997; 97US-0035847.  
 XX  
 PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
 XX  
 PI Blanchard BJ, Ingram VM;  
 DR WPI: 1998-398795/34.  
 XX  
 PT Inhibition of aggregation of, e.g. beta-amyloid peptide - by  
 PT administering decoy peptide or other calcium-influx inhibitor,  
 PT useful for, e.g. treating Alzheimer's disease  
 XX  
 PS Example 4; Page 43; 68pp; English.  
 XX  
 CC AAM64488-W64517 are decoy peptides that bind to a neurotoxic  
 CC beta-amyloid peptide (beta-AP) and reduces the ability of beta-AP's to  
 CC form aggregates that increase calcium influx into neuronal cells. Such  
 CC peptides can be used in the treatment of diseases associated with  
 CC neurotoxic aggregates of beta-AP specifically Alzheimer's disease. The  
 CC peptides are administered at 0.001-1000 (especially 0.2-20) mg/kg, by  
 CC injection and orally, or from slow-release implants.  
 CC  
 SO Sequence 14 AA;  
 QY  
 Db 1 GSNKGATIGLM 11  
 4 gsnkgatiglm 14  
 Query Match 100.0%; Score 54; DB 19; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.00044;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12  
 AAB91782 standard; Peptide; 14 AA.  
 ID AAB91782  
 XX  
 AC AAB91782;  
 XX  
 DT 22-JUN-2001 (first entry)  
 XX  
 DE Amyloid beta-protein fragment peptide SEQ ID NO:958.  
 XX  
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimidyl; maleimido group; amino;  
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.

XX  
 PN WO200069900-A2.  
 XX  
 PD 23-NOV-2000.  
 XX  
 PF 17-MAY-2000; 2000MO-US13576.  
 XX  
 PR 17-MAY-1999; 99US-0134406.  
 PR 10-SEP-1999; 99US-0153406.  
 PR 15-OCT-1999; 99US-0159783.  
 XX  
 PA (CONJ-) CONJUCHEM INC.  
 XX  
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;  
 DR WPI: 2001-112059/12.  
 XX  
 PT Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity  
 XX  
 PS Disclosure; Page 507; 733pp; English.  
 XX  
 CC The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutically active amino acid region (III) and a  
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to  
 CC a less therapeutically active amino acid region (IV), which covalently  
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity  
 CC in vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention.  
 CC  
 SO Sequence 14 AA;  
 QY  
 Db 1 GSNKGATIGLM 11  
 4 gsnkgatiglm 14  
 Query Match 100.0%; Score 54; DB 22; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.00044;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13  
 AAB91788 standard; Peptide; 14 AA.  
 ID AAB91788  
 XX  
 AC AAB91788;  
 XX  
 DT 22-JUN-2001 (first entry)  
 XX  
 DE Amyloid beta-protein fragment peptide SEQ ID NO:964.  
 XX  
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimidyl; maleimido group; amino;  
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200069900-A2.  
 XX  
 PD 23-NOV-2000.

|           |  |                 |
|-----------|--|-----------------|
| XX        | 17-MAY-2000;   | 2000WO-US13576. |
| XX        |  |                 |
| PR        | 17-MAY-1999;   | 99US-0134406.   |
| PR        | 10-SEP-1999;   | 99US-0153406.   |
| PR        | 15-OCT-1999;   | 99US-0159783.   |
| XX        |  |                 |
| PA        | (CONU-)  | CONUCHEM INC.   |
| XX        |  |                 |
| PI        | Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;                  |                 |
| DR        | WPI; 2001-112059/12.   |                 |
| XX        |  |                 |
| PT        | Modifying and attaching therapeutic peptides to albumin prevents         |                 |
| PT        | peptidase degradation, useful for increasing length of in vivo activity  |                 |
| XX        |  |                 |
| PS        | Disclosure; Page 509; 733pp; English.                                    |                 |
| XX        |  |                 |
| CC        | The present invention describes a modified therapeutic peptide (I)       |                 |
| CC        | comprising a therapeutically active amino acid region (III) and a        |                 |
| CC        | reactive group (II) (e.g. succinimidyl and maleimido groups) attached to |                 |
| CC        | a less therapeutically active amino acid region (IV), which covalently   |                 |
| CC        | bonds with amino/hydroxyl/thiol groups on blood components to form a     |                 |
| CC        | peptidase stabilised therapeutic peptide composed of 3-50 amino acids.   |                 |
| CC        | (I) are useful for modifying therapeutic peptides e.g. hormones, growth  |                 |
| CC        | factors and neurotransmitters, to protect them from peptidase activity   |                 |
| CC        | in vivo for the treatment of various disorders. Endogenous therapeutic   |                 |
| CC        | peptides are not suitable as drug candidates as they require frequent    |                 |
| CC        | administration due to rapid degradation by peptidases in the body.       |                 |
| CC        | Modifying and attaching therapeutic peptides to albumin prevents or      |                 |
| CC        | reduces the action of peptidases to increase length of activity (half    |                 |
| CC        | life) and specifically as bonding to large molecules decreases           |                 |
| CC        | intracellular uptake and interference with physiological processes.      |                 |
| CC        | AAB90829 to AAB92441 represent peptides which can be used in the         |                 |
| CC        | exemplification of the present invention.                                |                 |
| XX        |  |                 |
| SQ        | Sequence 14 AA:  |                 |
|           |  |                 |
|           | Query Match 100.0%; Score 54; DB 22; Length 14;                          |                 |
|           | Best Local Similarity 100.0%; Pred. NO. 0.00044;                         |                 |
|           | Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0.              |                 |
| QY        | 1 GSNKGAIIGLM 11   |                 |
|           |  |                 |
| DB        | 4 gsnkgaiiglm 14   |                 |
|           |  |                 |
| RESULT 14 |  |                 |
| ID        | AAB91815   |                 |
| XX        | AAB91815 standard; Peptide: 14 AA.                                       |                 |
| XX        |  |                 |
| AC        | AAB91815;  |                 |
| XX        |  |                 |
| DT        | 22-JUN-2001 (first entry)  |                 |
| XX        |  |                 |
| DE        | Amyloid beta-protein fragment peptide SEQ ID NO:991.                     |                 |
| XX        |  |                 |
| KW        | Protection; endogenous therapeutic peptide; peptidase; conjugation;      |                 |
| KW        | blood component; modification; succinimidyl; maleimido group; amino;     |                 |
| KW        | hydroxyl; thiol; hormone; growth factor; neurotransmitter.               |                 |
| XX        |  |                 |
| OS        | Homo sapiens.  |                 |
| OS        | Synthetic.   |                 |
| XX        |  |                 |
| PN        | WO200069900-A2.  |                 |
| XX        |  |                 |
| PD        | 23-NOV-2000.   |                 |
| XX        |  |                 |
| PF        | 17-MAY-2000; 2000WO-US13576.   |                 |
| XX        |  |                 |
| PR        | 17-MAY-1999; 99US-0134406.   |                 |

|           |  |               |
|-----------|--|---------------|
| PR        | 10-SEP-1999;   | 99US-0153406. |
| PR        | 15-OCT-1999;   | 99US-0159783. |
| XX        |  |               |
| PA        | (CONJ-) CONJUCHEM INC.   |               |
| XX        |  |               |
| PI        | Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;                  |               |
| XX        |  |               |
| DR        | WPI; 2001-112059/12.   |               |
| PT        |  |               |
| PT        | Modifying and attaching therapeutic peptides to albumin prevents         |               |
| PT        | peptidase degradation, useful for increasing length of in vivo activity  |               |
| XX        |  |               |
| PS        | Disclosure: Page 519; 733pp; English.                                    |               |
| CC        |  |               |
| CC        | The present invention describes a modified therapeutic peptide (I)       |               |
| CC        | comprising a therapeutically active amino acid region (III) and a        |               |
| CC        | reactive group (II) (e.g. succinimidy) and maleimido groups) attached to |               |
| CC        | a less therapeutically active amino acid region (IV), which covalently   |               |
| CC        | bonds with amino/hydroxyl/thiol groups on blood components to form a     |               |
| CC        | peptidase stabilised therapeutic peptide composed of 3-50 amino acids.   |               |
| CC        | (I) are useful for modifying therapeutic peptides e.g. hormones, growth  |               |
| CC        | factors and neurotransmitters, to protect them from peptidase activity   |               |
| CC        | in vivo for the treatment of various disorders. Endogenous therapeutic   |               |
| CC        | peptides are not suitable as drug candidates as they require frequent    |               |
| CC        | administration due to rapid degradation by peptidases in the body.       |               |
| CC        | Modifying and attaching therapeutic peptides to albumin prevents or      |               |
| CC        | reduces the action of peptidases to increase length of activity (half    |               |
| CC        | life) and specifically as bonding to large molecules decreases           |               |
| CC        | intracellular uptake and interference with physiological processes.      |               |
| CC        | AAB90829 to AAB92441 represent peptides which can be used in the         |               |
| CC        | exemplification of the present invention.                                |               |
| XX        |  |               |
| SQ        | Sequence 14 AA:  |               |
| OY        | 1 GSNKGAIIGLM 11   |               |
| DB        | 4 gsnkgaiiglm 14   |               |
|           |  |               |
| RESULT 15 |  |               |
| AAB91805  |  |               |
| ID        | AAB91805 standard; Peptide: 24 AA.                                       |               |
| XX        |  |               |
| AC        | AAB91805;  |               |
| XX        |  |               |
| DT        | 22-JUN-2001 (first entry)  |               |
| XX        |  |               |
| DE        | Amyloid beta-protein fragment peptide SEQ ID NO:981.                     |               |
| XX        |  |               |
| KW        | Protection; endogenous therapeutic peptide; peptidase; conjugation;      |               |
| KW        | blood component; modification; succinimidy; maleimido group; amino;      |               |
| XX        | hydroxyl; thiol; hormone; growth factor; neurotransmitter.               |               |
| OS        | Homo sapiens.  |               |
| OS        | Synthetic.   |               |
| XX        |  |               |
| PN        | WO200069900-A2.  |               |
| XX        |  |               |
| PD        | 23-NOV-2000.   |               |
| XX        |  |               |
| PF        | 17-MAY-2000; 2000WO-US13576.   |               |
| XX        |  |               |
| PR        | 17-MAY-1999; 99US-0134406.   |               |
| PR        | 10-SEP-1999; 99US-0153406.   |               |
| PR        | 15-OCT-1999; 99US-0159783.   |               |
| XX        |  |               |
| PA        | (CONJ-) CONJUCHEM INC.   |               |

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;  
 PI  
 XX  
 DR MPI; 2001-112059/12.

XX  
 PT Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity  
 PT

XX  
 PS Disclosure; Page 515; 733pp; English.

XX  
 CC The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutically active amino acid region (III) and a  
 CC reactive group (II) (e.g. succinimide and maleimide groups) attached to  
 CC a less therapeutically active amino acid region (IV), which covalently  
 CC bonds with amino/hydroxy/thiol groups on blood components to form a  
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity  
 CC in vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention.

XX  
 SQ Sequence 24 AA;

# Query Match

100.0%; Score 54; DB 22; Length 24;

Best Local Similarity 100.0%; Pred No. 0.00078;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGALIGLM 11

DB 9 gsnkgaliglm 19

Search completed: April 24, 2002, 09:17:36  
 Job time: 140 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:18:15 ; Search time 32.34 Seconds  
(without alignments)  
7.654 Million cell updates/sec

Title: US-09-689-469-4  
Perfect score: 54  
Sequence: 1 GSNKGATIGLM 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents, AA:\*  
1: /cgn2\_6/prodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/prodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description                          |
|------------|-------|-------------|--------|-------|--------------------------------------|
| 1          | 54    | 100.0       | 11     | 1     | US-07-744-767A-3 Sequence 3, Appl1   |
| 2          | 54    | 100.0       | 11     | 1     | US-08-306-872-2 Sequence 2, Appl1    |
| 3          | 54    | 100.0       | 11     | 1     | US-08-346-849-5 Sequence 5, Appl1    |
| 4          | 54    | 100.0       | 11     | 1     | US-08-304-585-3 Sequence 3, Appl1    |
| 5          | 54    | 100.0       | 11     | 1     | US-08-302-808-8 Sequence 8, Appl1    |
| 6          | 54    | 100.0       | 11     | 2     | US-08-433-734-3 Sequence 3, Appl1    |
| 7          | 54    | 100.0       | 11     | 2     | US-08-609-090-5 Sequence 5, Appl1    |
| 8          | 54    | 100.0       | 11     | 2     | US-08-986-948-8 Sequence 8, Appl1    |
| 9          | 54    | 100.0       | 11     | 2     | US-08-293-284A-5 Sequence 5, Appl1   |
| 10         | 54    | 100.0       | 11     | 4     | US-09-005-215-10 Sequence 10, Appl1  |
| 11         | 54    | 100.0       | 11     | 5     | PCT-US95-10989-2 Sequence 2, Appl1   |
| 12         | 54    | 100.0       | 14     | 4     | US-09-005-215-11 Sequence 11, Appl1  |
| 13         | 54    | 100.0       | 26     | 1     | US-08-304-585-7 Sequence 7, Appl1    |
| 14         | 54    | 100.0       | 34     | 2     | US-08-475-579A-4 Sequence 4, Appl1   |
| 15         | 54    | 100.0       | 35     | 1     | US-08-304-585-6 Sequence 6, Appl1    |
| 16         | 54    | 100.0       | 35     | 2     | US-08-612-785B-16 Sequence 16, Appl1 |
| 17         | 54    | 100.0       | 35     | 2     | US-08-612-785B-36 Sequence 36, Appl1 |
| 18         | 54    | 100.0       | 35     | 2     | US-08-612-785B-39 Sequence 39, Appl1 |
| 19         | 54    | 100.0       | 35     | 2     | US-08-612-785B-40 Sequence 40, Appl1 |
| 20         | 54    | 100.0       | 36     | 2     | US-08-609-090-6 Sequence 6, Appl1    |
| 21         | 54    | 100.0       | 38     | 1     | US-08-302-808-1 Sequence 1, Appl1    |
| 22         | 54    | 100.0       | 38     | 2     | US-07-737-371E-68 Sequence 68, Appl1 |
| 23         | 54    | 100.0       | 38     | 2     | US-08-986-948-1 Sequence 1, Appl1    |
| 24         | 54    | 100.0       | 39     | 1     | US-08-304-585-5 Sequence 5, Appl1    |
| 25         | 54    | 100.0       | 39     | 1     | US-08-302-808-2 Sequence 2, Appl1    |
| 26         | 54    | 100.0       | 39     | 2     | US-08-609-090-7 Sequence 7, Appl1    |
| 27         | 54    | 100.0       | 39     | 2     | US-08-682-245A-1 Sequence 1, Appl1   |

|    |    |       |    |   |                                      |
|----|----|-------|----|---|--------------------------------------|
| 28 | 54 | 100.0 | 39 | 2 | US-08-986-948-2 Sequence 2, Appl1    |
| 29 | 54 | 100.0 | 40 | 1 | US-07-744-767A-1 Sequence 1, Appl1   |
| 30 | 54 | 100.0 | 40 | 1 | US-08-235-400-2 Sequence 2, Appl1    |
| 31 | 54 | 100.0 | 40 | 1 | US-08-476-464A-2 Sequence 2, Appl1   |
| 32 | 54 | 100.0 | 40 | 1 | US-08-304-585-1 Sequence 1, Appl1    |
| 33 | 54 | 100.0 | 40 | 1 | US-08-304-585-8 Sequence 8, Appl1    |
| 34 | 54 | 100.0 | 40 | 1 | US-08-302-808-3 Sequence 3, Appl1    |
| 35 | 54 | 100.0 | 40 | 2 | US-08-433-734-1 Sequence 1, Appl1    |
| 36 | 54 | 100.0 | 40 | 2 | US-08-609-090-8 Sequence 8, Appl1    |
| 37 | 54 | 100.0 | 40 | 2 | US-07-737-371E-69 Sequence 69, Appl1 |
| 38 | 54 | 100.0 | 40 | 2 | US-08-682-245A-2 Sequence 2, Appl1   |
| 39 | 54 | 100.0 | 40 | 2 | US-08-986-948-3 Sequence 3, Appl1    |
| 40 | 54 | 100.0 | 40 | 2 | US-08-461-216-1 Sequence 1, Appl1    |
| 41 | 54 | 100.0 | 40 | 4 | US-08-959-148-1 Sequence 1, Appl1    |
| 42 | 54 | 100.0 | 40 | 5 | PCT-US92-06700-1 Sequence 1, Appl1   |
| 43 | 54 | 100.0 | 41 | 1 | US-07-819-361-1 Sequence 1, Appl1    |
| 44 | 54 | 100.0 | 41 | 1 | US-08-302-808-4 Sequence 4, Appl1    |
| 45 | 54 | 100.0 | 41 | 2 | US-08-682-245A-3 Sequence 3, Appl1   |

## ALIGNMENTS

RESULT 1  
US-07-744-767A-3  
; Sequence 3, Application US/07744767A  
; Patent No. 5434050  
; GENERAL INFORMATION:  
; APPLICANT: Maggio, John E.  
; APPLICANT: Mantly, Patrick W.  
; TITLE OF INVENTION: Labelled - Amyloid Peptide and Methods  
; TITLE OF INVENTION: for use in Detecting Alzheimer's Disease  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg & Woessner, P.A.  
; STREET: 3500 IDS Center  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07744, 767A  
; FILING DATE: 13-AUG-1991  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Muelling, Ann M.  
; REGISTRATION NUMBER: 33,977  
; REFERENCE/DOCKET NUMBER: 600, 226-US-01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-339-0331  
; TELEFAX: 612-339-3061  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-07-744-767A-3

Query Match 100.0%; Score 54; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00035;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11  
|||||  
Db 1 GSNKGATIGLM 11

RESULT 2  
US-08-306-872-2  
Sequence 2, Application US/08306872  
Patent No. 5514653  
GENERAL INFORMATION:  
APPLICANT: Perlmutter, David H.  
TITLE OF INVENTION: Method of Blocking the SEC Receptor  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scott J. Meyer, Monsanto/Searle, A3SG  
STREET: 800 N. Lindbergh Blvd.  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63167  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/306,872  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyer, Scott J.  
REGISTRATION NUMBER: 25,275  
REFERENCE/DOCKET NUMBER: WU-2833  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)694-3117  
TELEFAX: (314)694-5435  
INFORMATION FOR SEQ. ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-306-872-2

Query Match 100.0%; Score 54; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00035;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11  
Db 1 GSNKGAIIGLM 11

RESULT 3  
US-08-346-849-5  
Sequence 5, Application US/08346849  
Patent No. 5670483  
GENERAL INFORMATION:  
APPLICANT: Zhang, Shuangang  
APPLICANT: Lockshin, Curtis  
APPLICANT: Rich, Alexander  
APPLICANT: Holmes, Todd  
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY  
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES  
TITLE OF INVENTION: THEREFOR  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Milltia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02173-4799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/346,849  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/973,326  
FILING DATE: 28 DECEMBER 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: MIT-6008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ. ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-346-849-5

Query Match 100.0%; Score 54; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00035;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11  
Db 1 GSNKGAIIGLM 11

RESULT 4  
US-08-304-585-3  
Sequence 3, Application US/08304585  
Patent No. 5721106  
GENERAL INFORMATION:  
APPLICANT: Maggio, John E.  
APPLICANT: Mantlyn, Patrick W.  
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND  
TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Muelting, Raasch, Gebhardt & Schwappach, P.A.  
STREET: P.O. Box 361415  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55458-1415  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/304,585  
FILING DATE: 12-SEP-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Muelting, Ann M.  
REGISTRATION NUMBER: 33,977  
REFERENCE/DOCKET NUMBER: 110,00010120  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-305-1217  
TELEFAX: 612-305-1228  
INFORMATION FOR SEQ. ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant



MOLECULE TYPE: peptide  
US-08-304-585-3

Query Match 100.0%; Score 54; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00035;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIIGLM 11  
|1111111111|  
DB 1 GSNKGAIIIGLM 11

RESULT 5  
US-08-302-808-8  
; Sequence 8, Application US/08302808  
; Patent No. 5750349

GENERAL INFORMATION:  
APPLICANT: SUZUKI, No. 5750349uhlro  
APPLICANT: ODAKA, Asano  
APPLICANT: KITADA, Chieko  
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR  
DERIVATIVES AND USE THEREOF  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MA

COUNTRY: USA  
ZIP: 02019

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/302,808  
FILING DATE: 15-SEP-1994  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP94/00089  
FILING DATE: 24-JAN-1994  
APPLICATION NUMBER: 010132/1993  
FILING DATE: 25-JAN-1993  
APPLICATION NUMBER: 019035/1993  
FILING DATE: 05-FEB-1993  
APPLICATION NUMBER: 286985/1993  
FILING DATE: 16-NOV-1993  
APPLICATION NUMBER: 334773/1993  
FILING DATE: 28-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: DAVID, RESNICK S  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 44631  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3440  
TELEFAX: 617-523-6440

TELEX: 200291 STRB

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:  
US-08-302-808-8

Query Match 100.0%; Score 54; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00035;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIIGLM 11  
|1111111111|  
DB 1 GSNKGAIIIGLM 11

RESULT 6  
US-08-433-734-3  
; Sequence 3, Application US/08433734  
; Patent No. 5837473

GENERAL INFORMATION:  
APPLICANT: Magglio, John E.  
APPLICANT: Mantyh, Patrick W.  
TITLE OF INVENTION: Labelled  
-Amyloid Peptide and Methods  
for Use in Detecting Alzheimer's Disease  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Muelting, Raasch, Gebhardt & Schwappach, P.A.  
STREET: P.O. Box 581415  
CITY: Minneapolis

STATE: MN  
COUNTRY: USA  
ZIP: 55458-1415

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/433,734

FILING DATE: 03-MAY-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Muelting, Ann M.

REGISTRATION NUMBER: 33,977

REFERENCE/DOCKET NUMBER: 110.00010102

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-305-1220

TELEFAX: 612-305-1220

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-433-734-3

Query Match 100.0%; Score 54; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00035;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIIGLM 11  
|1111111111|  
DB 1 GSNKGAIIIGLM 11

RESULT 7  
US-08-609-090-5  
; Sequence 5, Application US/08609090  
; Patent No. 5840838

GENERAL INFORMATION:

APPLICANT: HENSLEY, Kenneth

APPLICANT: BUTTERFIELD, D. A.

APPLICANT: CARNEY, John M.

APPLICANT: AKSENOV, Michael

TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF

TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: LOWE PRICE LEBLANC & BECKER  
STREET: 99 Canal Center Plaza, Suite 300  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/609,090  
FILING DATE: 29-FEB-1996  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Kraus, Eric J.  
REGISTRATION NUMBER: 36,190  
REFERENCE/DOCKET NUMBER: 434-059  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-684-1111  
TELEFAX: 703-684-1124  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-609-090-5

Query Match 100.0%; Score 54; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00035;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
DB 1 GSNKGATIGLM 11

RESULT 8  
US-08-986-948-8  
Sequence 8, Application US/08986948  
Patent No. 5955317  
GENERAL INFORMATION:  
APPLICANT: SUZUKI, No. 5955317uharo  
APPLICANT: ODAKA, Asano  
APPLICANT: KITADA, Chieko  
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR  
DERIVATIVES AND USE THEREOF  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02019  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEO Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/986,948  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/302,808  
FILING DATE: 15-SEP-1994  
APPLICATION NUMBER: PCT/JP94/00089  
FILING DATE: 24-JAN-1994

APPLICATION NUMBER: 010132/1993  
FILING DATE: 25-JAN-1993  
APPLICATION NUMBER: 019035/1993  
FILING DATE: 05-FEB-1993  
APPLICATION NUMBER: 286985/1993  
FILING DATE: 16-NOV-1993  
APPLICATION NUMBER: 334773/1993  
FILING DATE: 28-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: DAVID, RESNICK S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 44631  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
TELEX: 200291 STRE  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
US-08-986-948-8

Query Match 100.0%; Score 54; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00035;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
DB 1 GSNKGATIGLM 11

RESULT 9  
US-08-293-284A-5  
Sequence 5, Application US/08293284A  
Patent No. 5955343  
GENERAL INFORMATION:  
APPLICANT: Holmes, Todd  
APPLICANT: Zhang, Shuangang  
APPLICANT: Rich, Alexander  
APPLICANT: Dipersio, C. Michael  
APPLICANT: Lockshin, Curtis  
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY  
SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
STREET: Two Millitia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02173-4799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/293,284A  
FILING DATE: 22-AUG-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/973,326  
FILING DATE: 28-DEC-1992  
ATTORNEY/AGENT INFORMATION:

NAME: Brook, David E.  
REGISTRATION NUMBER: 22,592  
REFERENCE/DOCKET NUMBER: MIT-6008A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-293-284A-5

Query Match 100.0%; Score 54; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00035;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
Db 1 GSNKGATIGLM 11

RESULT 10  
US-09-005-215-10  
Sequence 10, Application US/09005215  
Patent No. 6172043  
GENERAL INFORMATION:  
APPLICANT: Ingram, Vernon M.  
APPLICANT: Blanchard, Barbara J.  
TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S  
TITLE OF INVENTION: DISEASE CAUSED BY -AMYLOID PEPTIDES  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
STREET: 600 ATLANTIC AVENUE  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/005,215  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/035,847  
FILING DATE: 10-JAN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/960,188  
FILING DATE: 29-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Gates, Edward R.  
REGISTRATION NUMBER: 31,616  
REFERENCE/DOCKET NUMBER: M06566/7035  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
US-09-005-215-10

Query Match 100.0%; Score 54; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00035;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
Db 1 GSNKGATIGLM 11

RESULT 11  
PCT-US95-10989-2  
Sequence 2, Application PC/TUS9510989  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Method of Blocking the SEC Receptor  
NUMBER OF SEQUENCES: 8  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/10989  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/306,872  
FILING DATE: 09-SEP-1994  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US95-10989-2

Query Match 100.0%; Score 54; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.00035;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
Db 1 GSNKGATIGLM 11

RESULT 12  
US-09-005-215-11  
Sequence 11, Application US/09005215  
Patent No. 6172043  
GENERAL INFORMATION:  
APPLICANT: Ingram, Vernon M.  
APPLICANT: Blanchard, Barbara J.  
TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S  
TITLE OF INVENTION: DISEASE CAUSED BY -AMYLOID PEPTIDES  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
STREET: 600 ATLANTIC AVENUE  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/005,215  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/035,847  
FILING DATE: 10-JAN-1997  
PRIOR APPLICATION DATA: 08/960,188  
APPLICATION NUMBER: 08/960,188  
FILING DATE: 29-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Gates, Edward R.  
REGISTRATION NUMBER: 31,616  
REFERENCE/DOCKET NUMBER: M0656/7035  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-720-2441  
TELEFAX: 617-720-3500  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
US-09-005-215-11

Query Match 100.0%; Score 54; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.00044;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11  
DB 4 GSNKGATIGLM 14

RESULT 13  
US-08-304-585-7  
Sequence 7, Application US/08304585  
Patent No. 5721106  
GENERAL INFORMATION:  
APPLICANT: Magglio, John E.  
ATTORNEY/AGENT INFORMATION:  
NAME: Mantyh, Patrick W.  
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND  
METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Muehling, Raasch, Gebhardt & Schwappach, P.A.  
STREET: P.O. Box 581415  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55458-1415  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/304,585  
FILING DATE: 12-SEP-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Muehling, Ann M.  
REGISTRATION NUMBER: 33,977  
REFERENCE/DOCKET NUMBER: 110,00010120  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-305-1217  
TELEFAX: 612-305-1228  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide

US-08-304-585-7

Query Match 100.0%; Score 54; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.00084;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11  
DB 16 GSNKGATIGLM 26

RESULT 14  
US-08-475-579A-4  
Sequence 4, Application US/08475579A  
Patent No. 5854215  
GENERAL INFORMATION:  
APPLICANT: Mark A. Findeis et al.  
TITLE OF INVENTION: Modulators of (SYMBOL 98 \f "symbol")-Amyloid Peptide Aggre  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,579A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/404,831  
FILING DATE: 14-MAR-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kara, Catherine J.  
REGISTRATION NUMBER: P41,106  
REFERENCE/DOCKET NUMBER: PPI-002CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-475-579A-4

QY 1 GSNKGATIGLM 11  
DB 19 GSNKGATIGLM 29

RESULT 15  
US-08-304-585-6  
Sequence 6, Application US/08304585  
Patent No. 5721106  
GENERAL INFORMATION:  
APPLICANT: Magglio, John E.  
ATTORNEY/AGENT INFORMATION:  
NAME: Mantyh, Patrick W.

;; TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND  
;; TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE  
;; NUMBER OF SEQUENCES: 12  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Mueling, Raasch, Gebhardt & Schwappach, P.A.  
;; STREET: P.O. Box 581415  
;; CITY: Minneapolis  
;; STATE: MN  
;; COUNTRY: USA  
;; ZIP: 55458-1415  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/304,585  
;; FILING DATE: 12-SEP-1994  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mueling, Ann M.  
;; REGISTRATION NUMBER: 33,977  
;; REFERENCE/DOCKET NUMBER: 110.00010120  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 612-305-1217  
;; TELEFAX: 612-305-1228  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 35 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: not relevant  
;; TOPOLOGY: not relevant  
;; MOLECULE TYPE: peptide  
;; US-08-304-585-6

Query Match 100.0%; Score 54; DB 1; Length 35;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11  
|||||  
DB 25 GSNKGAIIGLM 35

Search completed: April 24, 2002, 09:18:15  
Job time: 174 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:24:25 ; Search time 63.44 Seconds  
(without alignments)  
25.362 Million cell updates/sec

Title: US-09-689-469-4  
Perfect score: 11  
Sequence: 1 GSNKGATIGLM 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 473505 seqs, 146272329 residues

Word size : 0

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- 1: SPTREMBL\_17.\*
- 2: sp.archaea.\*
- 3: sp.bacteria.\*
- 4: sp.fungi.\*
- 5: sp.human.\*
- 6: sp.invertebrate.\*
- 7: sp.mammal.\*
- 8: sp.mhc.\*
- 9: sp.organelle.\*
- 10: sp.phage.\*
- 11: sp.plant.\*
- 12: sp.rodent.\*
- 13: sp.virus.\*
- 14: sp.vertebrate.\*
- 15: sp.unclassified.\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description         |
|------------|-------|-------------|--------|-------|---------------------|
| 1          | 11    | 100.0       | 49     | 6     | 097917 bos taurus   |
| 2          | 11    | 100.0       | 79     | 11    | 035463 cricetus     |
| 3          | 11    | 100.0       | 82     | 4     | P78438 homo sapien  |
| 4          | 11    | 100.0       | 82     | 4     | P78438 homo sapien  |
| 5          | 11    | 100.0       | 82     | 4     | Q16014 homo sapien  |
| 6          | 11    | 100.0       | 82     | 4     | Q16019 homo sapien  |
| 7          | 11    | 100.0       | 82     | 4     | Q16020 homo sapien  |
| 8          | 11    | 100.0       | 97     | 4     | Q13778 homo sapien  |
| 9          | 11    | 100.0       | 534    | 13    | 093296 gallus galli |
| 10         | 11    | 100.0       | 569    | 13    | 093296 gallus galli |
| 11         | 11    | 100.0       | 607    | 11    | 098932 mus musculu  |
| 12         | 11    | 100.0       | 693    | 13    | 098560 xenopus lae  |
| 13         | 11    | 100.0       | 695    | 11    | P97487 mus musculu  |
| 14         | 11    | 100.0       | 695    | 11    | Q60436 cavia porce  |
| 15         | 11    | 100.0       | 695    | 13    | 09DGJ8 gallus galli |
| 16         | 11    | 100.0       | 695    | 13    | 098SF9 xenopus lae  |
| 17         | 11    | 100.0       | 699    | 13    | 057394 natke japon  |
| 18         | 11    | 100.0       | 737    | 13    | 093279 fugu rubrip  |
| 19         | 11    | 100.0       | 747    | 13    | Q91963 xenopus lae  |
|            |       |             | 751    | 13    | Q9DGJ7 gallus galli |

|    |    |       |     |    |                    |
|----|----|-------|-----|----|--------------------|
| 20 | 11 | 100.0 | 770 | 6  | 09TU10 sus scrofa  |
| 21 | 11 | 100.0 | 780 | 13 | 073683 tetraodon f |
| 22 | 10 | 90.9  | 612 | 13 | 0919E7 brachydanio |
| 23 | 9  | 81.8  | 33  | 4  | 09UC33 homo sapien |
| 24 | 7  | 63.6  | 247 | 2  | 09KBT2 bacillus ha |
| 25 | 7  | 63.6  | 828 | 7  | 09FGRL arbidopsis  |
| 26 | 6  | 54.5  | 20  | 4  | 09UCB6 homo sapien |
| 27 | 6  | 54.5  | 30  | 4  | 09UCA9 homo sapien |
| 28 | 6  | 54.5  | 130 | 6  | 029364 sus scrofa  |
| 29 | 6  | 54.5  | 131 | 5  | 024897 echinococu  |
| 30 | 6  | 54.5  | 143 | 11 | 09DBK2 mus musculu |
| 31 | 6  | 54.5  | 144 | 2  | 09AM08 plectonema  |
| 32 | 6  | 54.5  | 157 | 10 | 09C5F3 arabidopsis |
| 33 | 6  | 54.5  | 175 | 5  | 09VZ11 droscophila |
| 34 | 6  | 54.5  | 176 | 2  | 09KCS1 bacillus ha |
| 35 | 6  | 54.5  | 188 | 5  | 09NHZ2 droscophila |
| 36 | 6  | 54.5  | 190 | 5  | 024799 echinococu  |
| 37 | 6  | 54.5  | 192 | 5  | 093713 caenorhabd  |
| 38 | 6  | 54.5  | 192 | 5  | 09U4H8 caenorhabd  |
| 39 | 6  | 54.5  | 205 | 2  | 09WXS1 thermotoga  |
| 40 | 6  | 54.5  | 205 | 2  | 09KXK7 vibrio chol |
| 41 | 6  | 54.5  | 216 | 11 | 09JMD0 mus musculu |
| 42 | 6  | 54.5  | 216 | 11 | 09JMD6 mus musculu |
| 43 | 6  | 54.5  | 223 | 11 | 09Z1U9 mus musculu |
| 44 | 6  | 54.5  | 230 | 2  | 09KMA3 vibrio chol |
| 45 | 6  | 54.5  | 234 | 2  | 007221 mycobacteri |

ALIGNMENTS

|  |                 |               |                         |            |  |
|--|-----------------|---------------|-------------------------|------------|--|
| RESULT 1   |                 |               |                         |            |  |
| ID 097917  | PRELIMINARY;    | PRT;          | 49 AA.                  |            |  |
| AC 097917;   |                 |               |                         |            |  |
| DT 01-MAY-1999 (TREMBLrel. 10, Created)                                  |                 |               |                         |            |  |
| DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)                     |                 |               |                         |            |  |
| DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)                   |                 |               |                         |            |  |
| DE AMYLOID PRECURSOR PROTEIN (FRAGMENT).                                 |                 |               |                         |            |  |
| GN AFP.  |                 |               |                         |            |  |
| OS Bos taurus (Bovine).  |                 |               |                         |            |  |
| OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;               |                 |               |                         |            |  |
| OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;     |                 |               |                         |            |  |
| OC Bovidae; Bovine; Bos.   |                 |               |                         |            |  |
| OX NCBI_TaxID=9913;  |                 |               |                         |            |  |
| RN [1]   |                 |               |                         |            |  |
| RP SEQUENCE FROM N.A.  |                 |               |                         |            |  |
| RA Konfortov B.A., Licence V.E., Miller J.R.;                            |                 |               |                         |            |  |
| RT "Re-sequencing of DNA from a diverse panel of cattle reveals frequent |                 |               |                         |            |  |
| RT polymorphisms in both intron and exon."                               |                 |               |                         |            |  |
| RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.               |                 |               |                         |            |  |
| DR EMBL; A013033; CAB38017.1; -  |                 |               |                         |            |  |
| DR HSSP; P05067; IBA4.   |                 |               |                         |            |  |
| FT NON_TER   | 1               |               |                         |            |  |
| FT NON_TER   | 49              | 49            |                         |            |  |
| SO SEQUENCE  | 49 AA;          | 5183 MW;      | 6287463F0559BDED CRC64; |            |  |
| Query Match  | 100.0%;         | Score 11;     | DB 6;                   | Length 49; |  |
| Best Local Similarity  | 100.0%;         | Pred. No. 3;  | 7e-05;                  |            |  |
| Matches 11;  | Conservative 0; | Mismatches 0; | Indels 0;               | Gaps 0;    |  |
| RESULT 2   |                 |               |                         |            |  |
| ID 035463  | PRELIMINARY;    | PRT;          | 79 AA.                  |            |  |
| AC 035463;   |                 |               |                         |            |  |
| DT 01-JAN-1998 (TREMBLrel. 05, Created)                                  |                 |               |                         |            |  |
| DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)                     |                 |               |                         |            |  |

DT 01-MAR-2001 (TREMURel. 16, Last annotation update)  
 DE ALZHEIMER'S AMYLOID BETA PROTEIN PRECURSOR (FRAGMENT).  
 GN BETA APP.  
 OS Cricetus griseus (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Cricetus.  
 OX NCBI\_TaxID=10029;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sambamurti K., Pinnix I., Gandhi S.;  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF030413; AAB6608.1; -;  
 DR HSSP: P05067; 1QCM.  
 FT NON\_TER 1 79  
 FT NON\_TER 79 79  
 SQ SEQUENCE 79 AA; 8538 MW; 37E2C6C3BFF3E597 CRC64;

Query Match 100.0%; Score 11; DB 11; Length 79;  
 Best Local Similarity 100.0%; Pred. No. 5, 6e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
 DB 45 GSNKGATIGLM 55

RESULT 3  
 ID P78438 PRELIMINARY; PRT; 82 AA.  
 AC P78438;  
 DT 01-MAY-1997 (TREMURel. 03, Created)  
 DT 01-MAY-1997 (TREMURel. 03, Last sequence update)  
 DT 01-MAR-2001 (TREMURel. 16, Last annotation update)  
 DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).  
 GN APP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=89392030; PubMed=2675837;  
 RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,  
 RA Little S.P.;  
 RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows  
 RT similarity to soybean trypsin inhibitor."  
 RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).  
 RN [2]  
 RP SEQUENCE OF 19-48 FROM N.A.  
 RX MEDLINE=87120329; PubMed=2949367;  
 RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,  
 RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;  
 RT "Amyloid beta protein gene: CDNA, mRNA distribution, and genetic  
 RT linkage near the Alzheimer locus."  
 RL Science 235:880-884(1987).  
 RN [3]  
 RP SEQUENCE OF 32-63 FROM N.A.  
 RX MEDLINE=9305397; PubMed=1415269;  
 RA Kamino K., Orr H.T., Payami H., Wiseman E.M., Alonso M.E., Pulst S.M.,  
 RA Anderson L., O'dahl S., Nemens E., White J.A.;  
 RT "Linkage and mutational analysis of familial Alzheimer disease  
 RT kinds for the APP gene region."  
 RL Am. J. Hum. Genet. 51:998-1014(1992).  
 DR EMBL: M28270; AAAS1768.1; -;  
 DR EMBL: M29269; AAAS1768.1; JOINED.  
 DR EMBL: M15532; AAAS1564.1; -;  
 DR EMBL: S45136; AAB23646.1; -;  
 DR HSSP: P05067; 1BA4.  
 FT NON\_TER 1 82  
 FT NON\_TER 82 82  
 SQ SEQUENCE 82 AA; 8994 MW; 8DA9EA2B813A070E CRC64;

Query Match 100.0%; Score 11; DB 4; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 5, 8e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
 DB 41 GSNKGATIGLM 51

RESULT 4  
 ID Q16014 PRELIMINARY; PRT; 82 AA.  
 AC Q16014;  
 DT 01-NOV-1996 (TREMURel. 01, Created)  
 DT 01-NOV-1996 (TREMURel. 01, Last sequence update)  
 DT 01-MAR-2001 (TREMURel. 16, Last annotation update)  
 DE BETA-AMYLOID PEPTIDE PRECURSOR (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93236601; PubMed=8476439;  
 RA Denman R.B., Rosenczwaig R., Miller D.L.;  
 RT "A system for studying the effect(s) of familial Alzheimer disease  
 RT mutations on the processing of the beta-amyloid peptide precursor."  
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
 DR EMBL: S60721; AAB26263.2; -;  
 DR HSSP: P05067; 1BA4.  
 FT NON\_TER 1 82  
 FT NON\_TER 82 82  
 SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 100.0%; Score 11; DB 4; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 5, 8e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
 DB 42 GSNKGATIGLM 52

RESULT 5  
 ID Q16019 PRELIMINARY; PRT; 82 AA.  
 AC Q16019;  
 DT 01-NOV-1996 (TREMURel. 01, Created)  
 DT 01-NOV-1996 (TREMURel. 01, Last sequence update)  
 DT 01-MAR-2001 (TREMURel. 16, Last annotation update)  
 DE BETA-AMYLOID PEPTIDE PRECURSOR (FRAGMENT).  
 GN BETA APP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93236601; PubMed=8476439;  
 RA Denman R.B., Rosenczwaig R., Miller D.L.;  
 RT "A system for studying the effect(s) of familial Alzheimer disease  
 RT mutations on the processing of the beta-amyloid peptide precursor."  
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
 DR EMBL: S61380; AAB26264.2; -;  
 DR HSSP: P05067; 1BA4.  
 FT NON\_TER 1 82  
 FT NON\_TER 82 82  
 SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match 100.0%; Score 11; DB 4; Length 82;



Best Local Similarity 100.0%; Pred. No. 5.8e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
DB 42 GSNKGATIGLM 52

## RESULT 6

ID 016020 PRELIMINARY; PRT; 82 AA.  
AC 016020;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)  
DE BETA-AMYLOID PEPTIDE PRECURSOR (FRAGMENT).  
GN BETA APP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;

RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE-93236601; PubMed-8476439;  
RA Denman R.B., Rosenzweig R., Miller D.L.;  
RT "A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor.";  
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
DR EMBL; S61383; AAB2625.2; -.  
DR HSSP; P05067; 1BA4. 1  
FT NON\_TER 1  
FT SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match 100.0%; Score 11; DB 4; Length 82;  
Best Local Similarity 100.0%; Pred. No. 5.8e-05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
DB 42 GSNKGATIGLM 52

## RESULT 7

ID 013778 PRELIMINARY; PRT; 97 AA.  
AC 013778;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)  
DE AMYLOID PROTEIN (AD-AP) (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;

RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE-87120328; PubMed-3810169;  
RA Goldhaber D., Ierman M.I., McBride O.W., Saffioti U., Gajdusek D.C.;  
RT "Characterization and chromosomal localization of a cDNA encoding brain amyloid of Alzheimer's disease.";  
RL Science 235:877-880(1987).  
DR EMBL; M15533; AAA35540.1; -.  
DR HSSP; P05067; 1BA4.  
DR InterPro; IPR001868; A4\_APP.  
DR PRINTS; PR00203; AMYLOIDA4.  
FT NON\_TER 1  
FT SEQUENCE 97 AA; 10884 MW; E528CDBA48DE474E CRC64;

Query Match 100.0%; Score 11; DB 4; Length 97;  
Best Local Similarity 100.0%; Pred. No. 6.7e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
DB 23 GSNKGATIGLM 33

## RESULT 8

ID 093296 PRELIMINARY; PRT; 534 AA.  
AC 093296;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)  
DE AMYLOID PRECURSOR PROTEIN (FRAGMENT).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;

RN [1]  
RP SEQUENCE FROM N.A.  
RA Barnes N.Y., Ling L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,  
RA Milligan C.E.;  
RT "Increased production of amyloid precursor protein provides a substrate for Caspase 3 in dying motoneurons.";  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF042098; AAC25052.1; -.  
DR HSSP; P05067; 1BA4.  
DR InterPro; IPR001868; A4\_APP.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR PROSITE; PS00319; A4\_EXTRA; 1.  
DR PROSITE; PS00320; A4\_INTRA; 1.  
FT NON\_TER 1  
FT SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;

Query Match 100.0%; Score 11; DB 13; Length 534;  
Best Local Similarity 100.0%; Pred. No. 0.00029;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
DB 460 GSNKGATIGLM 470

## RESULT 9

ID 09PVL1 PRELIMINARY; PRT; 569 AA.  
AC 09PVL1;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)  
DE AMYLOID PROTEIN PRECURSOR (FRAGMENT).  
GN APP.

OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA TISSUE-BRAIN;  
RA Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;  
RT "What the evolution of the amyloid protein precursor supergene family tells us about its function.";  
RL Neurochem. Int. 0:0-0(2000).  
DR EMBL; AF030341; AAF12698.1; -.  
DR HSSP; P05067; 1BA4.  
DR InterPro; IPR001868; A4\_APP.  
DR Pfam; PF02177; A4\_EXTRA; 1.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR SMART; SM00006; A4\_EXTRA; 1.

DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 569 AA; 64753 MW; 0ABBBB851863A19D CRC64;

Query Match 100.0%; Score 11; DB 13; Length 569;  
 Best Local Similarity 100.0%; Pred. No. 0.0003;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11  
 DB 496 GSNKGATIGLM 506

RESULT 10  
 099K32 PRELIMINARY; PRT; 607 AA.  
 AC 099K32;  
 DT 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DE UNKNOWN (PROTEIN FOR IMAGE:3486773) (FRAGMENT).  
 OS Mus musculus (mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=MAMMARY TUMOR;  
 RA Strausberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC005490; AAH05490.1; -  
 FT NON\_TER 1  
 SQ SEQUENCE 607 AA; 68391 MW; BF802214CBA7D172 CRC64;

Query Match 100.0%; Score 11; DB 11; Length 607;  
 Best Local Similarity 100.0%; Pred. No. 0.00032;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
 DB 533 GSNKGATIGLM 543

RESULT 11  
 098SG0 PRELIMINARY; PRT; 693 AA.  
 AC 098SG0;  
 DT 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE BETA-AMYLLOID PRECURSOR PROTEIN A.  
 GN APP.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_Taxid=8355;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RA Van den Hurk W.H.;  
 RL Thesis (2001), Department of Biological Sciences,  
 RU University of Nijmegen, Nijmegen, Netherlands.  
 DR EMBL; AJ298150; CAC37193.1; -  
 KW Signal.  
 FT SIGNAL 1  
 SQ SEQUENCE 693 AA; 78568 MW; CAFID655C1AB53 CRC64;

Query Match 100.0%; Score 11; DB 13; Length 693;  
 Best Local Similarity 100.0%; Pred. No. 0.00036;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GSNKGATIGLM 11  
 DB 619 GSNKGATIGLM 629

RESULT 12  
 P97487 PRELIMINARY; PRT; 695 AA.  
 ID P97487;  
 AC P97487; P97942;  
 DT 01-MAY-1997 (TREMblrel. 03, Created)  
 DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE HIPPOCAMPAL AMYLOID PROTEIN.  
 GN APP.

OS Mus musculus (mouse).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SAMP8; TISSUE=HIPPOCAMPUS;  
 RA Flood J.F., Kumar V.B., Sasser T., Word I., Morley J.E.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 RN 12  
 RP SEQUENCE OF 581-662 FROM N.A.  
 RC STRAIN=129SV;  
 RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capecci M.,  
 RA Loring J.F., Goate A.M.;  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U84012; AAB41502.1; -  
 DR EMBL; U82624; AAB40919.1; -  
 DR HSSP; P05067; 10CM.  
 DR MGD; MGI:88059; App.  
 DR InterPro; IPR001868; A4\_APP.  
 DR Pfam; Pf02177; A4\_EXTRA; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 SQ SEQUENCE 695 AA; 78414 MW; 9A5FB2ED261236E CRC64;

Query Match 100.0%; Score 11; DB 11; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 0.00036;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11  
 DB 621 GSNKGATIGLM 631

RESULT 13  
 060496 PRELIMINARY; PRT; 695 AA.  
 ID 060496;  
 AC 060496;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.  
 OX NCBI\_Taxid=10141;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RA Beck M., Mueller D., Bigl V.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 CC -FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
 CC G(O).

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: TO OTHER SPECIES APP ANALOGUES.  
 DR EMBL: X97631; CAA66230.1; -.  
 DR HSSP: P05067; IBA4.  
 DR InterPro: IPR001868; A4\_APP.  
 DR Pfam: PF02177; A4\_EXTRA; 1.  
 DR PRINTS: PR00203; AMYLOIDA4.  
 DR SMART: SM00006; A4\_EXTRA; 1.  
 DR PROSITE: PS00319; A4\_EXTRA; 1.  
 DR PROSITE: PS00320; A4\_INTRA; 1.  
 SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 100.0%; Score 11; DB 11; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 0.00036;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
 DB 621 GSNKGATIGLM 631

## RESULT 14

O9DGJ8 PRELIMINARY; PRT; 695 AA.  
 AC O9DGJ8;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE BETA-AMYLROID PRECURSOR PROTEIN 695 ISOFORM.  
 OS Gallus gallus (Chicken).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 CC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sarasa M., Rodolosse A., Sorribas V.;  
 RT "Cloning of full-length chicken beta-amyloid precursor protein  
 RT isoforms".  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF289218; AAG00593.1; -.  
 DR InterPro: IPR001868; A4\_APP.  
 DR Pfam: PF02177; A4\_EXTRA; 1.  
 DR PRINTS: PR00203; AMYLOIDA4.  
 DR SMART: SM00006; A4\_EXTRA; 1.  
 DR PROSITE: PS00319; A4\_EXTRA; 1.  
 SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 100.0%; Score 11; DB 13; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 0.00036;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
 DB 621 GSNKGATIGLM 631

## RESULT 15

O98SF9 PRELIMINARY; PRT; 695 AA.  
 AC O98SF9;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE BETA-AMYLROID PRECURSOR PROTEIN B.  
 GN APP.  
 OS Xenopus laevis (African clawed frog).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
 CC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Van den Hurk W.H.;  
 RL Thesis (2001), Department of Biological Sciences,  
 DR University of Nijmegen, Nijmegen, Netherlands.  
 DR EMBL: AJ298151; CAC37194.1; -.  
 KW Signal.  
 FT SIGNAL.  
 SQ SEQUENCE 695 AA; 78803 MW; DC14EB02AFB0204A CRC64;

Query Match 100.0%; Score 11; DB 13; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 0.00036;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
 DB 621 GSNKGATIGLM 631

Search completed: April 24, 2002, 09:24:25  
 Job time: 249 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:19:00 ; Search time 38.71 Seconds

(without alignments)  
21.646 Million cell updates/sec

Title: US-09-689-469-4

Perfect score: 54

Sequence: 1 GSNKGATIGLM 11

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 54    | 100.0       | 42     | 2     | PN0512      |
| 2          | 54    | 100.0       | 57     | 2     | E60045      |
| 3          | 54    | 100.0       | 57     | 2     | F60045      |
| 4          | 54    | 100.0       | 57     | 2     | D60045      |
| 5          | 54    | 100.0       | 57     | 2     | B60045      |
| 6          | 54    | 100.0       | 57     | 2     | B60045      |
| 7          | 54    | 100.0       | 57     | 2     | B60045      |
| 8          | 54    | 100.0       | 82     | 2     | P00438      |
| 9          | 54    | 100.0       | 695    | 1     | A43795      |
| 10         | 54    | 100.0       | 695    | 1     | A27485      |
| 11         | 54    | 100.0       | 695    | 2     | S00550      |
| 12         | 54    | 100.0       | 747    | 2     | JH0773      |
| 13         | 54    | 100.0       | 770    | 1     | ORH044      |
| 14         | 41    | 75.9        | 247    | 2     | B83880      |
| 15         | 38    | 70.4        | 229    | 2     | B83971      |
| 16         | 38    | 70.4        | 300    | 2     | S47764      |
| 17         | 38    | 70.4        | 300    | 2     | B86028      |
| 18         | 37    | 68.5        | 216    | 2     | T29039      |
| 19         | 37    | 68.5        | 906    | 2     | A43817      |
| 20         | 36    | 66.7        | 305    | 2     | S75667      |
| 21         | 36    | 66.7        | 390    | 1     | TVMVCB      |
| 22         | 36    | 66.7        | 417    | 2     | F70681      |
| 23         | 36    | 66.7        | 496    | 2     | JC5170      |
| 24         | 36    | 66.7        | 661    | 1     | A42287      |
| 25         | 36    | 66.7        | 896    | 2     | B43817      |
| 26         | 35    | 64.8        | 238    | 2     | E70337      |
| 27         | 35    | 64.8        | 309    | 2     | G75286      |
| 28         | 35    | 64.8        | 411    | 2     | A44121      |
| 29         | 35    | 64.8        | 414    | 1     | I38977      |

|    |    |      |      |   |        |                     |
|----|----|------|------|---|--------|---------------------|
| 30 | 35 | 64.8 | 486  | 2 | B70504 | probable transmembr |
| 31 | 35 | 64.8 | 593  | 2 | A96783 | unknown protein P2  |
| 32 | 35 | 64.8 | 673  | 2 | B70528 | probable peptidase  |
| 33 | 35 | 64.8 | 699  | 2 | A96529 | hypothetical prote  |
| 34 | 34 | 63.0 | 269  | 2 | S65034 | cytochrome-c oxida  |
| 35 | 34 | 63.0 | 308  | 2 | S67657 | hypothetical prote  |
| 36 | 36 | 63.0 | 315  | 2 | S76043 | hypothetical prote  |
| 37 | 34 | 63.0 | 323  | 2 | S25513 | outer membrane pro  |
| 38 | 34 | 63.0 | 345  | 2 | E64458 | branched-chain am   |
| 39 | 34 | 63.0 | 503  | 2 | S73843 | general amino acid  |
| 40 | 34 | 63.0 | 605  | 2 | S67815 | protein-tyrosine k  |
| 41 | 34 | 63.0 | 660  | 2 | B70662 | probable membrane   |
| 42 | 34 | 63.0 | 1362 | 2 | T41534 | leptomycin B resis  |
| 43 | 33 | 61.1 | 161  | 2 | H71677 | invasion protein A  |
| 44 | 33 | 61.1 | 169  | 2 | B83640 | hypothetical prote  |
| 45 | 33 | 61.1 | 293  | 2 | J00380 | proteinase T (Ec 3  |

#### ALIGNMENTS

RESULT 1  
PN0512  
beta-amyloid protein - guinea pig (fragment)  
C:Species: Cavia porcellus (guinea pig)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
C:Accession: PN0512  
R:Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno  
Biochem. Biophys. Res. Commun. 193, 624-630, 1993  
A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra  
A:Reference number: PN0512, MID:9320653  
A:Accession: PN0512  
A:Molecule type: protein  
A:Residues: 1-42 <SH1>  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
C:Keywords: alternative splicing; amyloid

Query Match 100.0%; Score 54; DB 2; Length 42;  
Best Local Similarity 100.0%; Pred. No. 0.0021;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11  
DB 25 GSNKGATIGLM 35  
RESULT 2  
E60045  
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)  
C:Species: Ovis sp. (sheep)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: E60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d  
A:Reference number: A60045, MID:92017079  
A:Accession: E60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: EMBL:X56130  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 54; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 0.0028;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11  
DB 30 GSNKGATIGLM 40

RESULT 3

F60045

Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999

C:Accession: F60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; PMID:92017079

A:Accession: F60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56127; NID:q1895; PIDN:CA39592.1; PID:q1896

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best local Similarity 100.0%; Score 54; DB 2; Length 57;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
|||||

DB 30 GSNKGATIGLM 40

RESULT 4

G60045

Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)

C:Species: Cavia porcellus (guinea pig)

C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995

C:Accession: G60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; PMID:92017079

A:Accession: G60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56126

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best local Similarity 100.0%; Score 54; DB 2; Length 57;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
|||||

DB 30 GSNKGATIGLM 40

RESULT 5

D60045

Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995

C:Accession: D60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,

A:Reference number: A60045; PMID:92017079

A:Accession: D60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56124

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match  
Best local Similarity 100.0%; Score 54; DB 2; Length 57;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
|||||

DB 30 GSNKGATIGLM 40

RESULT 6

A60045

Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)

C:Species: Canis lupus familiaris (dog)

C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995

C:Accession: A60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; PMID:92017079

A:Accession: A60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56125

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best local Similarity 100.0%; Score 54; DB 2; Length 57;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
|||||

DB 30 GSNKGATIGLM 40

RESULT 7

B60045

Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)

C:Species: Ursus maritimus (polar bear)

C>Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999

C:Accession: B60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; PMID:92017079

A:Accession: B60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56128; NID:q2165; PIDN:CA39593.1; PID:q2166

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best local Similarity 100.0%; Score 54; DB 2; Length 57;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
|||||

DB 30 GSNKGATIGLM 40

RESULT 8

PQ0438

Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 30-Sep-1993 #sequence\_revision 19-Oct-1995 #text\_change 19-Oct-1995

C:Accession: PQ0438; C60045

R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.

Biochem. Biophys. Res. Commun. 188, 905-911, 1992

A>Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor

A:Reference number: PQ0438; PMID:93075180

A:Accession: PQ0438  
A:Molecule type: DNA  
A:Residues: 1-82 <DAV>  
A:Cross-references: GB:M83558; GB:M83657  
R:Jomuncione, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; MUID:92017079  
A:Accession: C60045  
A:Molecule type: mRNA  
A:Residues: 12-68 <JOH>  
A:Cross-references: EMBL:X56129  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 54; DB 2; Length 82;  
Best Local Similarity 100.0%; Pred. No. 0.004;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIGLM 11  
|||||  
Db 41 GSNKGAIIGLM 51

RESULT 9  
A49795  
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque  
C:Species: Macaca fascicularis (crab-eating macaque)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A49795  
R:Podlasky, M.B.; Tolan, D.R.; Selkoe, D.J.  
Am. J. Pathol. 138, 1423-1435, 1991  
A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a  
A:Reference number: A49795; MUID:91273117  
A:Accession: A49795  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-695 <POD>  
A:Cross-references: GB:M58727; NID:q342062; PIDN:AAA36829.1; PID:q342063  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing

Query Match 100.0%; Score 54; DB 1; Length 695;  
Best Local Similarity 100.0%; Pred. No. 0.032;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIGLM 11  
|||||  
Db 621 GSNKGAIIGLM 631

RESULT 10  
A27485  
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse  
N:Alternate names: proteinase nexin II  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 13-Aug-1999  
C:Accession: A27485; S19727; I49485  
R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.  
Biochem. Biophys. Res. Commun. 149, 665-671, 1987  
A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precu  
A:Reference number: A27485; MUID:86106489  
A:Accession: A27485  
A:Molecule type: mRNA  
A:Residues: 1-695 <YAM>  
A:Cross-references: GB:M18373; NID:q191568; PIDN:AAA37139.1; PID:q309085  
A:Experimental source: brain  
R:De Strooper, B.; van Leuven, F.; van den Berghe, H.  
Biochem. Biophys. Acta 1129, 141-143, 1991  
A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer  
A:Reference number: S19727; MUID:92096458

A:Accession: S19727  
A:Molecule type: mRNA  
A:Residues: 1-210 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>  
A:Cross-references: EMBL:X59379  
R:Rizumi, R.; Yamada, T.; Yoshikawa, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.  
Gene 112, 189-195, 1992  
A:Title: Positive and negative regulatory elements for the expression of the Alzheimer  
A:Reference number: I49485; MUID:92209998  
A:Accession: I49485  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-19 <RBS>  
A:Cross-references: GB:DJ0603; NID:q220328; PIDN:BAA01456.1; PID:q220329  
C:Genetics:  
A:Map position: 16c3  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 100.0%; Score 54; DB 2; Length 695;  
Best Local Similarity 100.0%; Pred. No. 0.032;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIGLM 11  
|||||  
Db 621 GSNKGAIIGLM 631

RESULT 11  
S00550  
Alzheimer's disease amyloid beta protein precursor - rat  
N:Alternate names: beta-A4 amyloid protein  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 13-Aug-1999  
C:Accession: S00550; A41245; A39620; S46251  
R:Shivers, B.D.; Halblach, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.  
EMBO J. 7, 1365-1370, 1988  
A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat br  
A:Reference number: S00550; MUID:88312583  
A:Accession: S00550  
A:Molecule type: mRNA  
A:Residues: 1-695 <SHI>  
A:Cross-references: EMBL:X07648; NID:q55616; PIDN:CAA30488.1; PID:q55617  
R:Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saltch, T.; Cole, G.  
Science 241, 223-226, 1988  
A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan co  
A:Reference number: A41245; MUID:88264430  
A:Accession: A41245  
A:Molecule type: protein  
A:Residues: 18-37 'X', 39-40 'X', 42-44 <SCH>  
A:Note: evidence for heparan sulfate attachment  
R:Hesse, U.; Behner, D.; Masters, C.L.; Multhaup, G.  
FEBS Lett. 349, 109-116, 1994  
A:Title: The beta-A4 amyloid precursor protein binding to copper.  
A:Reference number: S46251; MUID:94320627  
A:Contents: annotation; copper binding sites  
A:Note: rat peptides were isolated but not sequenced  
R:Potemkin, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.  
J. Biol. Chem. 266, 8464-8469, 1991  
A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat b  
A:Reference number: A39820; MUID:91217087  
A:Accession: A39820  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 18-32 <POT>  
A:Experimental source: brain  
C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein  
F:625-648/Domain: transmembrane #status predicted <TMM>

Query Match 100.0%; Score 54; DB 2; Length 695;

Best Local Similarity 100.0%; Pred. No. 0.032;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAITGLM 11  
|||||

Db 621 GSNKGAITGLM 631

RESULT 12

Alzheimer's disease amyloid beta protein precursor - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 13-Aug-1999

C:Accession: JH0773

R:Okado, H.; Okamoto, H.

Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992

A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental

A:Reference number: JH0773; PMID:93129227

A:Accession: JH0773

A:Molecule type: mRNA

A:Residues: 1-747 <OKA>

A:Cross-references: GB:S52417; NID:9263150; PIDN:AAB24853.1; PID:g263151

A:Experimental source: Larva

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

C:Keywords: alternative splicing; amyloid

F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 100.0%; Score 54; DB 2; Length 747;  
Best Local Similarity 100.0%; Pred. No. 0.034;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAITGLM 11  
|||||

Db 673 GSNKGAITGLM 683

RESULT 13

ORHUA4 Alzheimer's disease amyloid beta protein precursor [validated] - human

N:Alternative names: Alzheimer's disease amyloid A4 protein; coagulation factor XIA inhibi

N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1987 #sequence\_revision 28-Jul-1995 #text\_change 15-Sep-2000

C:Accession: S02260; S05194; A32277; A32260; A35466; I39452; I39453; I39453; I39453; A44

4688; A28883; A29302; A60803; J00038; S06121; A60353; A59011; A38384; S29076; S38252; S3

R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey

Nucleic Acids Res. 17, 517-522, 1989

A:Title: The Prec4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b

A:Reference number: S02260; PMID:89128427

A:Accession: S02260

A:Molecule type: DNA

A:Residues: 1-288, 'V', 365-770 <LEM1>

A:Cross-references: EMBL:X13466

A:Note: alternative splice form APP(695)

R:Lemaire, H.G.

submitted to the EMBL Data Library, November 1988

A:Reference number: S05194

A:Accession: S05194

A:Molecule type: DNA

A:Residues: 1-14, 'V', 17-288, 'V', 365-770 <LEM2>

A:Cross-references: EMBL:X13466; NID:935598; PIDN:CAA31830.1; PID:g871360

A:Note: alternative splice form APP(695)

R:La Faut, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.

Biochem. Biophys. Res. Commun. 159, 297-304, 1989

A:Title: Characterization of the 5'-end region and the first two exons of the beta-prote

A:Reference number: A32277; PMID:89165870

A:Accession: A32277

A:Molecule type: DNA

A:Residues: 1-75 <LAF>

A:Cross-references: GB:M24546; GB:M24547; NID:9341202; PIDN:AA013654.1; PID:g516074

R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.

Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989

A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simila

A:Reference number: A33260; PMID:89392030

A:Accession: A33260

A:Molecule type: DNA

A:Residues: 656-737 <JOH>

A:Cross-references: GB:M29270; NID:q178863; PIDN:AAA51768.1; PID:q178865

R:Prelli, F.; Levy, E.; van Dineen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B

Biochem. Biophys. Res. Commun. 170, 301-307, 1990

A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid

A:Reference number: A35486; PMID:90321244

A:Accession: A35486

A:Molecule type: DNA

A:Residues: 672-710 <PRE1>

A:Note: 693-Gln was found in DNA isolated from HCHWA-D patients

R:Toshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.

Gene 87, 257-263, 1990

A:Title: Genomic organization of the human amyloid beta-protein precursor gene.

A:Reference number: I39451; PMID:90236318

A:Accession: I39452

A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/

A:Molecule type: DNA

A:Residues: 1-770 <YOS1>

A:Cross-references: GB:M33112; NID:q178613; PIDN:AAB59502.1; PID:q178616

A:Accession: I39451

A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/

A:Molecule type: DNA

A:Residues: 1-530, 'OMLPVPAFWEAKYGR' <YOS2>

A:Cross-references: GB:M34875; NID:q178608; PIDN:AAB59501.1; PID:q178615

R:Toshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.

Gene 102, 291-292, 1991

A:Reference number: A59020; PMID:91340168

A:Contents: annotation; erratum

A:Note: revised physical map for reference I39451

R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Du

Science 248, 1124-1126, 1990

A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemo

A:Reference number: I39453; PMID:90260663

A:Accession: I39453

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 656-737 <LEV>

A:Cross-references: GB:M37896; NID:q178618; PIDN:AAA51727.1; PID:q178620

A:Note: a mutation with 693-Gln is presented

R:Murrell, J.; Parlow, M.; Ghetti, B.; Benson, M.D.

Science 254, 97-99, 1991

A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe

A:Reference number: I59562; PMID:92022553

A:Accession: I59562

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 689-716, 'F', 718-737 <MUR>

A:Cross-references: GB:S57665; NID:q236720; PIDN:AAB19991.1; PID:g236721

R:Kamino, K.; Orr, H.T.; Payant, H.; Wilsman, E.M.; Alonso, M.E.; Puls, S.M.; Anders

arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heaton, L.L.; Mart

Am, J. Hum. Genet. 51, 998-1014, 1992

A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t

A:Reference number: A44017; PMID:9305537

A:Accession: A44017

A:Molecule type: DNA

A:Residues: 687-692, 'G', 694-718 <KAM1>

A:Cross-references: GB:S45135; NID:q257377; PIDN:AAB23645.1; PID:g257378

A:Experimental source: familial Alzheimer disease family SB

A:Note: sequence extracted from NCBI backbone (NCBI:115574)

A:Accession: B44017

A:Molecule type: DNA

A:Residues: 687-718 <KAM2>

A:Cross-references: GB:S45136; NID:q257379; PIDN:AAB23646.1; PID:g257380

A:Experimental source: familial Alzheimer disease family LT

A:Note: sequence extracted from NCBI backbone (NCBI:115576)

R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.

Nature 325, 733-736, 1987



A>Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface  
 A:Reference number: A03134; MUID:87144572  
 A:Accession: A03134  
 A:Molecule type: mRNA  
 A:Residues: 1-288, 'V', 365-770 <KAN>  
 A:Cross-references: GB:Y00264; NID:928525; PIDN:CAA68374.1; PID:928526  
 A:Note: alternative splice form APP(695)  
 R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987  
 A>Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular  
 A:Reference number: A29030; MUID:87231971  
 A:Accession: A29030  
 A:Molecule type: mRNA  
 A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>  
 A:Cross-references: GB:M6765; NID:9178539; PIDN:AA51722.1; PID:9178540  
 A:Note: the authors translated the codon CAG for residue 647 as Asp  
 R:Goldhaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.  
 Science 235, 877-880, 1987  
 A>Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid  
 A:Reference number: A47584; MUID:87120328  
 A:Accession: A47584  
 A:Molecule type: mRNA  
 A:Residues: 674-756, 'S', 758-770 <GOL>  
 A:Cross-references: GB:M5533; NID:9178706; PIDN:AA35540.1; PID:9178707  
 A:Experimental source: brain  
 R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke  
 Science 235, 880-884, 1987  
 A>Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th  
 A:Reference number: A47585; MUID:87120329  
 A:Accession: A47585  
 A:Molecule type: mRNA  
 A:Residues: 674-703 <TAN1>  
 A:Cross-references: GB:M5533; NID:9177957; PIDN:AA51564.1; PID:9177958  
 R:Dykes, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle  
 EMBO J. 7, 949-957, 1988  
 A>Title: Identification, transmembrane orientation and biosynthesis of the amyloid A4 prec  
 A:Reference number: S02638; MUID:88296437  
 A:Accession: S02638  
 A:Molecule type: mRNA  
 A:Residues: 672-678 <DYR>  
 R:Tanzi, R.E.; McClatchey, A.I.; Lampetti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve  
 Nature 331, 528-530, 1988  
 A>Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat  
 A:Reference number: S00707; MUID:88122640  
 A:Accession: S00707  
 A:Molecule type: mRNA  
 A:Residues: 286-344, 'I', 365-366 <TAN2>  
 A:Cross-references: EMBL:X06982; NID:928817; PIDN:CAA30042.1; PID:9292612  
 A:Experimental source: promyelocytic leukemia cell line HL60  
 A:Note: alternative splice form APP(751)  
 R:Ponte, P.; Gonzalez-Demhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da  
 Nature 331, 525-527, 1988  
 A>Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitor  
 A:Reference number: S00925; MUID:88122639  
 A:Accession: S00925  
 A:Molecule type: mRNA  
 A:Residues: 1-344, 'I', 365-770 <PO2>  
 A:Cross-references: GB:X06989; EMBL:Y00297; NID:928720; PIDN:CAA30050.1; PID:928721  
 A:Note: alternative splice form APP(751)  
 R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.  
 Nature 331, 530-532, 1988  
 A>Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor  
 A:Reference number: A38949; MUID:88122641  
 A:Accession: A38949  
 A:Molecule type: mRNA  
 A:Residues: 287-367 <KIT>  
 A:Cross-references: GB:X06981; NID:928816; PIDN:CAA30041.1; PID:9292611  
 A:Experimental source: glioblastoma cell line  
 A:Note: alternative splice form APP(770)  
 R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton  
 Brain Res. Mol. Brain Res. 4, 121-131, 1988  
 A>Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three F  
 A:Reference number: A30320

A:Accession: A30320  
 A>Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 284-288, 'V', 365-770 <VIT1>  
 A:Accession: B30320  
 A>Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 122-288, 'V', 365-770 <VIT2>  
 A:Accession: C30320  
 A>Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 606-770 <VIT3>  
 R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta,  
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988  
 A>Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease  
 A:Reference number: A31087; MUID:88124954  
 A:Accession: A31087  
 A:Molecule type: mRNA  
 A:Residues: 507-770 <ZAI>  
 A:Cross-references: GB:M18734; NID:9178572; PIDN:AA51726.1; PID:9178573  
 A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue  
 8 as Val, GTC for residue 609 as Asp, AAT for residue 610 as Gly, and GGT for residue  
 A:Note: the cited Genbank accession number, J03594, is not in release 101.0  
 R:Masters, C.L.; Multhaup, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther,  
 Query Match 100.0%; Score 54; DB 1; Length 770;  
 Best local Similarity 100.0%; Pred. No. 0.035;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 GSNKGAITGL 11  
 Db 696 GSNKGAITGL 706  
 RESULT 14  
 B83880  
 3-oxoacyl-(acyl-carrier protein) reductase BH1842 [Imported] - Bacillus halodurans (s  
 C:Species: Bacillus halodurans  
 C:Date: 01-Dec-2000 #sequence-revision 01-Dec-2000 #text-change 31-Dec-2000  
 C:Accession: B83880  
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H  
 Nucleic Acids Res. 28, 4317-4331, 2000  
 A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a  
 A:Reference number: A83650; MUID:20263314  
 A:Accession: B83880  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-247 <STO>  
 A:Cross-references: GB:AP001513; GB:BA000004; NID:910174345; PIDN:BA805561.1; GSPDB:G  
 A:Experimental source: strain C-125  
 C:Genetics:  
 A:gene: BH1842  
 C:superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology  
 Query Match 75.9%; Score 41; DB 2; Length 247;  
 Best local Similarity 80.0%; Pred. No. 3.2;  
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 GSNKGAITGL 10  
 Db 156 GASKGAIIGL 165  
 RESULT 15  
 C69971  
 conserved hypothetical protein yrak - Bacillus subtilis  
 C:Species: Bacillus subtilis  
 C:Date: 05-Dec-1997 #sequence-revision 05-Dec-1997 #text-change 15-Oct-1999  
 C:Accession: C69971  
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber  
 C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;  
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,

Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koeltter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
y, M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,  
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serod  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.  
A:title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.  
A:Reference number: A69580; M0ID:98044033  
A:Accession: C69971  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-229 <RUN>  
A:Cross-references: GB:299117; GB:AL009126; NID:g2634966; PIDN:CAB14632.1; PID:e183920;  
A:Experimental source: strain 168  
C:Genetics:  
A:Gene: yrak

Query Match 70.4%; Score 38; DB 2; Length 229;  
Best Local Similarity 70.0%; Pred. No. 11;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GSMKGATIGL 10  
11:11:111  
DB 97 GSSSGAVIGL 106

Search completed: April 24, 2002, 09:19:01  
Job time: 200 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:20:38 ; Search time 21.42 Seconds

(without alignments)  
18.829 Million cell updates/sec

Title: US-09-689-469-4  
Perfect score: 54  
Sequence: 1 GSNKGATIGLM 11

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 3664827 residues  
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | % Match | Query length | ID         | Description          |
|------------|-------|---------|--------------|------------|----------------------|
| 1          | 54    | 100.0   | 57           | A4_PIG     | Q29023 sus scrofa    |
| 2          | 54    | 100.0   | 57           | A4_URDMA   | Q29149 ursus marit   |
| 3          | 54    | 100.0   | 58           | A4_CANFA   | Q28280 canis fami    |
| 4          | 54    | 100.0   | 58           | A4_RABIT   | Q28748 oryctolagus   |
| 5          | 54    | 100.0   | 58           | A4_SHEEP   | Q28757 ovis aries    |
| 6          | 54    | 100.0   | 59           | A4_BOVIN   | Q28053 bos taurus    |
| 7          | 54    | 100.0   | 751          | A4_SAISC   | Q95241 salmtr1 sc    |
| 8          | 54    | 100.0   | 770          | A4_HUMAN   | P05067 homo sapien   |
| 9          | 54    | 100.0   | 770          | A4_MOUSE   | P12023 mus musculu   |
| 10         | 54    | 100.0   | 770          | A4_RAT     | P08592 rattus norv   |
| 11         | 38    | 70.4    | 300          | DPPC_ECOLI | P37315 escherichia   |
| 12         | 37    | 68.5    | 906          | CBT_HUMAN  | P22681 homo sapien   |
| 13         | 36    | 66.7    | 305          | RSIB_STY3  | P74142 synchocyst    |
| 14         | 36    | 66.7    | 305          | CBT_MLVN   | P23092 cas-n-1 mu    |
| 15         | 36    | 66.7    | 496          | MGLA_TREPA | Q56342 treponema p   |
| 16         | 36    | 66.7    | 661          | RDGC_DROME | P40421 drosophila    |
| 17         | 36    | 66.7    | 896          | CBT_MOUSE  | P22682 mus musculu   |
| 18         | 35    | 64.8    | 146          | Y237_AQUAE | O66425 aquifex aeo   |
| 19         | 35    | 64.8    | 295          | DPPC_HAEIN | P51000 haemophilus   |
| 20         | 35    | 64.8    | 411          | RRL_SPTOL  | P326342 schistosacch |
| 21         | 34    | 63.0    | 269          | COX3_TIRIU | Q36837 trichophyto   |
| 22         | 34    | 63.0    | 315          | ERA_SYNY3  | O55526 synchocyst    |
| 23         | 34    | 63.0    | 503          | Y226_MYCPN | P75462 mycoplasma    |
| 24         | 34    | 63.0    | 605          | RTK2_GEOCY | P42159 geodia cydo   |
| 25         | 34    | 63.0    | 1362         | PMO1_SCHPO | P36619 schistosacch  |
| 26         | 33    | 61.1    | 161          | NMDH_RICPR | Q92419 rickettsia    |
| 27         | 33    | 61.1    | 293          | PRTT_TRIAL | P320015 bacillus su  |
| 28         | 33    | 61.1    | 368          | GRBB_BACSU | P39570 bacillus su   |
| 29         | 33    | 61.1    | 407          | VG02_HSV1  | O00126 ictalurid h   |
| 30         | 33    | 61.1    | 543          | SGUT_VIBPA | P96169 vibrio para   |
| 31         | 33    | 61.1    | 649          | PTMA_VIBCH | Q9KRG7 vibrio chol   |
| 32         | 33    | 61.1    | 653          | PPH1_HUMAN | O14829 homo sapien   |
| 33         | 33    | 61.1    | 687          | HS7E_DROME | P29845 drosophila    |

|    |    |      |      |   |            |                    |
|----|----|------|------|---|------------|--------------------|
| 34 | 33 | 61.1 | 700  | 1 | NONA_DROME | Q04047 drosophila  |
| 35 | 33 | 61.1 | 917  | 1 | SLAP_THETH | P35830 thymus aqu  |
| 36 | 33 | 61.1 | 1648 | 1 | RPO_CGMVS  | P19523 cucurbit gr |
| 37 | 32 | 59.3 | 139  | 1 | Y965_MYCTU | P71545 mycobacteri |
| 38 | 32 | 59.3 | 360  | 1 | Y463_MYCTU | O53411 mycobacteri |
| 39 | 32 | 59.3 | 473  | 1 | DLDH_BUCAT | P57303 buchnera ap |
| 40 | 32 | 59.3 | 496  | 1 | IA12_ARATH | O06402 arabidopsis |
| 41 | 32 | 59.3 | 547  | 1 | Y0T5_CAEEL | O09316 caenorhabdi |
| 42 | 32 | 59.3 | 576  | 1 | Y006_CAEEL | P34644 caenorhabdi |
| 43 | 32 | 59.3 | 589  | 1 | CAH_DUNSA  | P54212 dunaliella  |
| 44 | 32 | 59.3 | 595  | 1 | CRT1_NEUCR | P21334 neuropept   |
| 45 | 32 | 59.3 | 753  | 1 | PPH2_HUMAN | O14830 homo sapien |

## ALIGNMENTS

```

RESULT 1
AC A4_PIG STANDARD: PRT: 57 AA.
AC Q29023;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).
GN APP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:289-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X56127; CAA39592.1; -
DR HSP: P05067; IAML.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neuron; Transmembrane.
FT NON_TER 1
FT CHAIN 1 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN 1 33 57 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT NON_TER 57
SQ SEQUENCE 57 AA; 6172 MW; 84209D88BA82DFA CRC64;
Query Match 100.0%; Score 54; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GSNKGATIGLM 11

```

Db 30 GSNKGATIGLM 40

RESULT 2

AC\_URSMA STANDARD: PRT: 57 AA.

ID A4\_URSMA

AC 029149;

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID

DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).

GN APP.

OS Ursus maritimus (Polar bear) (Thalassos maritimus).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.

OX NCBI\_TaxID=29073;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Brain;

RC MEDLINE=92017079; PubMed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.:

"Conservation of the sequence of the Alzheimer's disease amyloid

peptide in dog, polar bear and five other mammals by cross-species

polymerase chain reaction analysis.";

RT Brain Res. Mol. Brain Res. 10:299-305(1991).

CC - FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO

INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN

G(O) (BY SIMILARITY).

- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

- SIMILARITY: BELONGS TO THE APP FAMILY.

-----

This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation

at the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial

entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

-----

DR EMBL; X56128; CAA39593.1; -

DR HSSP; P05067; IAML.

DR InterPro; IPR001868; A4\_APP.

DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.

DR PROSITE; PS00320; A4\_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON\_TER 1 1

FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).

FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 34 57 POTENTIAL.

FT NON\_TER 57 57

FT SEQUENCE 57 AA: 6172 MW: 84209888BA82DFA CRC64:

QY 1 GSNKGATIGLM 11

DB 30 GSNKGATIGLM 40

RESULT 3

AC\_URSMA STANDARD: PRT: 58 AA.

ID A4\_URSMA

AC 028280;

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID

DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).

GN APP.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI\_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Kidney;

RC MEDLINE=92017079; PubMed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.:

"Conservation of the sequence of the Alzheimer's disease amyloid

peptide in dog, polar bear and five other mammals by cross-species

polymerase chain reaction analysis.";

RT Brain Res. Mol. Brain Res. 10:299-305(1991).

CC - FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO

INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN

G(O) (BY SIMILARITY).

- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

- SIMILARITY: BELONGS TO THE APP FAMILY.

-----

This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation

at the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial

entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

-----

DR EMBL; X56125; CAA39590.1; -

DR HSSP; P05067; IAML.

DR InterPro; IPR001868; A4\_APP.

DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.

DR PROSITE; PS00320; A4\_INTRA; PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON\_TER 1 1

FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).

FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 35 58 POTENTIAL.

FT NON\_TER 58 58

FT SEQUENCE 58 AA: 6285 MW: 84699488A2E12DFA CRC64:

QY 1 GSNKGATIGLM 11

DB 31 GSNKGATIGLM 41

RESULT 4

AC\_URSMA STANDARD: PRT: 58 AA.

ID A4\_URSMA

AC 028748;

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID

DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).

GN APP.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI\_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Brain;

RC MEDLINE=92017079; PubMed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.:

"Conservation of the sequence of the Alzheimer's disease amyloid

peptide in dog, polar bear and five other mammals by cross-species

polymerase chain reaction analysis.";

```

RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X56129; CAA39594.1; -.
DR HSSP: P05067; IAML.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 54; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSNKGAITGLM 11
   |||||
Db 30 GSNKGAITGLM 40

RESULT 5
A4_SHEEP 5
ID A4_SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).
GN APP.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
RT FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
RT INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
RT G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X56124; CAA39589.1; -.
DR HSSP: P05067; IAML.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.

```

```

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X56130; CAA39595.1; -.
DR HSSP: P05067; IAML.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 54; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSNKGAITGLM 11
   |||||
Db 30 GSNKGAITGLM 40

RESULT 6
A4_BOVIN 6
ID A4_BOVIN STANDARD; PRT; 59 AA.
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP) (A-BETA)] (FRAGMENT).
GN APP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
RT FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
RT INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
RT G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X56124; CAA39589.1; -.
DR HSSP: P05067; IAML.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.

```

FT NON\_TER 1 1  
 FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).  
 FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 35 58 POTENTIAL.  
 FT DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).  
 FT NON\_TER 59 59  
 SQ SEQUENCE 59 AA; 6414 MW; F43469D48BA2E12D CRC64;

Query Match 100.0%; Score 54; DB 1; Length 59;  
 Best Local Similarity 100.0%; Pred. No. 0.0012;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11  
 |||||  
 Db 31 GSNKGATIGLM 41

RESULT 7

A4\_SAIISC STANDARD; PRT; 751 AA.

AC 095241;

DT 15-DEC-1998 (Rel. 37, Created)

DT 20-AUG-2001 (Rel. 40, Last sequence update)

DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR [CONTAINS: BETA-

DE AMYLOID PROTEIN (BETA-APP) (A-BETA)].

OS Saimiri sciureus (Common squirrel monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.

NCBI\_TaxID=9521;

[1]

SEQUENCE FROM N.A.

RC TISSUE=Liver, and Kidney;

RA MEDLINE=96108482; PubMed=8532114;

RA Levy E., Amorim A., Frangione B., Walker L.C.;

RT "Beta-amyloid precursor protein gene in squirrel monkeys with

RT cerebral amyloid angiopathy."

RL Neurobiol. Aging 16:805-808(1995).

CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO

CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN

CC G(O).

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION

CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC

CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE

CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF

CC PHOSPHORYLATION (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation-

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

DR PROSITE: PS50279; BPTI\_KUNITZ\_2; 1.  
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;  
 KM Signal; Serine protease inhibitor.

FT SIGNAL 1 17 BY SIMILARITY.

FT CHAIN 18 751 A4 PROTEIN.

FT DOMAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).

FT TRANSMEM 18 680 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 681 704 POTENTIAL.

FT TRANSMEM 705 751 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.

FT SITE 740 743 CLATHRIN-BINDING (BY SIMILARITY).

FT ACT\_SITE 301 302 REACTIVE BOND.

FT DISULFID 291 341 BY SIMILARITY.

FT DISULFID 300 324 BY SIMILARITY.

FT DISULFID 316 337 BY SIMILARITY.

FT CARBOHYD 523 523 N-LINKED (GLCNAC... ) (PROBABLE).

FT CARBOHYD 552 552 N-LINKED (GLCNAC... ) (PROBABLE).

FT CARBOHYD 552 552 N-LINKED (GLCNAC... ) (PROBABLE).

SQ SEQUENCE 751 AA; 84893 MW; 6C3E431089569049 CRC64;

Query Match 100.0%; Score 54; DB 1; Length 751;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGATIGLM 11  
 |||||  
 Db 677 GSNKGATIGLM 687

RESULT 8

A4\_HUMAN STANDARD; PRT; 770 AA.

AC P05067; P09000; Q16011;

DT 13-AUG-1987 (Rel. 05, Created)

DT 01-NOV-1991 (Rel. 20, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR (PROTEASE NEXIN-II)

DE (PN-II) (APP) [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)].

GN APP OR A4 OR CVA9 OR AD1.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI\_TaxID=9606;

[1]

SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA MEDLINE=87144572; PubMed=2881207;

RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,

RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;

RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a

RT cell-surface receptor."

RL Nature 325:733-736(1987).

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

EMBL: S81024; AAD14347.1;  
 InterPro: IPR001868; A4\_APP.  
 InterPro: IPR002223; Kunitz\_BPTI.  
 Pfam: PF002177; A4\_EXTRA; 1.  
 Pfam: PF00014; Kunitz\_BPTI; 1.  
 PRINTS: PRO0203; AMYLOID4.  
 PRINTS: PRO0204; BETAAMYLOID.  
 PRINTS: PRO0759; BASICPTASE.  
 SMART: SM00006; A4\_EXTRA; 1.  
 SMART: SM00131; KJ; 1.  
 PROSITE: PS00319; A4\_EXTRA; 1.  
 PROSITE: PS00320; A4\_INTRA; 1.  
 PROSITE: PS00280; BPTI\_KUNITZ\_1; 1.

RA Saito M., Tsukuni S., Sakaki Y.;  
RT "A novel method for making nested deletions and its application for  
RL sequencing of a 300 kb region of human APP locus.";  
RN Nucleic Acids Res. 25:1802-1808(1997).  
RP [15]  
RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.  
RA MEDLINE-8812640; PubMed-2893290;  
RA Tanzi R.E., McClatchey A.I., Lampertl E.D., Villa-Komaroff L.,  
RA Gusella J.F., Neve R.L.;  
RT "Protease inhibitor domain encoded by an amyloid protein precursor  
RT mRNA associated with Alzheimer's disease.";  
RL Nature 331:528-530(1988).  
RN [6]  
RP SEQUENCE OF 287-367 FROM N.A.  
RA MEDLINE-8812641; PubMed-2893291;  
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;  
RT "Novel precursor of Alzheimer's disease amyloid protein shows  
RT protease inhibitory activity.";  
RL Nature 331:530-532(1988).  
RN [7]  
RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.  
RA MEDLINE-87231971; PubMed-3035574;  
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;  
RT "Molecular cloning and characterization of a cDNA encoding the  
RT cerebrovascular and the neuritic plaque amyloid peptides.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).  
RN [8]  
RP SEQUENCE OF 507-770 FROM N.A.  
RA MEDLINE-88124954; PubMed-2893379;  
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,  
RA Marotta C.A.;  
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer  
RT disease brain: coding and noncoding regions of the fetal precursor  
RT mRNA are expressed in the cortex.";  
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).  
RN [9]  
RP SEQUENCE OF 672-681.  
RA MEDLINE-88035004; PubMed-3312495;  
RA Partridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,  
RA Tountouloute W.W., Huebner V., Shively J.E.;  
RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition  
RT and partial sequence of a 4,200-dalton peptide isolated from cortical  
RT microvessels.";  
RL J. Neurochem. 49:1394-1401(1987).  
RN [10]  
RP SEQUENCE OF 739-770 FROM N.A.  
RA MEDLINE-90236318; PubMed-2110105;  
RA Yoshikata S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;  
RT "Genomic organization of the human amyloid beta-protein precursor  
RT gene.";  
RL Gene 87:257-263(1990).  
RN [11]  
RP SEQUENCE OF 1-10 FROM N.A.  
RA TISSUE-LIVER;  
RC MEDLINE-89016647; PubMed-3140222;  
RA Schon E.A., Mita S., Sadlock J., Herbert J.;  
RT "A cDNA specifying the human amyloid beta precursor protein (ABP)  
RT encodes a 95-kDa polypeptide.";  
RL Nucleic Acids Res. 16:9351-9351(1988).  
RN [12]  
RP SEQUENCE OF 18-50.  
RA MEDLINE-87250462; PubMed-3597385;  
RA van Nostrand W.E., Cunningham D.D.;  
RT "Purification of protease nexin II from human fibroblasts.";  
RL J. Biol. Chem. 262:8508-8514(1987).  
RN [13]  
RP IDENTITY OF APP WITH NEXIN-II.  
RA MEDLINE-89384866; PubMed-2506449;  
RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,  
RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,  
RA Slinn S.;  
RT "The secreted form of the Alzheimer's amyloid precursor protein with  
RT the Kunitz domain is protease nexin-II.";  
RN Nature 341:144-147(1989).  
RN [14]  
RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.  
RA MEDLINE-90211252; PubMed-19669731;  
RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;  
RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's  
RT disease amyloid protein precursor.";  
RN Biochem. Biophys. Res. Commun. 167:716-721(1990).  
RN [15]  
RP COMPLEX WITH G10)  
RA MEDLINE-93188965; PubMed-8446172;  
RA Nishimoto I., Okamoto T., Matsura Y., Takahashi S., Okamoto T.,  
RA Murayama Y., Ogata E.;  
RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding  
RT protein G10.";  
RL Nature 362:75-79(1993).  
RN [16]  
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.  
RA MEDLINE-99215582; PubMed-10201399;  
RA Rossjohn J., Cappai R., Fell S.C., Henry A., McKinsty W.J.,  
RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,  
RA Parker M.W.;  
RT "Crystal structure of the N-terminal, growth factor-like domain of  
RT Alzheimer amyloid precursor protein.";  
RL Nat. Struct. Biol. 6:327-331(1999).  
RN [17]  
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.  
RA MEDLINE-91104913; PubMed-2125487;  
RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrodt C., Kossiakof A.A.;  
RT "X-ray crystal structure of the protease inhibitor domain of  
RT Alzheimer's amyloid beta-protein precursor.";  
RL Biochemistry 29:10018-10022(1990).  
RN [18]  
RP STRUCTURE BY NMR OF 289-344.  
RA MEDLINE-92031488; PubMed-1718421;  
RA Heald S.L., Tilton R.F., Jr., Hammond L.S., Lee A., Bayney R.M.,  
RA Kamarch M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,  
RA Tamburini P.P.;  
RT "Sequential NMR resonance assignment and structure determination of  
RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid  
RT precursor protein.";  
RL Biochemistry 30:10467-10478(1991).  
RN [19]  
RP STRUCTURE BY NMR OF 672-699.  
RA MEDLINE-94281210; PubMed-7516706;  
RA Talaoui J., Marciniowski K.J., Klopman G., Zagorski M.G.;  
RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";  
RL Biochemistry 33:7788-7796(1994).  
RN [20]  
RP STRUCTURE BY NMR OF 696-706.  
RA MEDLINE-97128622; PubMed-8973180;  
RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;  
RT "Three-dimensional structures of the amyloid beta peptide (25-35) in  
RT membrane-mimicking environment.";  
RL Biochemistry 35:16094-16104(1996).  
RN [21]  
RP STRUCTURE BY NMR OF 672-711.  
RA MEDLINE-98359783; PubMed-9693002;  
RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;  
RT "Solution structure of amyloid beta-peptide(1-40) in a water-miscible  
RT environment. Is the membrane-spanning domain where we think it is?";  
RL Biochemistry 37:11064-11077(1998).  
RN [22]  
RP STRUCTURE BY NMR OF 672-699.  
RA MEDLINE-20400066; PubMed-10940222;  
RA Foulson S.A., Watson A.A., Craik D.J.;  
RT "Solution structures in aqueous SDS micelles of two amyloid beta  
RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage  
RT site.";  
RL J. Struct. Biol. 130:142-152(2000).  
RN [23]  
RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.  
RA MEDLINE-88296437; PubMed-2900137;

RA Dykx T., Weidemann A., Multaup G., Salbaum J.M., Lemaire H.-G.,  
 RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;  
 RT "Identification, transmembrane orientation and biogenesis of the  
 RT amyloid A4 precursor of Alzheimer's disease.";  
 RL EMBL J. 7:949-957(1988).  
 RN [24]  
 RP REVIEW.  
 RX MEDLINE=92271194; PubMed=1589757;  
 RA Kosik K.S.;  
 RT "Alzheimer's disease: a cell biological perspective.";  
 RL Science 256:780-783(1992).  
 RN [25]

Query Match 100.0%; Score 54; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAITGLM 11  
 DB 696 GSNKGAITGLM 706

RESULT 9  
 A4\_MOUSE STANDARD; PRT; 770 AA.  
 ID A4\_MOUSE  
 AC P12023;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 20-ANG-2001 (Rel. 40, Last annotation update)  
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR  
 DE (AMYLOIDOGENIC GLYCOPROTEIN) (AC).  
 GN APP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.  
 RC STRAIN-BALB/C; TISSUE-Brain;  
 RX MEDLINE=92096458; PubMed=1756177;  
 RA de Strooper B., van Leuven F., van den Bergh H.;  
 RT "The amyloid beta protein precursor or proteinase nexin II from mouse  
 RT biochim. Biophys. Acta 1129:141-143(1991).  
 RL [12]  
 RN RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.  
 RC TISSUE-Brain;  
 RX MEDLINE=88106489; PubMed=3322280;  
 RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;  
 RT "Complementary DNA for the mouse homolog of the human amyloid beta  
 RT protein precursor.";  
 RL Biochem. Biophys. Res. Commun. 149:665-671(1987).  
 RN [3]  
 RP REVISIONS.  
 RA Yamada T.;  
 RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 289-364 FROM N.A.  
 RC STRAIN-CD-1; TISSUE-Placenta;  
 RX MEDLINE=89345111; PubMed=2569710;  
 RA Fukuchi K., Martin G.M., Deeb S.S.;  
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein  
 RT precursor of Mus domesticus.";  
 RL Nucleic Acids Res. 17:5396-5396(1989).  
 RN [5]  
 RP SEQUENCE OF 1-19 FROM N.A.  
 RX MEDLINE=92209998; PubMed=1555768;  
 RA Izumi R., Yamada T., Yoshikawa S.I., Sasaki H., Hattori M.,  
 RA Sakai Y.;  
 RT "Positive and negative regulatory elements for the expression of the  
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";  
 RL Gene 112:189-195(1992).  
 RN [6]

RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.  
 RC TISSUE-Brain, and Kidney;  
 RX MEDLINE=89149813; PubMed=2493250;  
 RA Yamada T., Sasaki H., Donura K., Goto I., Sakaki Y.;  
 RT "Structure and expression of the alternatively-spliced forms of mRNA  
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein  
 RT precursor.";  
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),  
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING.  
 CC -1- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS  
 CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND  
 CC LIVER.  
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION  
 CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC  
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE  
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF  
 CC PHOSPHORYLATION (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.

-----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

DR EMBL: X59379; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL: M18373; AAA37139.1; -;  
 DR EMBL: X15210; CAA33280.1; -;  
 DR EMBL: D10603; BAA01436.1; -;  
 DR EMBL: M24397; AAA39929.1; -;  
 DR PIR: A27485; A27485.  
 DR PIR: S04855; S04855.  
 DR PIR: S19727; S19727.  
 DR MGD: MGI:88059; APP.  
 DR InterPro: IPR001868; A4\_APP.  
 DR InterPro: IPR002223; Kunitz\_BPTI.  
 DR Pfam: PF02177; A4\_EXTRA; 1.  
 DR Pfam: PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS: PR00203; AMYLOIDA4.  
 DR PRINTS: PR00204; BETAAMYLOID.  
 DR PRINTS: PR00759; BASICPTASE.  
 DR SMART: SM00006; A4\_EXTRA; 1.  
 DR SMART: SM00131; KU; 1.  
 DR PROSITE: PS00319; A4\_EXTRA; 1.  
 DR PROSITE: PS00320; A4\_INTRA; 1.  
 DR PROSITE: PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE: PS0279; BPTI\_KUNITZ\_2; 1.  
 DR PROSITE: PS0279; Amyloid; Neurone; Transmembrane; Signal;  
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;  
 KW Alternative splicing; Serine protease inhibitor.  
 FT SIGNAL 1 17  
 FT CHAIN 18 770  
 FT  
 FT DOMAIN 18 699  
 FT TRANSMEM 700 723  
 FT DOMAIN 724 770  
 FT DOMAIN 673 745  
 FT DOMAIN 287 345  
 FT SITE 759 762  
 FT SITE 291 341  
 FT DISULFID 291 324  
 FT DISULFID 316 337  
 FT CARBOHYD 542 542  
 FT CARBOHYD 571 571  
 FT CARBOHYD 289 289  
 FT VARSPLIC 290 364  
 FT VARSPLIC 346 380  
 FT SEQUENCE 770 AA: 86752 MW: 265050DE0890CAF7A CRC64;



Query Match 100.0%; Score 54; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11  
 |||||||||  
 DB 696 GSNKGAIIGLM 706

RESULT 10  
 A4\_RAT STANDARD: PRT: 770 AA.  
 ID A4\_RAT  
 AC P08592;  
 DT 01-AUG-1998 (Rel. 08, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR  
 DE (AMYLOIDOGENIC GLYCOPROTEIN) (AG).  
 GN APP.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=88312583; PubMed=2900758;  
 RA Shivers B.D., Hilblich C., Multhaup G., Salbaum J.M., Beyreuther K.,  
 RA Seeburg P.H.;  
 RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern  
 RT in rat brain suggests a role in cell contact.";  
 RL EMBO J. 7:1365-1370(1988).  
 RN [2]  
 RP SEQUENCE OF 289-364 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=89183625; PubMed=2648331;  
 RA Kang J., Mueller-Hill B.;  
 RT "The sequence of the two extra exons in rat preA4.";  
 RL Nucleic Acids Res. 17:2130-2130(1989).  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695),  
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING.  
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION  
 CC WITH X11 ALPHA, BETA, AND GAMMA. THE SEQUENCE SPECIFIC  
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE  
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF  
 CC PHOSPHORYLATION (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: X07648; CAA30488.1;  
 DR EMBL: X14066; CAA32229.1;  
 DR PIR: S00550; S00550.  
 DR PIR: S03607; S03607.  
 DR InterPro: IPR001868; A4\_APP.  
 DR InterPro: IPR002223; Kunitz\_BPTI.  
 DR Pfam: PF02177; A4\_EXTRA.1.  
 DR Pfam: PF00014; Kunitz\_BPTI.1.  
 DR PRINTS: PR00203; AMYLOIDAA.  
 DR PRINTS: PR00204; BETAMAMLOID.  
 DR PRINTS: PR00759; BASICPTASE.  
 DR SMART: SMO0006; A4\_EXTRA.1.

DR SMART: SMO0131; KU: 1.  
 DR PROSITE: PS00319; A4\_EXTRA.1.  
 DR PROSITE: PS00320; A4\_INTRA.1.  
 DR PROSITE: PS00280; BPTI\_KUNITZ\_1.1.  
 DR PROSITE: PS00279; BPTI\_KUNITZ\_2.1.  
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;  
 KW Alternative splicing; Serine protease inhibitor.  
 FT SIGNAL 1 17  
 FT CHAIN 18 770  
 FT DOMAIN 18 699  
 FT TRANSMEM 700 723  
 FT DOMAIN 724 770  
 FT DOMAIN 673 715  
 FT DOMAIN 287 345  
 FT SITE 759 762  
 FT DISULFID 291 341  
 FT DISULFID 300 324  
 FT DISULFID 316 337  
 FT CARBOHYD 542 542  
 FT CARBOHYD 571 571  
 FT VARSPPLIC 289 289  
 FT VARSPPLIC 290 364  
 FT SEQUENCE 770 AA: 86704 MW: C26C9D6B82D929A7 CRC64;

Query Match 100.0%; Score 54; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11  
 |||||||||  
 DB 696 GSNKGAIIGLM 706

RESULT 11  
 ID DPEC\_ECOLI STANDARD: PRT: 300 AA.  
 AC P37315;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPEC.  
 GN DPEC OR B3542 OR 24959 OR ECS4422.  
 OS Escherichia coli, and  
 OS Escherichia coli O157:H7.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562, 83334;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG500;  
 RX MEDLINE=95231288; PubMed=7536291;  
 RA Abouhamed W.N., Manson M.D.;  
 RT "The dipeptide permease of Escherichia coli closely resembles other  
 RT bacterial transport systems and shows growth-phase-dependent  
 RT expression.";  
 RL Mol. Microbiol. 14:1077-1092(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RX MEDLINE=94316500; PubMed=8041620;  
 RA Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;  
 RT "Analysis of the Escherichia coli genome. V. DNA sequence of the  
 RT Nucleic Acids Res. 22:2576-2586(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927;  
 RX MEDLINE=21074935; PubMed=11206551;  
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
 RA Postal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

RA Grothbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoussis K.,  
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
RA Welch R.A., Blattner F.R.;  
RT "Genome sequence of enterohemorrhagic Escherichia coli O157:H7."  
RL Nature 409:529-533(2001).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=O157:H7 / RIMD 0509952;  
RX MEDLINE=21156231; PubMed=11258796;  
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tode T.,  
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,  
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;  
RT "Complete genome sequence of enterohemorrhagic Escherichia coli  
RT O157:H7 and genomic comparison with a laboratory strain K-12.";  
RL DNA Res. 8:11-22(2001).  
CC -1- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM  
CC FOR DIPEPTIDES; PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF  
CC THE SUBSTRATE ACROSS THE MEMBRANE.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.  
CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-  
CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE OPPBC  
CC SUBFAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: L08399; AAA3704.1; -;  
DR EMBL: U00039; AAB18520.1; -;  
DR EMBL: AE000431; AAC76567.1; -;  
DR EMBL: AE005580; AAG58686.1; -;  
DR EMBL: AP002565; BAB37845.1; -;  
DR Ecogene: EGI2626; dppc.  
DR InterPro: IPR000515; BPD.transp.  
DR Pfam: PF00528; BPD.transp.  
DR PROSITE: PS00402; BPD.TRANSF.INN.MEMBR.FALSE.NEG.  
KW Transmembrane; Inner membrane;  
KW Complete proteome.  
FT TRANSMEM 33 53 POTENTIAL.  
FT TRANSMEM 102 122 POTENTIAL.  
FT TRANSMEM 137 157 POTENTIAL.  
FT TRANSMEM 207 227 POTENTIAL.  
FT TRANSMEM 231 251 POTENTIAL.  
FT TRANSMEM 266 286 POTENTIAL.  
SQ SEQUENCE 300 AA; 32308 MW; C4DD7BD82286E62 CRC64;  
  
OY 3 NKGAIIIGLM 11  
DB 29 NKGAIVGLV 37  
  
Query Match 70.4%; Score 38; DB 1; Length 300;  
Best Local Similarity 66.7%; Pred. No. 5.9;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91232862; PubMed=2030914;  
RA Blake T.J., Shapiro M., Morse H.C. III, Langdon W.Y.;  
RT "The sequences of the human and mouse c-cbl proto-oncogenes show  
RT v-cbl was generated by a large truncation encompassing a proline-rich  
RT domain and a leucine zipper-like motif."  
RL Oncogene 6:653-657(1991).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 47-350.  
RX MEDLINE=99176421; PubMed=10078535;  
RA Meng W., Sawasaki S., Burakoff S.J., Eck M.J.;  
RT "Structure of the amino-terminal domain of Cbl complexed to its  
RT binding site on ZAP-70 kinase."  
RL Nature 398:84-90(1999).  
CC -1- FUNCTION: PARTICIPATES IN SIGNAL TRANSDUCTION IN HEMATOPOIETIC  
CC CELLS. ADAPTOR PROTEIN THAT FUNCTIONS AS A NEGATIVE REGULATOR OF  
CC MANY SIGNALING PATHWAYS THAT START FROM RECEPTORS AT THE CELL  
CC SURFACE.  
CC -1- SUBUNIT: ASSOCIATES WITH NCK VIA ITS SH3 DOMAIN.  
CC -1- SUBCELLULAR LOCATION: CYTOSOL.  
CC -1- PTM: PHOSPHORYLATED ON TYROSINE.  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
CC -1- SIMILARITY: CONTAINS 1 UBA DOMAIN.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: X57110; CAA40393.1; -;  
DR PIR: A43817; A43817.  
DR PDB: 1BA7; 27-APR-99.  
DR IPI: 165360; -;  
DR InterPro: IPR003153; Cbl\_N.  
DR InterPro: IPR000449; UBA.  
DR InterPro: IPR001841; ZnF\_Fing.  
DR Pfam: PF02622; Cbl\_N; 1.  
DR Pfam: PF00627; UBA; 1.  
DR Pfam: PF00097; zf-C3HC4; 1.  
DR SMART: SM00184; RING; 1.  
DR SMART: SM00165; UBA; 1.  
DR PROSITE: PS00518; ZINC\_FINGER\_C3HC4; 1.  
KW Proto-oncogene; Nuclear protein; Zinc-finger; Phosphorylation;  
KW 3D-structure.  
FT DOMAIN 124 127 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
FT ZN\_FING 381 419 RING-TYPE.  
FT DOMAIN 357 476 ASP/GLU-RICH (ACIDIC).  
FT DOMAIN 477 688 PRO-RICH.  
FT DOMAIN 689 834 ASP/GLU-RICH (ACIDIC).  
FT DOMAIN 856 895 UBA.  
FT MOD\_RES 700 700 PHOSPHORYLATION.  
FT MOD\_RES 774 774 PHOSPHORYLATION.  
SQ SEQUENCE 906 AA; 99646 MW; 7D686B050204AD8F CRC64;  
  
OY 1 GSNKAIIGLM 11  
DB 19 GSGSGGLIGLM 29  
  
Query Match 68.5%; Score 37; DB 1; Length 906;  
Best Local Similarity 63.6%; Pred. No. 26;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

RESULT 12  
CBL\_HUMAN  
ID CBL\_HUMAN STANDARD; PRT; 906 AA.  
AC P22681;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE SIGNAL TRANSDUCTION PROTEIN CBL (PROTO-ONCOGENE C-CBL).  
GN CBL OR CBL2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

RESULT 13  
RS1B\_SYNY3  
ID RS1B\_SYNY3 STANDARD; PRT; 305 AA.  
AC P74142;

```

DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE 30S RIBOSOMAL PROTEIN S1 HOMOLOG B.
GN RPS1B OR SLR1984.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugitani M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -1- FUNCTION: BINDS MRNA.
CC -1- SIMILARITY: BELONGS TO THE SLP FAMILY OF RIBOSOMAL PROTEINS.
CC -1- SIMILARITY: CONTAINS 3 'S1 MOTIF' DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: D90912; BAA18228.1; .
DR HSSP: P05055; ISRO.
DR InterPro: IPR003029; S1.
DR Pfam: PF00575; S1; 3.
DR SMART: SM00316; S1; 3.
DR RIBOSOMAL PROTEIN; Repeat; RNA-binding; Complete proteome.
FT REPEAT 29 98 S1 MOTIF 1.
FT REPEAT 116 180 S1 MOTIF 2.
FT REPEAT 194 262 S1 MOTIF 3.
SQ SEQUENCE 305 AA; 33795 MW; 358C35F778BE03F5 CRC64;

Query Match
Best Local Similarity 66.7%; Score 36; DB 1; Length 305;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GSNKGAIIG 9
Db 125 GTNKGGVG 133

RESULT 14
ID CBL_MLYCN STANDARD; PRT; 390 AA.
AC P23092;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1991 (Rel. 20, Last annotation update)
DE TRANSFORMING PROTEIN CBL.
GN V-CBL.
OS Cas-NS-1 murine leukemia virus.
OC Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11793;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89145204; PubMed=2784003;
RA Landon W.Y., Hartley J.W., Klincken S.P., Ruscetti S.K.,
RA Morse H.C. III;
RT "V-CBL, an oncogene from a dual-recombinant murine retrovirus that
RT induces early B-lineage lymphomas.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:1168-1172(1989).

```

```

CC -1- DISEASE: CBL INDUCES EARLY B-LINEAGE LYMPHOMAS.
CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-CBL
CC POLYPEPTIDE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: J04169; AAA42885.1; ALT_INIT.
DR PIR: B32325; TVMVCB.
DR InterPro: IPR003153; CBL_N.
DR Pfam: PF02262; Cbl_N; 1.
DR Transforming protein; Oncogene.
SQ SEQUENCE 390 AA; 43692 MW; EB72483746827AB0 CRC64;

Query Match
Best Local Similarity 66.7%; Score 36; DB 1; Length 390;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GSNKGAIIGLM 11
Db 50 GSGAGGLIGLM 60

RESULT 15
ID MG1A_TREPA STANDARD; PRT; 496 AA.
AC 056342;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GALACTOSIDE TRANSPORT ATP-BINDING PROTEIN MG1A HOMOLOG.
GN MG1A OR TP0685.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97080510; PubMed=8921855;
RA Porella S.F., Popova T.G., Hagman K.E., Penn C.W., Radolf J.D.,
RA Norgard M.V.;
RT "A mgl-like operon in Treponema pallidum, the syphilis spirochete,";
RL Gene 177:115-121(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=NICHOLS;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.R., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Uterback T.,
RA McDonald L., Artlich P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete.";
RL Science 281:375-388(1998).
CC -1- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
CC FOR GALACTOSIDES. PROBABLY RESPONSIBLE FOR ENERGY COUPLING TO
CC THE TRANSPORT SYSTEM (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
CC (ABC TRANSPORTERS). MG1A/RBSA SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

```

CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
DR EMBL; U48416; AAC44585.1; -.  
DR EMBL; AE001242; AAC65648.1; -.  
DR TIGR; TP0685; -.  
DR InterPro; IPR003593; AAA.  
DR InterPro; IPR003439; ABC\_transport.  
DR InterPro; IPR001687; ATP\_GTP\_A.  
DR Pfam; PF00005; ABC\_tran; 2.  
DR SMART; SM00382; AAA; 2.  
DR PROSITE; PS00211; ABC\_TRANSPORTER; 1.  
KW Transport; Sugar transport; Membrane; ATP-binding; Complete proteome.  
FT NP\_BIND 37 44  
FT NP\_BIND 37 44  
SQ SEQUENCE 496 AA; 55191 MW; B6F63D53C5CD1411 CRC64;

Query Match 66.7%; Score 36; DB 1; Length 496;  
Best Local Similarity 75.0%; Pred. No. 23;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 4 KGAITGLM 11  
Db 29 KGAVGSLM 36

Search completed: April 24, 2002, 09:20:39  
Job time: 253 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:20:10 ; Search time 62.94 Seconds  
(without alignments)  
25.564 Million cell updates/sec

Title: US-09-689-469-4  
Perfect score: 54  
Sequence: 1 GSNKGAIIGLM 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues  
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SPREMBL\_17.\*  
2: sp-archaea.\*  
3: sp-bacteria.\*  
4: sp-fungi.\*  
5: sp-human.\*  
6: sp-invertebrate.\*  
7: sp-mammal.\*  
8: sp-mhc.\*  
9: sp-organellar.\*  
10: sp-phage.\*  
11: sp-plant.\*  
12: sp-rodent.\*  
13: sp-virus.\*  
14: sp-vertebrate.\*  
15: sp-unclassified.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 54    | 100.0       | 49     | 6     | 097917 bos taurus  |
| 2          | 54    | 100.0       | 79     | 11    | 035463 cricetus    |
| 3          | 54    | 100.0       | 82     | 4     | P78438 homo sapien |
| 4          | 54    | 100.0       | 82     | 4     | Q16014 homo sapien |
| 5          | 54    | 100.0       | 82     | 4     | Q16019 homo sapien |
| 6          | 54    | 100.0       | 82     | 4     | Q16020 homo sapien |
| 7          | 54    | 100.0       | 97     | 4     | Q13778 homo sapien |
| 8          | 54    | 100.0       | 534    | 13    | 093296 gallus gall |
| 9          | 54    | 100.0       | 569    | 13    | 093296 gallus gall |
| 10         | 54    | 100.0       | 607    | 11    | 099K32 mus musculu |
| 11         | 54    | 100.0       | 693    | 11    | Q98K32 mus musculu |
| 12         | 54    | 100.0       | 695    | 11    | Q98S60 xenopus lae |
| 13         | 54    | 100.0       | 695    | 11    | P97487 mus musculu |
| 14         | 54    | 100.0       | 695    | 11    | Q60496 cavia porce |
| 15         | 54    | 100.0       | 695    | 13    | 09DGJ8 gallus gall |
| 16         | 54    | 100.0       | 695    | 13    | Q98SF9 xenopus lae |
| 17         | 54    | 100.0       | 699    | 13    | 057394 narke japon |
| 18         | 54    | 100.0       | 737    | 13    | 093279 fugu rubrip |
| 19         | 54    | 100.0       | 747    | 13    | 091963 xenopus lae |
|            |       |             | 751    | 13    | Q9DGJ7 gallus gall |

|    |    |       |     |    |                     |
|----|----|-------|-----|----|---------------------|
| 20 | 54 | 100.0 | 770 | 6  | Q9TU10 sus scrofa   |
| 21 | 54 | 100.0 | 780 | 13 | Q73683 tetradon f   |
| 22 | 48 | 88.9  | 612 | 13 | Q919E7 brachydanio  |
| 23 | 45 | 83.3  | 33  | 4  | Q9UC33 homo sapien  |
| 24 | 41 | 75.2  | 247 | 2  | Q9KBR2 bacillus ha  |
| 25 | 39 | 72.2  | 229 | 2  | Q9AE43 rhizobium l  |
| 26 | 38 | 70.4  | 229 | 2  | Q07937 bacillus su  |
| 27 | 37 | 68.5  | 173 | 5  | Q9NN73 leishmania   |
| 28 | 37 | 68.5  | 216 | 5  | Q10910 caenorhabdi  |
| 29 | 36 | 66.7  | 217 | 2  | Q38156 enterobacte  |
| 30 | 36 | 66.7  | 417 | 2  | P71757 mycobacteri  |
| 31 | 36 | 66.7  | 456 | 2  | Q9RDF0 streptomyce  |
| 32 | 36 | 66.7  | 456 | 2  | Q56341 treponema p  |
| 33 | 35 | 64.8  | 203 | 8  | Q79624 sarcodon im  |
| 34 | 35 | 64.8  | 235 | 11 | Q9DP62 mus musculu  |
| 35 | 35 | 64.8  | 238 | 2  | Q66729 aquilex aeo  |
| 36 | 35 | 64.8  | 270 | 11 | Q9D794 mus musculu  |
| 37 | 35 | 64.8  | 270 | 11 | Q9DP60 mus musculu  |
| 38 | 35 | 64.8  | 270 | 11 | Q9CQX3 delinococcus |
| 39 | 35 | 64.8  | 309 | 2  | Q9RS04 homo sapien  |
| 40 | 35 | 64.8  | 414 | 4  | Q13148 mycobacteri  |
| 41 | 35 | 64.8  | 466 | 2  | Q33206 mycobacteri  |
| 42 | 35 | 64.8  | 509 | 2  | Q9AP71 uncultured   |
| 43 | 35 | 64.8  | 515 | 5  | Q9VJ10 drosophila   |
| 44 | 35 | 64.8  | 593 | 10 | Q9FRL7 arabidopsis  |
| 45 | 35 | 64.8  | 673 | 2  | Q07178 mycobacteri  |

## ALIGNMENTS

|  |                          |
|--|--------------------------|
| RESULT 1   |                          |
| 097917   | PRELIMINARY; PRT: 49 AA. |
| AC 097917  |                          |
| DT 01-MAY-1999 (TREMBlrel. 10, Created)                                  |                          |
| DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)                     |                          |
| DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)                   |                          |
| DE ANGIOID PRECURSOR PROTEIN (FRAGMENT).                                 |                          |
| GN APP.  |                          |
| OS Bos taurus (Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;    |                          |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;     |                          |
| OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;     |                          |
| OC Bovidae; Bovinae; Bos.  |                          |
| OX NCBI_TaxID=9913;  |                          |
| RN [1]   |                          |
| RP SEQUENCE FROM N.A.  |                          |
| RA Konfortov B.A., Licence V.E., Miller J.R.;                            |                          |
| RT "Re-sequencing of DNA from a diverse panel of cattle reveals frequent |                          |
| RT polymorphisms in both intron and exon."                               |                          |
| RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.               |                          |
| DR EMBL: AJ133033; CAB38017.1; -   |                          |
| DR HSSP: P05067; IBA4.   |                          |
| FT NON_TER 1   |                          |
| FT NON_TER 49  |                          |
| FT NON_TER 1   |                          |
| SQ SEQUENCE 49 AA; 5183 MW; 6287463F0559BDED CRC64;                      |                          |

Query Match 100.0%; Score 54; DB 6; Length 49;  
Best Local Similarity 100.0%; Pred. No. 0.0053;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSNKGAIIGLM 11  
Db 8 GSNKGAIIGLM 18

RESULT 2  
ID 035463 PRELIMINARY; PRT: 79 AA.  
AC 035463;  
DT 01-JAN-1998 (TREMBlrel. 05, Created)  
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

DT 01-MAR-2001 (TREMUREL. 16, Last annotation update)  
DE ALZHEIMER'S AMYLOID BETA PROTEIN PRECURSOR (FRAGMENT).  
GN BETA APP.  
OS Crictetus griseus (Chinese hamster).  
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Crictetus.  
OX NCBI\_TaxID=10029;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sambamurti K., Pinnix I., Gandhi S.;  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF030413; AAB86608.1; -  
DR HSSP; P05067; 10CM.  
FT NON\_TER 1 1  
FT NON\_TER 79 79  
SQ SEQUENCE 79 AA; 8538 MW; 37F2CC63BFF3F597 CRC64;

Query Match 100.0%; Score 54; DB 11; Length 79;  
Best Local Similarity 100.0%; Pred. No. 0.0091;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIGLM 11  
DB 45 GSNKGAIIGLM 55  
RESULT 3  
P78438 PRELIMINARY; PRT; 82 AA.  
AC P78438;  
DT 01-MAY-1997 (TREMUREL. 03, Created)  
DT 01-MAY-1997 (TREMUREL. 03, Last sequence update)  
DT 01-MAR-2001 (TREMUREL. 16, Last annotation update)  
DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).  
GN APP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=89392030; PubMed=2675837;  
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,  
RA Little S.P.;  
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows  
RT similarity to soybean trypsin inhibitor."  
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).  
RN [2]  
RP SEQUENCE OF 19-48 FROM N.A.  
RX MEDLINE=87120329; PubMed=2949367;  
RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,  
RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;  
RT "Amyloid beta protein gene: CDNA, mRNA distribution, and genetic  
RT linkage near the Alzheimer locus."  
RL Science 235:880-884(1987).  
RN [3]  
RP SEQUENCE OF 32-63 FROM N.A.  
RX MEDLINE=93035397; PubMed=1415269;  
RA Kamino K., Ort H.T., Payami H., Wajsbman E.M., Alonso M.E., Pulst S.M.,  
RA Anderson L., O'dahl S., Nemens E., White J.A.;  
RT "Linkage and mutational analysis of familial Alzheimer disease  
RT kinds for the APP gene-1014(1992).  
RL Am. J. Hum. Genet. 51:998-1014(1992).  
DR EMBL; M29270; AAAS1768.1; -  
DR EMBL; M29269; AAAS1768.1; JOINED.  
DR EMBL; M15532; AAAS1564.1; -  
DR EMBL; S45136; AAB23646.1; -  
DR HSSP; P05067; 1BA4.  
FT NON\_TER 1 1  
SQ SEQUENCE 82 AA; 8994 MW; 8DA9EA2B813A070E CRC64;

Query Match 100.0%; Score 54; DB 4; Length 82;  
Best Local Similarity 100.0%; Pred. No. 0.0095;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIGLM 11  
DB 41 GSNKGAIIGLM 51

RESULT 4  
Q16014 PRELIMINARY; PRT; 82 AA.  
ID Q16014;  
AC Q16014;  
DT 01-NOV-1996 (TREMUREL. 01, Created)  
DT 01-NOV-1996 (TREMUREL. 01, Last sequence update)  
DT 01-MAR-2001 (TREMUREL. 16, Last annotation update)  
DE BETA-AMYLOID PEPTIDE PRECURSOR (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93236601; PubMed=8476439;  
RA Denman R.B., Rosencwaig R., Miller D.L.;  
RT "A system for studying the effect(s) of familial Alzheimer disease  
RT mutations on the processing of the beta-amyloid peptide precursor."  
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
DR EMBL; S60721; AAB26263.2; -  
DR HSSP; P05067; 1BA4.  
FT NON\_TER 1 1  
FT NON\_TER 82 82  
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 100.0%; Score 54; DB 4; Length 82;  
Best Local Similarity 100.0%; Pred. No. 0.0095;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIGLM 11  
DB 42 GSNKGAIIGLM 52

RESULT 5  
Q16019 PRELIMINARY; PRT; 82 AA.  
ID Q16019;  
AC Q16019;  
DT 01-NOV-1996 (TREMUREL. 01, Created)  
DT 01-NOV-1996 (TREMUREL. 01, Last sequence update)  
DT 01-MAR-2001 (TREMUREL. 16, Last annotation update)  
DE BETA-AMYLOID PEPTIDE PRECURSOR (FRAGMENT).  
GN BETA APP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93236601; PubMed=8476439;  
RA Denman R.B., Rosencwaig R., Miller D.L.;  
RT "A system for studying the effect(s) of familial Alzheimer disease  
RT mutations on the processing of the beta-amyloid peptide precursor."  
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
DR EMBL; S61380; AAB26264.2; -  
DR HSSP; P05067; 1BA4.  
FT NON\_TER 1 1  
FT NON\_TER 82 82  
SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match 100.0%; Score 54; DB 4; Length 82;

Best Local Similarity 100.0%; Pred. No. 0.0095;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
|||||  
DB 42 GSNKGATIGLM 52

## RESULT 6

ID Q16020 PRELIMINARY; PRT; 82 AA.  
AC Q16020;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE BETA-AMYLOID PEPTIDE PRECURSOR (FRAGMENT).  
GN BETA APP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=93236601; PubMed=8476439;  
RA Denman R.B., Rosenzweig R., Miller D.L.;  
RT "A system for studying the effect(s) of familial Alzheimer disease  
mutations on the processing of the beta-amyloid peptide precursor.";  
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
DR EMBL; S61383; AAB2625.2; -.  
DR HSSP; P05067; 1BA4.  
FT NON\_TER 1  
FT 82  
SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match 100.0%; Score 54; DB 4; Length 82;  
Best Local Similarity 100.0%; Pred. No. 0.0095;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
|||||  
DB 42 GSNKGATIGLM 52

## RESULT 7

ID Q13778 PRELIMINARY; PRT; 97 AA.  
AC Q13778;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE AMYLOID PROTEIN (AD-AP) (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=87120328; PubMed=3810169;  
RA Goldgaber D., Lerman M.I., McBride O.W., Saffioti U., Gajdusek D.C.;  
RT "Characterization and chromosomal localization of a cDNA encoding  
RT brain amyloid of Alzheimer's disease.";  
RL Science 235:877-880(1987).  
DR EMBL; M15533; AAA35540.1; -.  
DR HSSP; P05067; 1BA4.  
DR InterPro; IPR001868; A4\_APP.  
DR PRINTS; PR00203; AMYLOIDA4.  
FT NON\_TER 1  
SQ SEQUENCE 97 AA; 10884 MW; E528CDB48DE474E CRC64;

Query Match 100.0%; Score 54; DB 4; Length 97;  
Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
|||||  
DB 23 GSNKGATIGLM 33

## RESULT 8

ID Q93296 PRELIMINARY; PRT; 534 AA.  
AC Q93296;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE AMYLOID PRECURSOR PROTEIN (FRAGMENT).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Barnes N.Y., Ling L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,  
RA Milligan C.E.;  
RT "Increased production of amyloid precursor protein provides a  
RT substrate for Caspase 3 in dying motoneurons.";  
RL Submitted (JAN-1998) to the EMBL/GenBank/DDa databases.  
DR EMBL; AF042098; AAC25052.1; -.  
DR HSSP; P05067; 1BA4.  
DR InterPro; IPR001868; A4\_APP.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR PROSITE; PS00319; A4\_EXTRA; 1.  
DR PROSITE; PS00320; A4\_INTRA; 1.  
FT NON\_TER 1  
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;

Query Match 100.0%; Score 54; DB 13; Length 534;  
Best Local Similarity 100.0%; Pred. No. 0.078;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
|||||  
DB 460 GSNKGATIGLM 470

## RESULT 9

ID Q9PVL1 PRELIMINARY; PRT; 569 AA.  
AC Q9PVL1;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE AMYLOID PROTEIN PRECURSOR (FRAGMENT).  
GN APP.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA TISSUE-BRAIN;  
RA Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;  
RT "What the evolution of the amyloid protein precursor supergene family  
RT tells us about its function.";  
RL Neurochem. Int. 0:0-0(2000).  
DR EMBL; AF030341; AAF12698.1; -.  
DR HSSP; P05067; 1BA4.  
DR InterPro; IPR001868; A4\_APP.  
DR Pfam; PF02177; A4\_EXTRA; 1.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR SMART; SM00006; A4\_EXTRA; 1.

DR PROSITE: PS00319; A4\_EXTRA; 1.  
 DR PROSITE: PS00320; A4\_INTRA; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 569 AA; 64753 MW; 0AB8BB851863A19D CRC64;

Query Match 100.0%; Score 54; DB 13; Length 569;  
 Best Local Similarity 100.0%; Pred. No. 0.084;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
 DB 496 GSNKGATIGLM 506

RESULT 10  
 ID 099K32 PRELIMINARY; PRT; 607 AA.  
 AC 099K32;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE UNKNOWN (PROTEIN FOR IMAGE:3486773) (FRAGMENT).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=MAMMARY TUMOR;  
 RA Strausberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC005490; AA05490.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 607 AA; 68391 MW; BF802214CBA7D172 CRC64;

Query Match 100.0%; Score 54; DB 11; Length 607;  
 Best Local Similarity 100.0%; Pred. No. 0.091;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
 DB 533 GSNKGATIGLM 543

RESULT 11  
 ID 098SG0 PRELIMINARY; PRT; 693 AA.  
 AC 098SG0;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE BETA-AMYLLOID PRECURSOR PROTEIN A.  
 GN APP.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_Taxid=8335;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Van den Hurk W.H.;  
 RL Thesis (2001). Department of Biological Sciences,  
 University of Nijmegen, Nijmegen, Netherlands.  
 DR EMBL: AJ296150; CAC37193.1; -.  
 KW Signal.  
 FT SIGNAL 1  
 SQ SEQUENCE 693 AA; 78568 MW; CAFID655C1AB653 CRC64;

Query Match 100.0%; Score 54; DB 13; Length 693;  
 Best Local Similarity 100.0%; Pred. No. 0.11;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 GSNKGATIGLM 11  
 DB 619 GSNKGATIGLM 629

RESULT 12  
 ID P97487 PRELIMINARY; PRT; 695 AA.  
 AC P97487; P97942;  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE HIPPOCAMPAL AMYLOID PROTEIN.  
 GN APP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SAMP8; TISSUE=HIPPOCAMPUS;  
 RA Flood J.F., Kumar V.B., Sasser T., Word L., Morley J.E.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 581-662 FROM N.A.  
 RC STRAIN-129SV;  
 RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capecchi M.,  
 RL Loring J.F., Goate A.M.;  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U84012; AAB41502.1; -.  
 DR EMBL: U82624; AAB40919.1; -.  
 DR HSP: P05067; 10CM.  
 DR MGD; MGI:88059; App.  
 DR InterPro; IPR001868; A4\_APP.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 SQ SEQUENCE 695 AA; 78414 MW; 9A5FB2ED261236E CRC64;

Query Match 100.0%; Score 54; DB 11; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 0.11;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGATIGLM 11  
 DB 621 GSNKGATIGLM 631

RESULT 13  
 ID 060496 PRELIMINARY; PRT; 695 AA.  
 AC 060496;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.  
 OX NCBI\_Taxid=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RA Beck M., Mueller D., Bigl V.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO  
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN  
 CC G(O).



CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: TO OTHER SPECIES APP ANALOGUES.  
 DR EMBL: X97631; CAA66230.1; -.  
 DR HSSP: P05067; IBA4.  
 DR InterPro: IPR001868; A4\_APP.  
 DR Pfam: PF02177; A4\_EXTRA; 1.  
 DR PRINTS: PR00203; AMYLOIDA4.  
 DR SMART: SM00006; A4\_EXTRA; 1.  
 DR PROSITE: PS00319; A4\_EXTRA; 1.  
 DR PROSITE: PS00320; A4\_INTRA; 1.  
 SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 100.0%; Score 54; DB 11; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 0.11;  
 Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIGLM 11  
 |||||  
 DB 621 GSNKGAIIGLM 631

RESULT 14

ID Q9DGCJ8 PRELIMINARY; PRT; 695 AA.  
 AC Q9DGCJ8;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sarasa M., Rodolose A., Sorribas V.;  
 RT "Cloning of full-length chicken beta-amyloid precursor protein  
 RT isoforms";  
 RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF289218; AAG00593.1; -.  
 DR InterPro: IPR001868; A4\_APP.  
 DR Pfam: PF02177; A4\_EXTRA; 1.  
 DR PRINTS: PR00203; AMYLOIDA4.  
 DR SMART: SM00006; A4\_EXTRA; 1.  
 DR PROSITE: PS00319; A4\_EXTRA; 1.  
 SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 100.0%; Score 54; DB 13; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 0.11;  
 Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIGLM 11  
 |||||  
 DB 621 GSNKGAIIGLM 631

RESULT 15

ID Q98SF9 PRELIMINARY; PRT; 695 AA.  
 AC Q98SF9;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE BETA-AMYLOID PRECURSOR PROTEIN B.  
 GN APP.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Van den Hurk W.H.;  
 RL Thesis (2001), Department of Biological Sciences,  
 DR University of Nijmegen, Nijmegen, Netherlands.  
 DR EMBL: AJ298151; CAC37194.1; -.  
 KW Signal.  
 FT SIGNAL. 1  
 SQ SEQUENCE 695 AA; 78803 MW; DC14EB02AFB0204A CRC64;

Query Match 100.0%; Score 54; DB 13; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 0.11;  
 Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GSNKGAIIGLM 11  
 |||||  
 DB 621 GSNKGAIIGLM 631

Search completed: April 24, 2002, 09:20:11  
 Job time: 240 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:21:50 ; Search time 66.52 seconds  
(without alignments)  
33.406 Million cell updates/sec

Title: US-09-689-469-5

Perfect score: 30  
Sequence: 1 AONITARIGEPVLKCKGAPKKPPQRLKWK 30

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 522463 seqs, 74073290 residues

Word size : 0

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A.Geneseq\_1101.\*

1: /SID58/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID58/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID58/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID58/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID58/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SID58/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SID58/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SID58/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SID58/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SID58/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SID58/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SID58/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SID58/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SID58/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SID58/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SID58/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SID58/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SID58/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SID58/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID58/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID58/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID58/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description                  |
|------------|-------|-------------|--------|-------|------------------------------|
| 1          | 30    | 100.0       | 30     | 20    | AAV09349 Human RAGE V-domain |
| 2          | 30    | 100.0       | 30     | 21    | AAV52134 Human Receptor to   |
| 3          | 30    | 100.0       | 318    | 18    | AAW44200 Human mature recep  |
| 4          | 30    | 100.0       | 318    | 18    | AAW33754 Human RAGE polypep  |
| 5          | 30    | 100.0       | 332    | 21    | AAV52130 Human Receptor to   |
| 6          | 30    | 100.0       | 340    | 18    | AAW44199 Human Soluble rece  |
| 7          | 30    | 100.0       | 340    | 18    | AAW33753 Human RAGE polypep  |
| 8          | 30    | 100.0       | 404    | 22    | AAW44214 Extracellular cirt  |
| 9          | 16    | 53.3        | 16     | 18    | AAW44214 Human soluble RAGE  |
| 10         | 16    | 53.3        | 16     | 18    | AAW33768 Human RAGE polypep  |
| 11         | 15    | 50.0        | 15     | 18    | AAW44208 Human soluble RAGE  |

|    |    |      |      |    |          |          |
|----|----|------|------|----|----------|----------|
| 12 | 13 | 15   | 50.0 | 15 | 18       | AAW33762 |
| 13 | 15 | 13   | 43.3 | 30 | 20       | AAV09350 |
| 14 | 11 | 36.7 | 30   | 20 | AAV09351 |          |
| 15 | 10 | 33.3 | 10   | 18 | AAW44209 |          |
| 16 | 10 | 33.3 | 10   | 18 | AAW44201 |          |
| 17 | 10 | 33.3 | 10   | 18 | AAW33763 |          |
| 18 | 10 | 33.3 | 10   | 18 | AAW33755 |          |
| 19 | 10 | 33.3 | 10   | 20 | AAV09353 |          |
| 20 | 10 | 33.3 | 10   | 21 | AAV52135 |          |
| 21 | 10 | 33.3 | 30   | 20 | AAV09352 |          |
| 22 | 9  | 30.0 | 30   | 18 | AAW23337 |          |
| 23 | 7  | 23.3 | 178  | 22 | AAW36499 |          |
| 24 | 6  | 20.0 | 10   | 18 | AAW27362 |          |
| 25 | 6  | 20.0 | 10   | 20 | AAW92647 |          |
| 26 | 6  | 20.0 | 49   | 22 | AAW36735 |          |
| 27 | 6  | 20.0 | 105  | 21 | AAW57767 |          |
| 28 | 6  | 20.0 | 116  | 21 | AAW41577 |          |
| 29 | 6  | 20.0 | 155  | 21 | AAW22865 |          |
| 30 | 6  | 20.0 | 155  | 21 | AAW54142 |          |
| 31 | 6  | 20.0 | 160  | 21 | AAW22864 |          |
| 32 | 6  | 20.0 | 160  | 21 | AAW54141 |          |
| 33 | 6  | 20.0 | 213  | 19 | AAW60564 |          |
| 34 | 6  | 20.0 | 218  | 22 | AAW73217 |          |
| 35 | 6  | 20.0 | 369  | 21 | AAW52004 |          |
| 36 | 6  | 20.0 | 399  | 16 | AAW71032 |          |
| 37 | 6  | 20.0 | 400  | 21 | AAW52003 |          |
| 38 | 6  | 20.0 | 415  | 22 | AAW85144 |          |
| 39 | 6  | 20.0 | 422  | 21 | AAW52002 |          |
| 40 | 6  | 20.0 | 456  | 21 | AAW20758 |          |
| 41 | 6  | 20.0 | 456  | 21 | AAW50449 |          |
| 42 | 6  | 20.0 | 481  | 16 | AAW71033 |          |
| 43 | 6  | 20.0 | 481  | 19 | AAW40814 |          |
| 44 | 6  | 20.0 | 481  | 21 | AAW20757 |          |
| 45 | 6  | 20.0 | 481  | 21 | AAW50448 |          |

#### ALIGNMENTS

|          |  |
|----------|--|
| RESULT 1 |  |
| AAV09349 | AAV09349 standard; peptide: 30 AA.                                       |
| ID       |  |
| XX       |  |
| AC       | AAV09349:  |
| XX       |  |
| DT       | 09-JUL-1999 (first entry)  |
| XX       |  |
| DE       | Human RAGE V-domain peptide SEQ ID NO:1.                                 |
| XX       |  |
| KW       | RAGE: V-domain; receptor for advanced glycation endproduct;              |
| KW       | ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome; |
| KW       | senility; renal failure; hyperlipidaemic atherosclerosis; dementia;      |
| KW       | neuronal cytotoxicity; head trauma; autoimmune lateral sclerosis;        |
| KW       | multiple sclerosis; amyloidosis; autoimmune disease; inflammation;       |
| KW       | tumour; cancer; male impotence; wound healing; periodontal disease;      |
| KW       | neuropathy; retinopathy; nephropathy; neuronal degeneration.             |
| XX       |  |
| OS       | Homo sapiens.  |
| XX       |  |
| PN       | W0918987-A1.   |
| XX       |  |
| PD       | 22-APR-1999.   |
| XX       |  |
| PF       | 09-OCT-1998; 98WC-US21346.   |
| XX       |  |
| PR       | 09-OCT-1997; 97US-0948131.   |
| XX       |  |
| PA       | (UYCO ) UNIV COLUMBIA NEW YORK.  |
| XX       |  |
| PI       | Iamster I, Schmidt AM, Stern D, Yan SD;                                  |
| XX       |  |
| DR       | WPI; 1999-277439/23.   |

PT New peptides based on an advanced glycation end product receptor are  
PT useful for treating Alzheimer's disease and Down's syndrome  
XX  
XX  
PS Claim 2; Page 78; 101pp; English.

CC The present invention describes novel isolated peptides (1) having an  
CC amino acid sequence corresponding to an amino acid sequence of a  
CC V-domain of a receptor for an advanced glycation end product (RAGE).  
CC Also described are methods for: (1) inhibiting an amyloid-beta peptide  
CC (ABP) interaction with a receptor for RAGE when the receptor is on the  
CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)  
CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting  
CC extracellular assembly of an ABP into a fibril; (5) inhibiting  
CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration  
CC of a microglial cell into senile plaques; (7) inhibiting activation of a  
CC microglial cell by an ABP; (8) treating a subject with a condition  
CC associated with an interaction of an ABP with a receptor for RAGE on a  
CC cell; (9) evaluating the ability of an agent to inhibit binding of an  
CC ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)  
CC inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting  
CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction  
CC with a receptor for RAGE when the receptor is on the surface of a cell;  
CC and (13) treating a subject with a condition associated with an  
CC interaction of an RAGE with a receptor for RAGE on a cell. The methods  
CC can be used for treating conditions associated with an interaction of an  
CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's  
CC disease, senility, renal failure, hyperlipidemic atherosclerosis,  
CC neuronal cytotoxicity, Down's syndrome, dementia associated with head  
CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,  
CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,  
CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy  
CC or neuronal degeneration.  
XX  
SQ Sequence 30 AA;

Query Match 100.0%; Score 30; DB 20; Length 30;  
Best Local Similarity 100.0%; Pred. No. 4e-25;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTTARIGEPVLKCKGAPKPPQRLWK 30  
DB 1 agntarigepvlkckgapkppqrlwkw 30

RESULT 2  
AA52134  
ID AAY52134 standard; protein; 30 AA.  
XX  
XX AAY52134;

DT 28-JAN-2000 (first entry)

DE Human Receptor to AGE (RAGE) amino acid sequence fragment #3.

KW Soluble receptor for advanced glycation endproducts; RAGE; tumour;  
KM invasion; metastasis; amphoterin; neuron; inhibit; therapy.

OS Homo sapiens.

PN WO954485-A1.

PD 28-OCT-1999.

PF 16-APR-1999; 99WO-US08427.

PR 17-APR-1998; 98US-0062365.

PA (UYCO ) UNIV COLUMBIA NEW YORK.

PT Schmidt AM, Stern D;

XX  
XX WPI; 2000-013260/01.

XX  
XX Inhibiting tumour invasion or spreading by administration of soluble  
PT receptor for advanced glycation endproducts -  
XX  
XX  
PS Claim 29; Page 62; 86pp; English.

CC This is the amino acid sequence of a fragment of the human soluble  
CC Receptor for Advanced Glycation Endproducts (RAGE). RAGE interacts with  
CC a range of physiologically and pathophysiologically relevant ligands  
CC when considering tumour invasion. In normal developing neurons RAGE  
CC colocalizes with amphoterin which is a matrix associated polypeptide.  
CC The expression of both RAGE and amphoterin decreases after birth, but  
CC both have increased expression in tumours. RAGE polypeptides  
CC AAY52132-Y52135 are used in the invention in a method for inhibiting  
CC tumour invasion and metastasis. The method involves inhibiting tumour  
CC invasion and metastasis via administration of a therapeutically effective  
CC amount of the pharmaceutical composition containing a RAGE polypeptide.  
CC The invention also relates to a method for evaluating the ability of an  
CC agent to inhibit tumour invasion in a local cellular environment. RAGE  
CC can be administered to a patient in a pharmaceutically acceptable  
CC carrier.  
XX  
SQ Sequence 30 AA;

Query Match 100.0%; Score 30; DB 21; Length 30;  
Best Local Similarity 100.0%; Pred. No. 4e-25;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTTARIGEPVLKCKGAPKPPQRLWK 30  
DB 1 agntarigepvlkckgapkppqrlwkw 30

RESULT 3  
AAW44200  
ID AAW44200 standard; protein; 318 AA.  
XX  
XX AAW44200;

DT 14-MAY-1998 (first entry)

DE Human mature receptor to an advanced glycosylation end product.

KW Human; soluble receptor; advanced glycosylation end product; RAGE;  
KM AGE; antibody; vascular permeability; diabetes mellitus.

OS Homo sapiens.

FT Key Location/Qualifiers  
FT Misc-difference 66 /note="encoded by CCR"

PN WO9739125-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01834.

PR 16-APR-1996; 96US-0633148.

PA (SCHD ) SCHERING PATENTE AG.

PI Hollander DA, Morser MJ, Nagashima M;

DR WPI; 1997-558580/51.

DR N-PSDB; AAV12395.

PT Anti-advanced glycosylation end product polypeptide antibody -  
PT prevents receptor binding and therefore reduces vascular  
PT permeability, useful to treat diabetes mellitus

XX  
XX Claim 2; Page 42-43; 90pp; English.

CC This is a human advanced glycosylation end-product receptor (RAGE)  
CC polypeptide (318 amino acid residues). The RAGE polypeptide and its  
CC active fragments or their mimetics, inhibit interaction between advanced  
CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They  
CC are used to treat diseases associated with AGE/RAGE interaction, such as  
CC increased vascular permeability, diabetes mellitus (particularly  
CC complications such as micro- or macro- vasculopathy or occlusive vascular  
CC disorders such as neuropathy, nephropathy, retinopathy or  
CC atherosclerosis) or haemodialysis-associated amyloidosis, also activation  
CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or

CC This is the amino acid sequence of the human soluble Receptor for  
CC Advanced Glycation Endproducts (RAGE). RAGE interacts with a range of  
CC physiologically and pathophysiologically relevant ligands when  
CC considering tumour invasion. In normal developing neurons RAGE  
CC colocalises with amphoterin which is a matrix associated polypeptide.  
CC The expression of both RAGE and amphoterin decreases after birth, but  
CC both have increased expression in tumours. RAGE polypeptides  
CC AA52132-Y52135 are used in the invention in a method for inhibiting  
CC tumour invasion and metastasis. The method involves inhibiting tumour  
CC invasion and metastasis via administration of a therapeutically effective  
CC amount of the pharmaceutical composition containing a RAGE polypeptide.  
CC The invention also relates to a method for evaluating the ability of an  
CC agent to inhibit tumour invasion in a local cellular environment. RAGE  
CC can be administered to a patient in a pharmaceutically acceptable  
CC carrier.

SQ Sequence 332 AA:

Query Match 100.0%; Score 30; DB 21; Length 332;  
Best Local Similarity 100.0%; Pred. No. 2,9e-24;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGEPVLKCKGAPKPPORLEWK 30  
|||||  
DB 1 agnitarigepvlkckgapkppqrllewk 30

RESULT 6  
AAM44199  
ID AAM44199 standard; Protein: 340 AA.

AC AAM44199;

DT 14-MAY-1998 (first entry)

DE Human soluble receptor to an advanced glycosylation end product.

KW Human; soluble receptor; advanced glycosylation end product; RAGE;

KM AGE; antibody; vascular permeability; diabetes mellitus.

XX Homo sapiens.

OS

PN WO9739125-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01834.

PR 16-APR-1996; 96US-0633148.

PT (SCHD ) SCHERING PATENTE AG.

PI Hollander DA, Morser MJ, Nagashima M;

XX WPI: 1997-558580/51.

DR N-PSDB; AAV12394.

XX Anti-advanced glycosylation end product polypeptide antibody

PT prevents receptor binding and therefore reduces vascular

permeability, useful to treat diabetes mellitus

PS Claim 2; Page 40-41; 90pp; English.

XX The present sequence represents a soluble human receptor to an advanced

CC glycosylation end product (RAGE) polypeptide. The present invention

CC describes an isolated antibody (Ab), specifically immunoreactive with

CC RAGE. Advanced glycosylation end products (AGE) of proteins are

CC non-enzymatically glycosylated proteins, which accumulate in vascular

CC tissue in aging, and at an accelerated rate in individuals with

CC diabetes. The Ab, which prevents the interaction between an AGE and its

CC receptor (RAGE), reduces vascular permeability. The Ab can be used to

CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive

CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis

CC associated amyloidosis or atherosclerosis. The Ab can also be used for

CC the isolation and purification of human RAGE polypeptide.

SQ Sequence 340 AA:

Query Match 100.0%; Score 30; DB 18; Length 340;  
Best Local Similarity 100.0%; Pred. No. 3e-24;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGEPVLKCKGAPKPPORLEWK 30  
|||||  
DB 23 agnitarigepvlkckgapkppqrllewk 52

RESULT 7  
AAM33753  
ID AAM33753 standard; Protein: 340 AA.

AC AAM33753;

DT 08-MAY-1998 (first entry)

DE Human RAGE polypeptide (340 amino acid residues).

KW Advanced glycosylation end-product receptor; RAGE; screening; AGE;

KM vascular permeability; diabetes mellitus; treatment; atherosclerosis;

XX Alzheimer's disease.

XX Homo sapiens.

OS

PN WO9739121-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01832.

PR 16-APR-1996; 96US-0633147.

PT (SCHD ) SCHERING AG.

PI Morser MJ, Nagashima M;

XX WPI: 1997-526458/48.

DR N-PSDB; AAV06517.

PT New soluble advanced glycosylation end-product receptor polypeptide

PT - used for reducing vascular permeability, complications of diabetes

PT etc., also for purification and to screen for modulators

PS Claim 3; Fig 1A; 91pp; English.

XX This is a human advanced glycosylation end-product receptor (RAGE)

CC polypeptide (340 amino acid residues). The RAGE polypeptides and its

CC active fragments or their mimetics, inhibit interaction between advanced

CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They

CC are used to treat diseases associated with AGE/RAGE interaction, such as

CC increased vascular permeability, diabetes mellitus (particularly

CC complications such as micro- or macro- vasculopathy or occlusive vascular

CC disorders such as neuropathy, nephropathy, retinopathy or

CC atherosclerosis) or haemodialysis-associated amyloidosis, also activation

CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or

CC age-related disorders such as oxidative stress. These RAGE polypeptides

CC are also used, when immobilised, to purify AGE from a protein mixture and

CC to screen for compounds that are agonists and antagonists of AGE/RAGE

CC interaction. They can also be used diagnostically to detect abnormal

CC levels of AGE. Antibodies against RAGE polypeptides are useful as

CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of

CC interaction between AGE and RAGE or other receptors and for purification

CC and quantification of RAGE polypeptides. The encoding nucleic acids are

CC used to express recombinant RAGE and as probes for isolating related

CC genes.

SQ Sequence 340 AA:

Query Match 100.0%; Score 30; DB 18; Length 340;  
Best Local Similarity 100.0%; Pred. No. 3e-24;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGEPVLKCKGAPKPPORLEWK 30  
|||||  
DB 23 agnitarigepvlkckgapkppqrllewk 52

RESULT 8

AAB81925  
ID AAB81925 standard; protein: 404 AA.

```

XX AAB81925;
AC
XX
XX 15-JUN-2001 (first entry)
DT
XX
DE Extracorporeal circulation material receptor protein.
XX
XX Extracorporeal circulation; carbonyl stress product; receptor;
KW diabetes; vascular lesion; excretory dysfunction.
XX
XX Unidentified.
OS
XX
XX WO200118060-A1.
PN
XX
XX 15-MAR-2001.
PD
XX
XX 08-SEP-2000; 2000WO-JP06172.
PE
XX
XX 08-SEP-1999; 99JP-0254463.
PR
XX
XX (TORA ) TORAY IND INC.
PA
XX
XX Shimizu S, Kubota M, Akiyama H, Usui M;
PI WPI; 2001-290314/30.
DR
XX
XX Material for extracorporeal circulation, applicable in selective
PT elimination of diabetic complication factors such as carbonyl stress
PT products caused by abnormally promoted carbonyl stress from excretory
PT dysfunction in vascular lesions
PS
XX
XX Claim 1: Page 31-32; 36pp; Japanese.
PS
XX
XX The present invention describes a material for extracorporeal circulation
CC which is made from a water-insoluble carrier immobilized with a protein
CC having the sequence shown here. The materials of the invention, including
CC adsorbents, are for extracorporeal circulation, which are applicable in
CC the selective elimination of diabetic complication factors from a body
CC fluid, and are therefore useful in treating vascular lesions like
CC arteriosclerosis due to carbonyl stress products caused by abnormally
CC promoted carbonyl stress from excretory dysfunction.
CC
XX
XX Sequence 404 AA:
SQ

```

Query Match 100.0%; Score 30; DB 22; Length 404;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-24;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 AONITARIGEPVLKCKGAPKKRPQRLWK 30
   |||||||
DB 23 agnitarigepvlkckgapkppqrlwkw 52

```

RESULT 9  
 AAW44214  
 ID AAW44214 standard; peptide; 16 AA.  
 AC  
 XX AAW44214;  
 AC  
 XX 14-MAY-1998 (first entry)  
 DT  
 XX  
 XX Human soluble RAGE immunologically active fragment SEQ ID NO.18.  
 DE  
 XX  
 XX Human; soluble receptor; advanced glycosylation end product; RAGE;  
 KW AGE; antibody; vascular permeability; immunologically active fragment;  
 KW diabetes mellitus.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO9739125-A1.  
 PN  
 XX  
 XX 23-OCT-1997.  
 PD

```

XX
XX 11-APR-1997; 97WO-EP01834.
PF
XX
XX 16-APR-1996; 96US-0633148.
PR
XX
XX (SCHD ) SCHERING PATENTE AG.
PA
XX
XX Hollander DA, Morser MJ, Nagashima M;
PI WPI; 1997-558580/51.
DR
XX
XX Anti-advanced glycosylation end product polypeptide antibody
PT prevents receptor binding and therefore reduces vascular
PT permeability, useful to treat diabetes mellitus
PS
XX
XX Claim 2; Page 49; 90pp; English.
PS
XX
XX The present sequence represents an immunologically active fragment
CC of a soluble human receptor to an advanced glycosylation end
CC product (RAGE) polypeptide. The present invention describes
CC an isolated antibody (Ab), specifically immunoreactive with
CC RAGE. Advanced glycosylation end products (AGE) of proteins are
CC non-enzymatically glycosylated proteins, which accumulate in vascular
CC tissue in aging, and at an accelerated rate in individuals with
CC diabetes. The Ab, which prevents the interaction between an AGE and it's
CC receptor (RAGE), reduces vascular permeability. The Ab can be used to
CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive
CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis
CC associated amyloidosis or arteriosclerosis. The Ab can also be used for
CC the isolation and purification of human RAGE polypeptide.
CC
XX
XX Sequence 16 AA:
SQ

```

Query Match 53.3%; Score 16; DB 18; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2e-10;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 AONITARIGEPVLKCK 16
   |||||||
DB 1 agnitarigepvlkck 16

```

RESULT 10  
 AAW33768  
 ID AAW33768 standard; peptide; 16 AA.  
 AC  
 XX AAW33768;  
 AC  
 XX 08-MAY-1998 (first entry)  
 DT  
 XX  
 XX Human RAGE polypeptide fragment 14.  
 DE  
 XX  
 XX Advanced glycosylation end-product receptor; RAGE; screening; AGE;  
 KW vascular permeability; diabetes mellitus; treatment; arteriosclerosis;  
 KW Alzheimer's disease.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO9739121-A1.  
 PN  
 XX  
 XX 23-OCT-1997.  
 PD  
 XX  
 XX 11-APR-1997; 97WO-EP01832.  
 PF  
 XX  
 XX 16-APR-1996; 96US-0633147.  
 PR  
 XX  
 XX (SCHD ) SCHERING AG.  
 PA  
 XX  
 XX Morser MJ, Nagashima M;  
 PI WPI; 1997-526458/48.  
 DR  
 XX





CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or  
CC age-related disorders such as oxidative stress. These RAGE polypeptides  
CC are also used, when immobilised, to purify AGE from a protein mixture and  
CC to screen for compounds that are agonists and antagonists of AGE/RAGE  
CC interaction. They can also be used diagnostically to detect abnormal  
CC levels of AGE. Antibodies against RAGE polypeptides are useful as  
CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of  
CC interaction between AGE and RAGE or other receptors and for purification  
CC and quantification of RAGE polypeptides. The encoding nucleic acids are  
CC used to express recombinant RAGE and as probes for isolating related  
CC genes.  
XX  
SQ Sequence 15 AA;

Query Match 50.0%; Score 15; DB 18; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.2e-09;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AQNTARIGEPLVLK 15  
DB 1 aqntarigeplvlk 15

RESULT 13  
AAV09350  
ID AAV09350 standard; peptide; 30 AA.  
XX  
AC AAV09350;  
XX  
DT 09-JUL-1999 (first entry)  
XX  
DE Mouse RAGE V-domain peptide SEQ ID NO:2.  
XX

RAGE; V-domain; receptor for advanced glycation endproduct;  
KW ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;  
KW senility; renal failure; hyperlipidaemic atherosclerosis; dementia;  
KW neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;  
KW multiple sclerosis; amyloidosis; autoimmune disease; inflammation;  
KW tumour; cancer; male impotence; wound healing; periodontal disease;  
KW neuropathy; retinopathy; nephropathy; neuronal degeneration.  
XX  
XX  
OS Mus sp.

PN WO9918987-A1.

XX 22-APR-1999.

XX 09-OCT-1998; 98WO-US21346.

XX 09-OCT-1997; 97US-0948131.

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX Lamster I, Schmidt AM, Stern D, Yan SD;

DR WPI; 1999-277439/23.

PT New peptides based on an advanced glycation end product receptor are  
PT useful for treating Alzheimer's disease and Down's syndrome  
XX  
XX  
PS Claim 3; Page 78; 101pp; English.

CC The present invention describes novel isolated peptides (1) having an  
CC amino acid sequence corresponding to an amino acid sequence of a  
CC V-domain of a receptor for an advanced glycation end product (RAGE).  
CC Also described are methods for: (1) inhibiting an amyloid-beta peptide  
CC (ABP) interaction with a receptor for RAGE when the receptor is on the  
CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)  
CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting  
CC extracellular assembly of an ABP into a fibril; (5) inhibiting  
CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration  
CC of a microglial cell into senile plaques; (7) inhibiting activation of a

CC microglial cell by an ABP; (8) treating a subject with a condition  
CC associated with an interaction of an ABP with a receptor for RAGE on a  
CC cell; (9) evaluating the ability of an agent to inhibit binding of an  
CC ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)  
CC inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting  
CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction  
CC with a receptor for RAGE when the receptor is on the surface of a cell;  
CC and (13) treating a subject with a condition associated with an  
CC interaction of an RAGE with a receptor for RAGE on a cell. The methods  
CC can be used for treating conditions associated with an interaction of an  
CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's  
CC disease, senility, renal failure, hyperlipidaemic atherosclerosis,  
CC neuronal cytotoxicity, Down's syndrome, dementia associated with head  
CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,  
CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,  
CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy  
CC or neuronal degeneration.  
XX  
SQ Sequence 30 AA;

Query Match 43.3%; Score 13; DB 20; Length 30;  
Best Local Similarity 100.0%; Pred. No. 5.2e-07;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QNTARIGEPLVL 14  
DB 2 qntarigeplvl 14

RESULT 14  
AAV09351  
ID AAV09351 standard; peptide; 30 AA.  
XX  
AC AAV09351;  
XX  
DT 09-JUL-1999 (first entry)  
XX  
DE Rat RAGE V-domain peptide SEQ ID NO:3.

RAGE; V-domain; receptor for advanced glycation endproduct;  
KW ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;  
KW senility; renal failure; hyperlipidaemic atherosclerosis; dementia;  
KW neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;  
KW multiple sclerosis; amyloidosis; autoimmune disease; inflammation;  
KW tumour; cancer; male impotence; wound healing; periodontal disease;  
KW neuropathy; retinopathy; nephropathy; neuronal degeneration.  
XX  
XX  
OS Rattus sp.

PN WO9918987-A1.

XX 22-APR-1999.

XX 09-OCT-1998; 98WO-US21346.

XX 09-OCT-1997; 97US-0948131.

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX Lamster I, Schmidt AM, Stern D, Yan SD;

DR WPI; 1999-277439/23.

PT New peptides based on an advanced glycation end product receptor are  
PT useful for treating Alzheimer's disease and Down's syndrome  
XX  
XX  
PS Claim 4; Page 78; 101pp; English.

CC The present invention describes novel isolated peptides (1) having an  
CC amino acid sequence corresponding to an amino acid sequence of a  
CC V-domain of a receptor for an advanced glycation end product (RAGE).  
CC Also described are methods for: (1) inhibiting an amyloid-beta peptide

CC (ABP) interaction with a receptor for RAGE when the receptor is on the  
 CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)  
 CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting  
 CC extracellular assembly of an ABP into a fibril; (5) inhibiting  
 CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration  
 CC of a microglial cell into senile plaques; (7) inhibiting activation of a  
 CC microglial cell by an ABP; (8) treating a subject with a condition  
 CC associated with an interaction of an ABP with a receptor for RAGE on a  
 CC cell; (9) evaluating the ability of an agent to inhibit binding of an  
 CC ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)  
 CC inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting  
 CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction  
 CC with a receptor for RAGE when the receptor is on the surface of a cell;  
 CC and (13) treating a subject with a condition associated with an  
 CC interaction of an RAGE with a receptor for RAGE on a cell. The methods  
 CC can be used for treating conditions associated with an interaction of an  
 CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's  
 CC disease, senility, renal failure, hyperlipidemic atherosclerosis,  
 CC neuronal cytotoxicity, Down's syndrome, dementia associated with head  
 CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,  
 CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,  
 CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy  
 CC or neuronal degeneration.  
 CC  
 SQ Sequence 30 AA;

Query Match 36.7%; Score 11; DB 20; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 QNTARIGEPV 12  
 |||||  
 Db 2 qntarigepl 12

RESULT 15  
 AAM44209

ID AAM44209 standard; peptide; 10 AA.

AC AAM44209;

DT 14-MAY-1998 (first entry)

DE Human soluble RAGE immunologically active fragment SEQ ID NO:13.

KW Human; soluble receptor; advanced glycosylation end product; RAGE;  
 AGE; antibody; vascular permeability; immunologically active fragment;  
 diabetes mellitus.

OS Homo sapiens.

PN WO9739125-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01834.

PR 16-APR-1996; 96US-0633148.

PA (SCHD ) SCHERING PATENTE AG.

PI Hollander DA, Morser MJ, Nagashima M;

WPI; 1997-558580/51.

XX Anti-advanced glycosylation end product polypeptide antibody  
 PT prevents receptor binding and therefore reduces vascular  
 PT permeability, useful to treat diabetes mellitus  
 PS Claim 2; Page 47; 90pp; English.

CC The present sequence represents an immunologically active fragment

CC of a soluble human receptor to an advanced glycosylation end  
 CC product (RAGE) polypeptide. The present invention describes  
 CC an isolated antibody (Ab), specifically immunoreactive with  
 CC RAGE. Advanced glycosylation end products (AGE) of proteins are  
 CC non-enzymatically glycosylated proteins, which accumulate in vascular  
 CC tissue in ageing, and at an accelerated rate in individuals with  
 CC diabetes. The Ab, which prevents the interaction between an AGE and it's  
 CC receptor (RAGE), reduces vascular permeability. The Ab can be used to  
 CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive  
 CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis  
 CC associated amyloidosis or atherosclerosis. The Ab can also be used for  
 CC the isolation and purification of human RAGE polypeptide.  
 CC  
 SQ Sequence 10 AA;

Query Match 33.3%; Score 10; DB 18; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.00033;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 CKGAPKKRPQ 25  
 |||||  
 Db 1 ckgapkxrpq 10

Search completed: April 24, 2002, 09:21:51  
 Job time: 250 sec



**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:22:29 ; Search time 32.21 Seconds  
(without alignments)  
20.959 Million cell updates/sec

Title: US-09-689-469-5  
Perfect score: 30  
Sequence: 1 AONTARIGEPLVLKCKGAPKKPPQRLKWK 30

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 212252 seqs, 22503292 residues

Word size : 0

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PTDUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/Dackfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 30    | 100.0       | 318    | 2  | US-08-633-148-4    |
| 2          | 30    | 100.0       | 340    | 2  | US-08-633-148-2    |
| 3          | 23    | 76.7        | 278    | 2  | US-08-432-016-5    |
| 4          | 23    | 76.7        | 278    | 2  | US-08-684-594-5    |
| 5          | 16    | 53.3        | 16     | 2  | US-08-633-148-18   |
| 6          | 15    | 50.0        | 15     | 2  | US-08-633-148-12   |
| 7          | 10    | 33.3        | 10     | 2  | US-08-633-148-5    |
| 8          | 10    | 33.3        | 10     | 2  | US-08-633-148-13   |
| 9          | 6     | 20.0        | 10     | 4  | US-08-685-558A-2   |
| 10         | 6     | 20.0        | 479    | 1  | US-08-416-788-2    |
| 11         | 6     | 20.0        | 481    | 1  | US-08-173-436A-2   |
| 12         | 6     | 20.0        | 481    | 2  | US-08-748-485-8    |
| 13         | 6     | 20.0        | 513    | 4  | US-08-685-558A-18  |
| 14         | 6     | 20.0        | 741    | 1  | US-08-277-231A-4   |
| 15         | 6     | 20.0        | 741    | 2  | US-08-473-750-7    |
| 16         | 6     | 20.0        | 741    | 2  | US-08-477-326-7    |
| 17         | 6     | 20.0        | 1103   | 3  | US-09-162-373-1    |
| 18         | 6     | 20.0        | 1103   | 4  | US-09-467-946-1    |
| 19         | 6     | 20.0        | 1958   | 4  | US-07-945-283-2    |
| 20         | 5     | 16.7        | 11     | 1  | US-08-336-343A-23  |
| 21         | 5     | 16.7        | 14     | 1  | US-08-137-117D-153 |
| 22         | 5     | 16.7        | 14     | 1  | US-08-137-117D-155 |
| 23         | 5     | 16.7        | 14     | 1  | US-08-137-117D-158 |
| 24         | 5     | 16.7        | 14     | 2  | US-08-436-717-153  |
| 25         | 5     | 16.7        | 14     | 2  | US-08-436-717-155  |
| 26         | 5     | 16.7        | 14     | 2  | US-08-436-717-158  |
| 27         | 5     | 16.7        | 20     | 4  | US-08-602-999A-134 |

|    |   |      |     |   |                    |                   |
|----|---|------|-----|---|--------------------|-------------------|
| 28 | 5 | 16.7 | 20  | 4 | US-09-242-131A-1   | Sequence 1, Appl  |
| 29 | 5 | 16.7 | 20  | 4 | US-09-615-283-1    | Sequence 1, Appl  |
| 30 | 5 | 16.7 | 22  | 4 | US-09-242-131A-7   | Sequence 7, Appl  |
| 31 | 5 | 16.7 | 22  | 4 | US-09-615-283-7    | Sequence 7, Appl  |
| 32 | 5 | 16.7 | 26  | 2 | US-08-637-759B-326 | Sequence 326, App |
| 33 | 5 | 16.7 | 26  | 2 | US-08-871-355A-326 | Sequence 326, App |
| 34 | 5 | 16.7 | 49  | 4 | US-09-085-305-22   | Sequence 22, Appl |
| 35 | 5 | 16.7 | 59  | 4 | US-09-085-305-21   | Sequence 21, Appl |
| 36 | 5 | 16.7 | 63  | 2 | US-08-637-759B-191 | Sequence 191, App |
| 37 | 5 | 16.7 | 63  | 3 | US-08-871-355A-191 | Sequence 191, App |
| 38 | 5 | 16.7 | 72  | 4 | US-09-188-930-153  | Sequence 153, App |
| 39 | 5 | 16.7 | 72  | 4 | US-09-188-930-304  | Sequence 304, App |
| 40 | 5 | 16.7 | 80  | 4 | US-09-085-305-23   | Sequence 23, Appl |
| 41 | 5 | 16.7 | 86  | 1 | US-08-497-312-27   | Sequence 27, Appl |
| 42 | 5 | 16.7 | 90  | 4 | US-09-085-305-24   | Sequence 24, Appl |
| 43 | 5 | 16.7 | 98  | 1 | US-08-211-202-130  | Sequence 130, App |
| 44 | 5 | 16.7 | 98  | 1 | US-08-211-202-140  | Sequence 140, App |
| 45 | 5 | 16.7 | 117 | 3 | US-08-545-809A-91  | Sequence 91, Appl |

#### ALIGNMENTS

RESULT 1  
US-08-633-148-4  
; Sequence 4, Application US/08633148  
; Patent No. 5864018  
; GENERAL INFORMATION:  
; APPLICANT: MORSE, MICHAEL J.  
; APPLICANT: NAGASHIMA, MARIKO  
; APPLICANT: HOLLANDER, DORIS A.  
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION  
; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP  
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: U.S.A.  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/633,148  
; FILING DATE: 16-APR-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MORPHY ESO., MATTHEW B.  
; REGISTRATION NUMBER: 39,787  
; REFERENCE/DOCKET NUMBER: 014618-005600US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 318 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-633-148-4

Query Match 100.0%; Score 30; DB 2; Length 318;  
Best Local Similarity 100.0%; Pred. No. 1.2e-24;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 AONTARIGEPLVLKCKGAPKKPPQRLKWK 30  
|||||

Db 1 AONITARIIGEPVLKCKGAPKPPORLEWK 30

RESULT 2

US-08-633-148-2

Sequence 2, Application US/08633148

Patent No. 5864018

GENERAL INFORMATION:

APPLICANT: MORSE, MICHAEL J.

APPLICANT: MAGASHIMA, NARIKO

APPLICANT: HOLLANDER, DORIS A.

TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION

TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP

STREET: TWO EMBARCADERO CENTER, 8TH FLOOR

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: U.S.A.

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/633,148

FILING DATE: 16-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURPHY ESQ., MATTHEW B.

REGISTRATION NUMBER: 39,787

REFERENCE/DOCKET NUMBER: 014618-00560005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ. ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 340 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-633-148-2

Query Match 100.0%; Score 30; DB 2; Length 340;

Best Local Similarity 100.0%; Pred. No. 1.3e-24;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONITARIIGEPVLKCKGAPKPPORLEWK 30

Db 23 AONITARIIGEPVLKCKGAPKPPORLEWK 52

RESULT 3

US-08-432-016-5

Sequence 5, Application US/08432016

Patent No. 5968768

GENERAL INFORMATION:

APPLICANT: HAYNES, BARTON F.

APPLICANT: ARUEFO, ALEJANDRO

APPLICANT: PATEL, DHAVALKUMAR

APPLICANT: BOWEN, MICHAEL A.

APPLICANT: MAROUDAT, HANS

TITLE OF INVENTION: CD6 LIGAND

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/432,016

FILING DATE: 01-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/333,350

FILING DATE: 02-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/143,903

FILING DATE: 02-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955

REFERENCE/DOCKET NUMBER: 1579-95

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ. ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 278 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-432-016-5

Query Match 76.7%; Score 23; DB 2; Length 278;

Best Local Similarity 100.0%; Pred. No. 2.9e-17;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 IGEPLVLKCKGAPKPPORLEWK 30

Db 1 IGEPLVLKCKGAPKPPORLEWK 23

RESULT 4

US-08-684-594-5

Sequence 5, Application US/08684594

Patent No. 5998172

GENERAL INFORMATION:

APPLICANT: HAYNES, BARTON F.

APPLICANT: ARUEFO, ALEJANDRO

APPLICANT: PATEL, DHAVALKUMAR

APPLICANT: BOWEN, MICHAEL A.

APPLICANT: MAROUDAT, HANS

TITLE OF INVENTION: CD6 LIGAND

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/684,594

FILING DATE: 18-JUL-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/432,016



APPLICANT: HOLLANDER, DORIS A.  
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION  
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USBS THEREFOR  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP  
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: U.S.A.  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/633,148  
FILING DATE: 16-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY ESO., MATTHEW B.  
REGISTRATION NUMBER: 39,787  
REFERENCE/DOCKET NUMBER: 014618-00560005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
SEQUENCE CHARACTERISTICS:  
INFORMATION FOR SEQ. ID NO: 5:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-633-148-5

Query Match 33.3%; Score 10; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00012;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CKGAPKKPPQ 25  
DB 1 CKGAPKKPPQ 10

RESULT 8  
US-08-633-148-13  
Sequence 13, Application US/08633148  
Patent No. 5864018  
GENERAL INFORMATION:  
APPLICANT: MORSE, MICHAEL J.  
APPLICANT: HOLLANDER, DORIS A.  
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION  
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USBS THEREFOR  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP  
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: U.S.A.  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/633,148  
FILING DATE: 16-APR-1996  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY ESO., MATTHEW B.  
REGISTRATION NUMBER: 39,787  
REFERENCE/DOCKET NUMBER: 014618-00560005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ. ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-633-148-13

Query Match 33.3%; Score 10; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00012;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CKGAPKKPPQ 25  
DB 1 CKGAPKKPPQ 10

RESULT 9  
US-08-685-558A-2  
Sequence 2, Application US/08685558A  
Patent No. 6225081  
GENERAL INFORMATION:  
APPLICANT: SHIMOMURA, Takeshi  
APPLICANT: KAWAGUCHI, Toshiya  
APPLICANT: KITAMURA, Naomi  
APPLICANT: MIYAZAWA, Keiji  
TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME  
TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,558A  
FILING DATE: 24-JUL-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JPA Hei 7-187135  
FILING DATE: 24-JUL-1995  
INFORMATION FOR SEQ. ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: Internal fragment  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: MKN45  
US-08-685-558A-2

Query Match 20.0%; Score 6; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



OY 10 EPLVLK 15  
|||||  
DB 5 EPLVLK 10

RESULT 10  
US-08-416-788-2  
; Sequence 2, Application US/08416788  
; Patent No. 5780245  
; GENERAL INFORMATION:  
; APPLICANT: Marcoux, Luc  
; TITLE OF INVENTION: No. 5780245el Polypeptides Having a Serotonin  
; TITLE OF INVENTION: Receptor Activity, Nucleic Acids Coding for These  
; TITLE OF INVENTION: Polypeptides and Uses  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcoia Road, 3043  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426-0107  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/416,788  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/FR93/01012  
; FILING DATE: 13-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 92-12280  
; FILING DATE: 14-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, Julie K.  
; REGISTRATION NUMBER: 38,619  
; REFERENCE/DOCKET NUMBER: EX92008-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610)454-3839  
; TELEFAX: (610)454-3808  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 479 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-416-788-2

Query Match 20.0%; Score 6; DB 1; Length 479;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 KPPQRL 27  
|||||  
DB 253 KPPQRL 258

RESULT 11  
US-08-173-436A-2  
; Sequence 2, Application US/08173436A  
; Patent No. 5698444  
; GENERAL INFORMATION:  
; APPLICANT: Baez, Melvyn  
; APPLICANT: Kirsar, Jonathan D.  
; TITLE OF INVENTION: SEROTONIN RECEPTOR PROTEIN AND RELATED  
; TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Eli Lilly and Company  
; STREET: Lilly Corporate Center/Patent Division  
; CITY: Indianapolis  
; STATE: IN  
; COUNTRY: US  
; ZIP: 46285  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/173,436A  
; FILING DATE: 23-DEC-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gaylo, Paul J.  
; REGISTRATION NUMBER: 36,808  
; REFERENCE/DOCKET NUMBER: X-9367  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 317-276-0756  
; TELEFAX: 317-276-3861  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 481 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-173-436A-2

Query Match 20.0%; Score 6; DB 1; Length 481;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 KPPQRL 27  
|||||  
DB 254 KPPQRL 259

RESULT 12  
US-08-748-485-8  
; Sequence 8, Application US/08748485  
; Patent No. 5817480  
; GENERAL INFORMATION:  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Murty, Lynn E.  
; TITLE OF INVENTION: NOVEL HISTAMINE H2 RECEPTOR  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/748,485  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0159 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 481 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 475198  
US-08-748-485-8

Query Match 20.0%; Score 6; DB 2; Length 481;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 KPPQRL 27  
Db 254 KPPQRL 259

RESULT 13  
US-08-685-558A-18  
Sequence 18, Application US/08685558A  
Patent No. 6225081  
GENERAL INFORMATION:  
APPLICANT: SHIMOMURA, Takeshi  
APPLICANT: KAWAGUCHI, Toshiya  
APPLICANT: KITAMURA, Naomi  
APPLICANT: MIYAZAWA, Keiji  
TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME  
TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SUGHRUE, MIOM, ZINN, MACPEAK & SEAS  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,558A  
FILING DATE: 24-JUL-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JPA Hei 7-187135  
FILING DATE: 24-JUL-1995  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 513 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: MKN45  
US-08-685-558A-18

Query Match 20.0%; Score 6; DB 4; Length 513;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EPLVLK 15  
Db 177 EPLVLK 182

RESULT 14  
US-08-277-231A-4  
Sequence 4, Application US/08277231A  
Patent No. 5643725  
GENERAL INFORMATION:  
APPLICANT: Green, Bruce A.  
APPLICANT: Brinton, Charles C.  
TITLE OF INVENTION: Sequence and Analysis of LKP Pili  
Patent No. 5643725  
TITLE OF INVENTION: Structural Genes and The LKP Pili Operon of No. 5643725type  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Millitia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/277,231A  
FILING DATE: 19-JUL-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Carroll, Alice O.  
REGISTRATION NUMBER: 32,542  
REFERENCE/DOCKET NUMBER: ACC94-02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 741 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-277-231A-4

Query Match 20.0%; Score 6; DB 1; Length 741;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TARIGE 10  
Db 157 TARIGE 162

RESULT 15  
US-08-473-750-7  
Sequence 7, Application US/08473750  
Patent No. 5834187  
Patent No. 5834187 5786143  
GENERAL INFORMATION:  
APPLICANT: Green, Bruce A.  
APPLICANT: Brinton, Jr., Charles C.  
TITLE OF INVENTION: Sequence and Analysis of LKP Pili  
Patent No. 5834187  
Patent No. 5834187 5786143  
TITLE OF INVENTION: Structural Gene and the LKP Pili Operon of No. 5834187 5786  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Millitia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/473,750  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/277,321  
FILING DATE: 19-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Carroll, Alice O.  
REGISTRATION NUMBER: 33,542  
REFERENCE/DOCKET NUMBER: ACC94-02B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 741 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-473-750-7

Query Match 20.0%; Score 6; DB 2; Length 741;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 6; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

OY 5 TARIGE 10  
| | | | |  
Db 157 TARIGE 162

Search completed: April 24, 2002, 09:22:30  
Job time: 249 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:23:16 ; Search time 38.65 seconds  
(without alignments)  
59.126 Million cell updates/sec

Title: US-09-689-469-5  
30  
Sequence: 1 AONITARIGEPVLKCKGAPKPPQRLKWK 30

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description                 |
|------------|-------|-------------|--------|-------|-----------------------------|
| 1          | 30    | 100.0       | 404    | 1     | I61596 advanced glycosyla   |
| 2          | 13    | 43.3        | 402    | 1     | T09062 probable advanced    |
| 3          | 10    | 33.3        | 416    | 1     | A42879 advanced glycosyla   |
| 4          | 7     | 23.3        | 223    | 2     | H64065 mutator muth - Hae   |
| 5          | 7     | 23.3        | 330    | 2     | E81998 pseudouridylylate sy |
| 6          | 7     | 23.3        | 330    | 2     | H81225 ribosomal large ch   |
| 7          | 7     | 23.3        | 537    | 1     | J01619 cell fusion glycop   |
| 8          | 7     | 23.3        | 595    | 2     | B86212 protein F24B9.20 l   |
| 9          | 6     | 20.0        | 96     | 2     | T07822 cystein proteinase   |
| 10         | 6     | 20.0        | 110    | 2     | S64538 hypothetical prote   |
| 11         | 6     | 20.0        | 155    | 2     | T46154 hypothetical prote   |
| 12         | 6     | 20.0        | 209    | 2     | E70536 hypothetical prote   |
| 13         | 6     | 20.0        | 230    | 2     | A75260 hypothetical prote   |
| 14         | 6     | 20.0        | 234    | 1     | Q08E43 membrane antigen g   |
| 15         | 6     | 20.0        | 238    | 2     | H64181 ABC-type transport   |
| 16         | 6     | 20.0        | 257    | 2     | D70552 hypothetical prote   |
| 17         | 6     | 20.0        | 271    | 2     | A70415 molybdopter in bios  |
| 18         | 6     | 20.0        | 282    | 2     | T07303 cell division inh    |
| 19         | 6     | 20.0        | 298    | 2     | T51746 RNA helicase RH17    |
| 20         | 6     | 20.0        | 326    | 2     | H83187 hypothetical prote   |
| 21         | 6     | 20.0        | 334    | 2     | D83164 conserved hypothet   |
| 22         | 6     | 20.0        | 359    | 2     | T35179 oxidoreductase alp   |
| 23         | 6     | 20.0        | 387    | 2     | C96670 hypothetical prote   |
| 24         | 6     | 20.0        | 389    | 2     | C93667 probable integrase   |
| 25         | 6     | 20.0        | 429    | 2     | T23984 hypothetical prote   |
| 26         | 6     | 20.0        | 468    | 2     | H69133 argininosuccinate    |
| 27         | 6     | 20.0        | 471    | 2     | S30585 hypothetical prote   |
| 28         | 6     | 20.0        | 474    | 2     | B82227 exodeoxyribonuclea   |
| 29         | 6     | 20.0        | 479    | 2     | C86275 hypothetical prote   |

|    |   |      |     |   |                           |
|----|---|------|-----|---|---------------------------|
| 30 | 6 | 20.0 | 481 | 2 | S43687 serotonin receptor |
| 31 | 6 | 20.0 | 481 | 2 | S49442 serotonin receptor |
| 32 | 6 | 20.0 | 504 | 2 | S27269 serotonin receptor |
| 33 | 6 | 20.0 | 509 | 2 | T36710 hypothetical prote |
| 34 | 6 | 20.0 | 511 | 2 | JE0312 3-ketosteroid-deta |
| 35 | 6 | 20.0 | 548 | 2 | T05671 hypothetical prote |
| 36 | 6 | 20.0 | 560 | 2 | T05278 hypothetical prote |
| 37 | 6 | 20.0 | 562 | 2 | T24462 hypothetical prote |
| 38 | 6 | 20.0 | 567 | 2 | A84748 hypothetical prote |
| 39 | 6 | 20.0 | 608 | 2 | C83322 excludinase ABC s  |
| 40 | 6 | 20.0 | 609 | 2 | G84832 ATP-dependent RNA  |
| 41 | 6 | 20.0 | 635 | 2 | E71733 threonine--trna 11 |
| 42 | 6 | 20.0 | 714 | 2 | A70983 probable fusa2 pro |
| 43 | 6 | 20.0 | 748 | 2 | S54505 hypothetical prote |
| 44 | 6 | 20.0 | 754 | 1 | BAB0H peptide-aspartate   |
| 45 | 6 | 20.0 | 757 | 2 | I38423 aspartyl beta-hydr |

#### ALIGNMENTS

RESULT 1  
I61596  
advanced glycosylation end-products receptor precursor - human  
N:Alternate names: advanced glycosylation end product-binding protein, 35K; glycoprot  
C:Species: Homo sapiens (man)  
C>Date: 24-May-1996 #sequence\_revision 07-Feb-1997 #text\_change 16-Jul-1999  
C:Accession: I61596; B42879; S27968  
R:Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko,  
Genomics 23, 408-419, 1994  
A>Title: Three genes in the human MHC class III region near the junction with the cla  
nterpart of mouse mammary tumor gene int-3.  
A:Reference number: A55562; M0ID:95137587  
A:Accession: I61596  
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
A:Molecule type: DNA  
A:Residues: 1-404 <RES>  
A:Cross-references: GB:D28769; NID:q561657; PIDN:BA005958.1; PID:q561659  
R:Nepper, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.;  
J. Biol. Chem. 267, 14998-15004, 1992  
A>Title: Cloning and expression of a cell surface receptor for advanced glycosylation  
A:Reference number: A42879; M0ID:92340547  
A:Accession: B42879  
A:Molecule type: mRNA  
A:Residues: 'G', '2-99', 'R', '101-404 <NE>  
A:Cross-references: EMBL:M91211; NID:q190845; PIDN:AAA03574.1; PID:q190846  
A:Experimental source: Lung  
A:Note: sequence extracted from NCBI backbone (NCBI:109438)  
C:Comment: Advanced glycosylation end products are heterogeneous nonenzymatically gly  
cellular function, thus contributing to tissue lesions in diabetes.  
C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide  
ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.  
C:Genetics:  
A:Gene: GDB:AGER  
A:Cross-references: GDB:306354; OMIM:600214  
A:Map position: 6p21.3-6p21.3  
A:Introns: 18/1; 53/3; 119/1; 140/3; 170/1; 231/1; 274/3; 322/1; 331/1; 373/2  
C:Function:  
A:Description: neuronal receptor for amphoterin, a DNA-binding protein involved in ne  
C:Superfamily: advanced glycosylation end products receptor; immunoglobulin homology  
C:Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-404/Product: advanced glycosylation end products receptor #status predicted <MAT  
F:23-344/Domain: extracellular #status predicted <EXT>  
F:31-101/Domain: immunoglobulin homology <IM1>  
F:137-210/Domain: immunoglobulin homology <IM2>  
F:252-303/Domain: immunoglobulin homology <IM3>  
F:345-362/Domain: transmembrane #status predicted <TMW>  
F:363-404/Domain: intracellular #status predicted <INT>  
F:25,81/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:38-99,144-208,259-301/Disulfide bonds: #status predicted

```

Query Match          100.0%; Score 30; DB 1; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.7e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AQNTARIGEPVLVKCKGAKRPPORLEWK 30
    |||||||
Db 23 AQNTARIGEPVLVKCKGAKRPPORLEWK 52

RESULT 2
T09062
probable advanced glycosylation end-products receptor precursor - mouse
N:Alternate names: RAGE
C:Species: Mus musculus (house mouse)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000
C:Accession: T09062
R:Rowen, L.; Mahairas, G.; Qln, S.; Ahern, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; So
submitted to the EMBL Data Library, October 1997
A:Description: Sequence of the mouse major histocompatibility locus class III region.
A:Reference number: Z16543
A:Accession: T09062
A:Status: preliminary; translated from GB/EMBL/DBDUT
A:Molecule type: DNA
A:Residues: 1-402 <ROW>
A:Cross-references: EMBL:AF030001; NID:q2564945; PID:q2564950
C:Genetics:
A:Gene: RAGE
A:Map position: 17
A:introns: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1; 272/3; 320/1; 329/1; 371/2
C:Superfamily: advanced glycosylation end products receptor; Immunoglobulin homology
C:Keywords: receptor; transmembrane protein
F:31-100/Domain: immunoglobulin homology <IMM>

Query Match          43.3%; Score 13; DB 2; Length 402;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 QNTARIGEPLVL 14
    |||||||
Db 24 QNTARIGEPLVL 36

RESULT 3
A42879
advanced glycosylation end-products receptor precursor - bovine
N:Alternate names: advanced glycosylation end product-binding protein, 35k; glycoprotein
C:Species: Bos primigenius taurus (cattle)
C>Date: 04-Mar-1993 #sequence_revision 07-Feb-1997 #text_change 16-Jul-1999
C:Accession: A42879; A42878; S27949
R:Neepert, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; St
J. Biol. Chem. 267, 14998-15004, 1992
A:Title: Cloning and expression of a cell surface receptor for advanced glycosylation en
A:Reference number: A42879; MUID:92340547
A:Accession: A42879
A:Molecule type: mRNA
A:Residues: 1-416 <NEE>
A:Cross-references: GB:M91212; NID:q163650; PIDN:AAA03575.1; PID:q163651
A:Experimental source: Lung
A:Note: sequence extracted from NCBI backbone (NCBIP:109436)
A:Note: parts of this sequence, including the amino end of the mature protein, were dete
R.Schmidt, A.M.; Vianna, M.; Gerlach, M.; Brett, J.; Ryan, J.; Kao, J.; Esposito, C.; He
J. Biol. Chem. 267, 14987-14997, 1992
A:Title: Isolation and characterization of two binding proteins for advanced glycosylati
A:Reference number: A42878; MUID:92340546
A:Accession: A42878
A:Molecule type: protein
A:Residues: 23-24, 'X', '26-37', 'X', '39-49', 'XX', '52-54' <SCH>
A:Experimental source: endothelial cells
A:Note: sequence extracted from NCBI backbone (NCBIP:109434)
C:Comment: Advanced glycosylation end products are heterogeneous nonenzymatically glycos
cellular function, thus contributing to tissue lesions in diabetes.
C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide on

```

```

ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.
C:Function:
A:Description: neuronal receptor for amphotericin, a DNA-binding protein involved in ne
C:Superfamily: advanced glycosylation end products receptor; immunoglobulin homology
C:Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-416/Product: advanced glycosylation end-products receptor RAGE #status predicted
F:23-354/Domain: extracellular #status predicted <EXT>
F:31-100/Domain: immunoglobulin homology <IM1>
F:136-209/Domain: immunoglobulin homology <IM2>
F:262-313/Domain: immunoglobulin homology <IM3>
F:355-372/Domain: transmembrane #status predicted <TM>
F:373-416/Domain: intracellular #status predicted <INT>
F:25,80/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:38-98,143-207,269-311/Disulfide bonds: #status predicted

Query Match          33.3%; Score 10; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 CKGAPKRPQ 25
    |||||||
Db 38 CKGAPKRPQ 47

RESULT 4
H64065
mutator mult - Haemophilus influenzae (strain Rd KW20)
N:Alternate names: DNA mismatch protein
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 26-Aug-1999
C:Accession: H64065
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kinkness, E.F.; Kerlavage
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glöck, A.; Kelley, J.M.; Weidman
, D.M.; Brandon, R.C.; Fine, L.D.; Fitchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.W.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630
A:Accession: H64065
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-223 <TIGR>
A:Cross-references: GB:U32723; GB:I42023; NID:g1573363; PIDN:AAC22062.1; PID:g1573374
C:Genetics:
A:Gene: mult
C:Superfamily: mutator mult

Query Match          23.3%; Score 7; DB 2; Length 223;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ITARIGE 10
    |||||||
Db 165 ITARIGE 171

RESULT 5
E81998
pseudouridylylate synthase (BC 4.2.1.70) C RNA-specific NMA0070 [imported] - Neisseria
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churche, C.; Klee, S.R.; Mo
; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491
A:Reference number: AB1775; MUID:20222556
A:Accession: E81998
A:Status: preliminary
A:Molecule type: DNA

```

A:Residues: 1-330 <PAR>  
A:Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CA833386.1; PID:g737884  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: rLUC; NMA0070  
C:Superfamily: conserved hypothetical protein H10176  
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 23.3%; Score 7; DB 2; Length 330;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GEPVLK 15  
|||||||  
DB 304 GEPVLK 310

RESULT 6  
H81225  
ribosomal large chain pseudouridine synthase C NMB0198 [imported] - Neisseria meningitidis  
C:Species: Neisseria meningitidis  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C:Accession: H81225  
R:Reteljin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
Li, H.; Qin, H.; Yamahayan, J.; Gill, J.; Scarlato, V.; Maignan, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A:Authors: Grandt, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A:Reference number: AB1000; MUID:20175755  
A:Accession: H81225  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-330 <TEM>  
A:Cross-references: GB:AE002377; GB:AE002098; NID:g7225416; PIDN:AAF40655.1; PID:g722541  
A:Experimental source: serogroup B, strain MC58  
C:Genetics:  
A:Gene: NMB0198  
C:Superfamily: conserved hypothetical protein H10176

Query Match 23.3%; Score 7; DB 2; Length 330;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GEPVLK 15  
|||||||  
DB 304 GEPVLK 310

RESULT 7  
J01619  
cell fusion glycoprotein precursor - pneumonia virus of mice  
N:Alternate names: F protein  
N:Contents: cell fusion glycoprotein F1; cell fusion glycoprotein F2  
C:Species: pneumonia virus of mice  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 25-Oct-1996  
C:Accession: J01619  
R:Chambers, P.; Pringle, C.R.; Easton, A.J.  
J. Gen. Virol. 73, 1717-1724, 1992  
A:Title: Sequence analysis of the gene encoding the fusion glycoprotein of pneumonia vir  
A:Reference number: J01619; MUID:92333256  
A:Accession: J01619  
A:Molecule type: mRNA  
A:Residues: 1-537 <CHA>  
A:Cross-references: GB:S40186  
C:Genetics:  
A:Gene: F  
C:Superfamily: cell fusion glycoprotein  
C:Keywords: glycoprotein; membrane fusion; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-101/Product: cell fusion glycoprotein F2 #status predicted <PG2>

F:102-537/Product: cell fusion glycoprotein F1 #status predicted <FG1>  
F:491-514/Domain: transmembrane #status predicted <TM>  
F:463,468/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 23.3%; Score 7; DB 1; Length 537;  
Best Local Similarity 100.0%; Pred. No. 9.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GEPVLK 15  
|||||||  
DB 434 GEPVLK 440

RESULT 8  
B86212  
protein F24B9.20 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: B86212  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon  
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Malt, R.; Marzia  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: AB6141; MUID:21016719  
A:Accession: B86212  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-595 <STO>  
A:Cross-references: GB:AE005172; NID:g8439898; PIDN:AAF75084.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: F24B9.20  
A:Map position: 1

Query Match 23.3%; Score 7; DB 2; Length 595;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 RIGEPV 13  
|||||||  
DB 550 RIGEPV 556

RESULT 9  
T07822  
cystein proteinase inhibitor - cucumber  
C:Species: Cucumis sativus (cucumber)  
C:Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 20-Jun-2000  
C:Accession: T07822  
R:Yamakawa, S.  
submitted to the EMBL Data Library, May 1998  
A:Description: Cystein proteinase inhibitor.  
A:Reference number: T07822  
A:Accession: T07822  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-96 <YAM>  
A:Cross-references: EMBL:AB014760; PIDN:BAA28867.1  
A:Note: root-specific  
C:Superfamily: cystatin; cystatin homology  
C:Keywords: cysteine proteinase inhibitor

Query Match 20.0%; Score 6; DB 2; Length 96;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LVLKCK 17  
|||||  
Db 59 LVLKCK 64

## RESULT 10

S64538  
hypothetical protein YGR215W - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein G7821

C:Species: Saccharomyces cerevisiae

C:Date: 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 20-Jun-2000

C:Accession: S64538

R:Rieger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.  
submitted to the Protein Sequence Database, May 1996

A:Reference number: S64071

A:Accession: S64538

A:Molecule type: DNA

A:Residues: 1-110 <R1E>

A:Cross-references: EMBL:Z73000; NID:q1323386; PID:q1323387; GSPDB:GN00007; MIPS:YGR215W

A:Experimental source: strain S288C

C:Genetics:

A:Gene: MIPS:YGR215W

A:Map position: 7R

C:Superfamily: Saccharomyces cerevisiae hypothetical protein YGR215W

Query Match 20.0%; Score 6; DB 2; Length 110;

Best Local Similarity 100.0%; Pred. No. 29;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 KGAPKK 22  
|||||

Db 88 KGAPKK 93

## RESULT 11

T46154

hypothetical protein T4D2.10 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 04-Feb-2000

C:Accession: T46154

R:Myakura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;  
submitted to the Protein Sequence Database, December 1999

A:Reference number: Z23025

A:Accession: T46154

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-155 <NYA>

A:Cross-references: EMBL:AL132958

A:Experimental source: cultivar Columbia; BAC clone T4D2

C:Genetics:

A:Map position: 3

A:Introns: 118/3

A:Note: T4D2.10

Query Match 20.0%; Score 6; DB 2; Length 155;

Best Local Similarity 100.0%; Pred. No. 39;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 KCKGAP 20  
|||||

Db 139 KCKGAP 144

## RESULT 12

E70536

hypothetical protein RV0804 - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999

C:Accession: E70536

R:Colet, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squires, S.  
Nature 393, 537-544, 1998

A:Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.

A:Title: Deciphering the Biology of Mycobacterium tuberculosis from the complete geno

A:Reference number: A70500; M0ID:98295987

A:Accession: E70536

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-209 <COL>

A:Cross-references: GB:Z95618; GB:AL123456; NID:93261788; PIDN:CAB09107.1; PID:e31727

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: RV0804

Query Match 20.0%; Score 6; DB 2; Length 209;

Best Local Similarity 100.0%; Pred. No. 49;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GEPLVL 14  
|||||

Db 151 GEPLVL 156

## RESULT 13

A75260

hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000

C:Accession: A75260

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.

; M.; Shen, M.; Yamathayan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zaleski, C.;

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; M0ID:20036896

A:Accession: A75260

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-230 <WHI>

A:Cross-references: GB:AE002084; GB:AE000513; NID:96460372; PIDN:AAF12096.1; PID:9646

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR2550

A:Map position: 1

Query Match 20.0%; Score 6; DB 2; Length 230;

Best Local Similarity 100.0%; Pred. No. 53;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ARIGEP 11  
|||||

Db 121 ARIGEP 126

## RESULT 14

Q08543

membrane antigen gp85 - human herpesvirus 4 (strain B95-8)

C:Species: human herpesvirus 4, Epstein-Barr virus

C:Date: 25-Feb-1985 #sequence\_revision 25-Feb-1985 #text\_change 16-Jul-1999

C:Accession: F43044; A03787; S33040

R:Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrall, B.G.

Mol. Biol. Med. 1, 21-45, 1983

A:Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr v1

A:Reference number: A93065; M0ID:85035713

A:Accession: F43044

A:Molecule type: DNA

A:Residues: 1-234 <BAN>

A:Cross-references: EMBL:V01555; NID:959074; PIDN:CAA24835.1; PID:91334899

R:Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.  
Nature 310, 207-211, 1984



A:Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.  
A:Reference number: A03794; MUID:8427067  
A:Contents: annotation: protein coding region  
C:Superfamily: Epstein-Barr virus membrane antigen gp85

Query Match 20.0%; Score 6; DB 1; Length 234;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITA 6  
|||||  
Db 108 AONITA 113

## RESULT 15

H64181  
ABC-type transport system probable membrane spanning protein - Haemophilus influenzae (S  
C:Species: Haemophilus influenzae  
C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 21-Aug-1998  
C:Accession: H64181  
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.  
; Goearney, J.D.; Scott, J.; Shiley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.  
Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,  
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630  
A:Accession: H64181  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-238 <TIGR>  
A:Cross-references: GB:IA2023; TIGR:HI1079  
C:Superfamily: histidine permease protein M

Query Match 20.0%; Score 6; DB 2; Length 238;  
Best Local Similarity 100.0%; Pred. No. 55;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITA 6  
|||||  
Db 195 AONITA 200

Search completed: April 24, 2002, 09:23:17  
Job time: 246 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:17:36 ; Search time 66.28 Seconds  
(Without alignments)  
33.527 Million cell updates/sec

Title: US-09-689-469-5  
Perfect score: 162  
Sequence: 1 AONITRICEPLVLCKGAPKPPQRLMK 30

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: A.Geneseq\_1101.\*  
2: /SID8/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
3: /SID8/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
4: /SID8/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
5: /SID8/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
6: /SID8/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
7: /SID8/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
8: /SID8/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
9: /SID8/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
10: /SID8/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
11: /SID8/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
12: /SID8/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
13: /SID8/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
14: /SID8/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
15: /SID8/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
16: /SID8/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
17: /SID8/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
18: /SID8/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
19: /SID8/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
20: /SID8/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
21: /SID8/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
22: /SID8/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
23: /SID8/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description          |
|------------|-------|-------------|--------|----------|----------------------|
| 1          | 162   | 100.0       | 30     | AA09349  | Human RAGE V-domain  |
| 2          | 162   | 100.0       | 30     | AA52134  | Human Receptor to    |
| 3          | 162   | 100.0       | 318    | AA44200  | Human mature recep   |
| 4          | 162   | 100.0       | 318    | AAW33754 | Human RAGE polypep   |
| 5          | 162   | 100.0       | 332    | AA52130  | Human Receptor to    |
| 6          | 162   | 100.0       | 340    | AAW4199  | Human soluble rece   |
| 7          | 162   | 100.0       | 340    | AAW33753 | Human RAGE polypep   |
| 8          | 162   | 100.0       | 404    | AAW81925 | Extracellular cir    |
| 9          | 149   | 92.0        | 30     | AA09350  | Mouse RAGE V-domain  |
| 10         | 149   | 89.5        | 30     | AA09352  | Bovine RAGE V-domain |
| 11         | 133   | 82.1        | 30     | AA09351  | Rat RAGE V-domain    |

|    |      |      |      |          |                    |
|----|------|------|------|----------|--------------------|
| 12 | 127  | 78.4 | 30   | AAW23337 | N-terminal sequenc |
| 13 | 81   | 50.0 | 16   | AAW44214 | Human soluble RAGE |
| 14 | 81   | 50.0 | 16   | AAW33768 | Human RAGE polypep |
| 15 | 72   | 44.4 | 15   | AAW44208 | Human soluble RAGE |
| 16 | 72   | 44.4 | 15   | AAW33762 | Human RAGE polypep |
| 17 | 60   | 37.0 | 10   | AAW44209 | Human soluble RAGE |
| 18 | 60   | 37.0 | 10   | AAW44201 | Human soluble RAGE |
| 19 | 60   | 37.0 | 10   | AAW33763 | Human RAGE polypep |
| 20 | 60   | 37.0 | 10   | AAW33755 | Human RAGE polypep |
| 21 | 55.5 | 34.3 | 1496 | AAW81030 | Human RAGE polypep |
| 22 | 55.5 | 34.3 | 1496 | AAW70469 | Human RAGE polypep |
| 23 | 55   | 34.0 | 312  | AAW50904 | Human p53 target m |
| 24 | 54   | 33.3 | 602  | AAW51705 | Human PRO245 prote |
| 25 | 54   | 33.3 | 602  | AAW32900 | Neurotrophic facto |
| 26 | 53.5 | 33.0 | 767  | AAW25696 | Chicken neurotroph |
| 27 | 53.5 | 33.0 | 1101 | AAW08008 | Human protein sequ |
| 28 | 53   | 32.7 | 298  | AAW75220 | Human H16-1 prote  |
| 29 | 53   | 32.7 | 298  | AAW53220 | Human secreted pro |
| 30 | 53   | 32.7 | 753  | AAW83927 | Human T85 protein. |
| 31 | 53   | 32.7 | 1649 | AAW08404 | Human ROBO1 protei |
| 32 | 52.5 | 32.4 | 1651 | AAW13566 | Human Robo 1 polyp |
| 33 | 52   | 32.1 | 4412 | AAW53666 | Sequence g1/101742 |
| 34 | 52   | 32.1 | 298  | AAW85457 | Secreted protein e |
| 35 | 52   | 32.1 | 298  | AAW27273 | Human confuency r  |
| 36 | 52   | 32.1 | 298  | AAW27275 | Murine confuency   |
| 37 | 52   | 32.1 | 303  | AAW00512 | Human junctional a |
| 38 | 52   | 32.1 | 303  | AAW23693 | Human EST encoded  |
| 39 | 52   | 32.1 | 312  | AAW08060 | Human PRO245 prote |
| 40 | 52   | 32.1 | 312  | AAW13354 | A33 related anti   |
| 41 | 52   | 32.1 | 312  | AAW13354 | Amino acid sequenc |
| 42 | 52   | 32.1 | 312  | AAW34421 | Human PRO245 prote |
| 43 | 52   | 32.1 | 312  | AAW24401 | Human PRO245 prote |
| 44 | 52   | 32.1 | 312  | AAW70668 | Human PRO245 prote |
| 45 | 52   | 32.1 | 312  | AAW00821 | Human immune respo |

## ALIGNMENTS

|          |  |
|----------|--|
| RESULT 1 |  |
| AA09349  | AA09349 standard; peptide; 30 AA.  |
| XX       | XX   |
| XX       | XX   |
| AC       | AA09349;   |
| XX       | XX   |
| DT       | 09-JUL-1999 (first entry)  |
| XX       | XX   |
| XX       | XX   |
| DE       | Human RAGE V-domain peptide SEQ ID NO:1.                                 |
| XX       | XX   |
| KW       | RAGE: V-domain; receptor for advanced glycation endproduct;              |
| KW       | ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome; |
| KW       | senility; renal failure; hyperlipidemic atherosclerosis; dementia;       |
| KW       | neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;       |
| KW       | multiple sclerosis; amyloidosis; autoimmune disease; inflammation;       |
| KW       | tumour; cancer; male impotence; wound healing; periodontal disease;      |
| KW       | neuropathy; retinopathy; nephropathy; neuronal degeneration.             |
| XX       | XX   |
| OS       | homo sapiens.  |
| XX       | XX   |
| PN       | WO918987-A1.   |
| XX       | XX   |
| PD       | 22-APR-1999.   |
| XX       | XX   |
| PF       | 09-OCT-1998; 98WO-US21346.   |
| XX       | XX   |
| PR       | 09-OCT-1997; 97US-0948131.   |
| XX       | XX   |
| PA       | (UYCO ) UNIV COLUMBIA NEW YORK.  |
| XX       | XX   |
| PI       | Lamster I, Schmidt AM, Stern D, Yan SD;                                  |
| XX       | XX   |
| DR       | WPI; 1999-277439/23.   |
| XX       | XX   |

PT New peptides based on an advanced glycation end product receptor are  
 PT useful for treating Alzheimer's disease and Down's syndrome  
 XX  
 PS Claim 2; Page 78; 101pp; English.

CC The present invention describes novel isolated peptides (1) having an  
 CC amino acid sequence corresponding to an amino acid sequence of a  
 CC V-domain of a receptor for an advanced glycation end product (RAGE).  
 CC Also described are methods for: (1) inhibiting an amyloid-beta peptide  
 CC (Aβ) interaction with a receptor for RAGE when the receptor is on the  
 CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)  
 CC inhibiting formation of an Aβ fibril on a cell; (4) inhibiting  
 CC extracellular assembly of an Aβ into a fibril; (5) inhibiting  
 CC aggregation of Aβ on the surface of a cell; (6) inhibiting infiltration  
 CC of a microglial cell into senile plaques; (7) inhibiting activation of a  
 CC microglial cell by an Aβ; (8) treating a subject with a condition  
 CC associated with an interaction of an Aβ with a receptor for RAGE on a  
 CC cell; (9) evaluating the ability of an agent to inhibit binding of an  
 CC Aβ with a V-domain of a receptor for RAGE on the surface of a cell; (10)  
 CC inhibiting activation of a NF-κappaB gene in a cell; (11) inhibiting  
 CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction  
 CC with a receptor for RAGE when the receptor is on the surface of a cell;  
 CC and (13) treating a subject with a condition associated with an  
 CC interaction of an RAGE with a receptor for RAGE on a cell. The methods  
 CC can be used for treating conditions associated with an interaction of an  
 CC Aβ or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's  
 CC disease, senility, renal failure, hyperlipidemic atherosclerosis,  
 CC neuronal cytotoxicity, Down's syndrome, dementia associated with head  
 CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,  
 CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,  
 CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy  
 CC or neuronal degeneration.  
 CC  
 SQ Sequence 30 AA;

Query Match 100.0%; Score 162; DB 20; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-15;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTTARIGEPVLKCKGAPKPPQRLWK 30  
 DB 1 agntartigepvlkckgapkppqrlew 30

RESULT 2

AA52134  
 ID AAY52134 standard; protein; 30 AA.

AC AAY52134;

DT 28-JAN-2000 (first entry)

DE Human Receptor to AGE (RAGE) amino acid sequence fragment #3.

KW Soluble receptor for advanced glycation endproducts; RAGE; tumour;  
 KM invasion; metastasis; amphoterin; neuron; inhibit; therapy.

OS Homo sapiens.

PN WO954485-A1.

PD 28-OCT-1999.

PF 16-APR-1999; 99WO-US08427.

PR 17-APR-1998; 98US-0062365.

PA (UYCO ) UNIV COLUMBIA NEW YORK.

PT Schmidt AM, Stern D;

DR WPI; 2000-013260/01.

XX  
 PT Inhibiting tumour invasion or spreading by administration of soluble  
 PT receptor for advanced glycation endproducts -  
 XX  
 PS Claim 29; Page 62; 88pp; English.

CC This is the amino acid sequence of a fragment of the human soluble  
 CC Receptor for Advanced Glycation Endproducts (RAGE). RAGE interacts with  
 CC a range of physiologically and pathophysiologically relevant ligands  
 CC when considering tumour invasion. In normal developing neurons RAGE  
 CC colocalizes with amphoterin which is a matrix associated polypeptide.  
 CC The expression of both RAGE and amphoterin decreases after birth, but  
 CC AAY52132-Y52135 are used in the invention in a method for inhibiting  
 CC tumour invasion and metastasis. The method involves inhibiting tumour  
 CC invasion and metastasis via administration of a therapeutically effective  
 CC amount of the pharmaceutical composition containing a RAGE polypeptide.  
 CC The invention also relates to a method for evaluating the ability of an  
 CC agent to inhibit tumour invasion in a local cellular environment. RAGE  
 CC can be administered to a patient in a pharmaceutically acceptable  
 CC carrier.

SQ Sequence 30 AA;

Query Match 100.0%; Score 162; DB 21; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-15;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTTARIGEPVLKCKGAPKPPQRLWK 30  
 DB 1 agntartigepvlkckgapkppqrlew 30

RESULT 3

AAW44200  
 ID AAW44200 standard; Protein; 318 AA.

AC AAW44200;

DT 14-MAY-1998 (first entry)

DE Human mature receptor to an advanced glycosylation end product.

KW Human: soluble receptor; advanced glycosylation end product; RAGE;  
 KM AGE; antibody; vascular permeability; diabetes mellitus.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Misc-difference 66 /note="encoded by CCR"

PN WO9739125-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01834.

PR 16-APR-1996; 96US-0633148.

PA (SCHD ) SCHERING PATENTE AG.

PI Hollander DA, Morser MJ, Nagashima M;

DR WPI; 1997-558580/51.

DR N-PDB; AAY12395.

PT Anti-advanced glycosylation end product polypeptide antibody -  
 PT prevents receptor binding and therefore reduces vascular  
 PT permeability, useful to treat diabetes mellitus

XX Claim 2; Page 42-43; 90pp; English.

XX The present sequence represents a mature human receptor to an advanced  
CC glycosylation end product (RAGE) polypeptide. The present invention  
CC describes an isolated antibody (Ab), specifically immunoreactive with  
CC RAGE. Advanced glycosylation end products (AGE) of proteins are  
CC non-enzymatically glycosylated proteins, which accumulate in vascular  
CC tissue in ageing, and at an accelerated rate in individuals with  
CC diabetes. The Ab, which prevents the interaction between an AGE and its  
CC receptor (RAGE), reduces vascular permeability. The Ab can be used to  
CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive  
CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis  
CC associated amyloidosis or atherosclerosis. The Ab can also be used for  
CC the isolation and purification of human RAGE polypeptide.  
XX

SQ Sequence 318 AA:

Query Match 100.0%; Score 162; DB 18; Length 318;

Best Local Similarity 100.0%; Pred. No. 2.7e-14;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGEPVLKCKGAPKKPPQRLWK 30  
1 aqnlrtarigepvlkckgapkkppqrlewk 30

Db 1 aqnlrtarigepvlkckgapkkppqrlewk 30

RESULT 4

AAW33754

ID AAW33754 standard; Protein; 318 AA.

AC AAW33754;

DT 08-MAY-1998 (first entry)

DE Human RAGE polypeptide (318 amino acid residues).

XX Advanced glycosylation end-product receptor; RAGE; screening; AGE;

KW vascular permeability; diabetes mellitus; treatment; atherosclerosis;

KM Alzheimer's disease.

XX Homo sapiens.

XX WO9739121-A1.

XX 23-OCT-1997.

PD 11-APR-1997; 97WO-EP01832.

XX 16-APR-1996; 96US-0633147.

PR (SCHD ) SCHERING AG.

XX Morser MJ, Nagashima M;

PI WPI; 1997-526458/48.

DR N-PSDB; AAV06518.

XX New soluble advanced glycosylation end-product receptor polypeptide

PT -used for reducing vascular permeability, complications of diabetes

PT etc., also for purification and to screen for modulators

PS Claim 3; Fig 1B; 91pp; English.

XX This is a human advanced glycosylation end-product receptor (RAGE)

CC polypeptide (318 amino acid residues). The RAGE polypeptides and its

CC active fragments or their mimetics, inhibit interaction between advanced

CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They

CC are used to treat diseases associated with AGE/RAGE interaction, such as

CC increased vascular permeability, diabetes mellitus (particularly

CC complications such as micro- or macro- vasculopathy or occlusive vascular

CC disorders such as neuropathy, nephropathy, retinopathy or

CC atherosclerosis) or haemodialysis-associated amyloidosis, also activation

CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or

CC age-related disorders such as oxidative stress. These RAGE polypeptides  
CC are also used, when immobilised, to purify AGE from a protein mixture and  
CC to screen for compounds that are agonists and antagonists of AGE/RAGE  
CC interaction. They can also be used diagnostically to detect abnormal  
CC levels of AGE. Antibodies against RAGE polypeptides are useful as  
CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of  
CC interaction between AGE and RAGE or other receptors and for purification  
CC and quantification of RAGE polypeptides. The encoding nucleic acids are  
CC used to express recombinant RAGE and as probes for isolating related  
CC genes.  
XX

SQ Sequence 318 AA:

Query Match 100.0%; Score 162; DB 18; Length 318;

Best Local Similarity 100.0%; Pred. No. 2.7e-14;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGEPVLKCKGAPKKPPQRLWK 30  
1 aqnlrtarigepvlkckgapkkppqrlewk 30

Db 1 aqnlrtarigepvlkckgapkkppqrlewk 30

RESULT 5

AA52130

ID AA52130 standard; protein; 332 AA.

AC AA52130;

DT 28-JAN-2000 (first entry)

DE Human Receptor to AGE (RAGE) amino acid sequence.

XX Soluble receptor for advanced glycation endproducts; RAGE; tumour;

KW invasion; metastasis; amphoterin; neuron; inhibit; therapy.

XX Homo sapiens.

XX WO954485-A1.

XX 28-OCT-1999.

PD 16-APR-1999; 99WO-US08427.

XX 17-APR-1998; 98US-0062365.

PR (UYCO ) UNIV COLUMBIA NEW YORK.

PA Schmidt AM, Stern D;

PI WPI; 2000-013260/01.

XX Inhibiting tumour invasion or spreading by administration of soluble

PT receptor for advanced glycation endproducts -

PS Disclosure: Page 10-11; 88pp; English.

XX This is the amino acid sequence of the human soluble Receptor for

CC Advanced Glycation Endproducts (RAGE). RAGE interacts with a range of

CC physiologically and pathophysiologically relevant ligands when

CC considering tumour invasion. In normal developing neurons RAGE

CC colocalizes with amphoterin which is a matrix associated polypeptide.

CC The expression of both RAGE and amphoterin decreases after birth, but

CC both have increased expression in tumours. RAGE polypeptides

CC AA52132-Y52133 are used in the invention in a method for inhibiting

CC tumour invasion and metastasis. The method involves inhibiting tumour

CC invasion and metastasis via administration of a therapeutically effective

CC amount of the pharmaceutical composition containing a RAGE polypeptide.

CC The invention also relates to a method for evaluating the ability of an

CC agent to inhibit tumour invasion in a local cellular environment. RAGE

CC can be administered to a patient in a pharmaceutically acceptable

CC carrier.

SQ Sequence 332 AA;

Query Match 100.0%; Score 162; DB 21; Length 332;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-14;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGEPVLKCKGAPKPPORLEWK 30  
 ||||||||||||||||||||||||||||  
 Db 1 agnitarigepvlkckgapkppqrllewk 30

RESULT 6

AAW44199  
 ID AAW44199 standard; Protein; 340 AA.

AC AAW44199;

DT 14-MAY-1998 (first entry)

DE Human soluble receptor to an advanced glycosylation end product.

KW Human; soluble receptor; advanced glycosylation end product; RAGE;

XX AGE; antibody; vascular permeability; diabetes mellitus.

OS Homo sapiens.

XX MO9739125-A1.

XX 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01834.

PR 16-APR-1996; 96US-0633148.

XX (SCHD ) SCHERING PATENTE AG.

PA Hollander DA, Morser MJ, Nagashima M;

PI WPI; 1997-558580/51.

DR N-PSDB; AAV12394.

XX Anti-advanced glycosylation end product polypeptide antibody

PT prevents receptor binding and therefore reduces vascular

PT permeability, useful to treat diabetes mellitus

PS Claim 2; Page 40-41; 90pp; English.

XX The present sequence represents a soluble human receptor to an advanced

CC glycosylation end product (RAGE) polypeptide. The present invention

CC describes an isolated antibody (Ab), specifically immunoreactive with

CC RAGE. Advanced glycosylation end products (AGE) of proteins are

CC non-enzymatically glycosylated proteins, which accumulate in vascular

CC tissue in ageing, and at an accelerated rate in individuals with

CC diabetes. The Ab, which prevents the interaction between an AGE and it's

CC receptor (RAGE), reduces vascular permeability. The Ab can be used to

CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive

CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis

CC associated amyloidosis or atherosclerosis. The Ab can also be used for

CC the isolation and purification of human RAGE polypeptide.

SQ Sequence 340 AA;

Query Match 100.0%; Score 162; DB 18; Length 340;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-14;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGEPVLKCKGAPKPPORLEWK 30  
 ||||||||||||||||||||||||||||  
 Db 23 agnitarigepvlkckgapkppqrllewk 52

RESULT 7

AAW33753  
 ID AAW33753 standard; Protein; 340 AA.

AC AAW33753;

DT 08-MAY-1998 (first entry)

DE Human RAGE polypeptide (340 amino acid residues).

KW Advanced glycosylation end-product receptor; RAGE; screening; AGE;

XX vascular permeability; diabetes mellitus; treatment; atherosclerosis;

XX Alzheimer's disease.

OS Homo sapiens.

XX MO9739121-A1.

XX 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01832.

PR 16-APR-1996; 96US-0633147.

XX (SCHD ) SCHERING AG.

PA Morser MJ, Nagashima M;

PI WPI; 1997-526458/48.

DR N-PSDB; AAV06517.

XX New soluble advanced glycosylation end-product receptor polypeptide

PT - used for reducing vascular permeability; complications of diabetes

PT etc., also for purification and to screen for modulators

XX Claim 3; Fig 1A; 91pp; English.

PS This is a human advanced glycosylation end-product receptor (RAGE)

CC polypeptide (340 amino acid residues). The RAGE polypeptides and its

CC active fragments or their mimetics, inhibit interaction between advanced

CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They

CC are used to treat diseases associated with AGE/RAGE interaction, such as

CC increased vascular permeability, diabetes mellitus (particularly

CC complications such as micro- or macro- vasculopathy or occlusive vascular

CC disorders such as neuropathy, nephropathy, retinopathy or

CC atherosclerosis) or haemodialysis-associated amyloidosis, also activation

CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or

CC age-related disorders such as oxidative stress. These RAGE polypeptides

CC are also used, when immobilised, to purify AGE from a protein mixture and

CC to screen for compounds that are agonists and antagonists of AGE/RAGE

CC interaction. They can also be used diagnostically to detect abnormal

CC levels of AGE. Antibodies against RAGE polypeptides are useful as

CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of

CC interaction between AGE and RAGE or other receptors and for purification

CC and quantification of RAGE polypeptides. The encoding nucleic acids are

CC used to express recombinant RAGE and as probes for isolating related

SQ Sequence 340 AA;

Query Match 100.0%; Score 162; DB 18; Length 340;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-14;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGEPVLKCKGAPKPPORLEWK 30  
 ||||||||||||||||||||||||||||  
 Db 23 agnitarigepvlkckgapkppqrllewk 52

RESULT 8

AAW81925  
 ID AAW81925 standard; Protein; 404 AA.

```

XX AC AAB81925;
XX XX
XX 15-JUN-2001 (first entry)
XX DT
XX DE Extracorporeal circulation material receptor protein.
XX DE Extracorporeal circulation; carbonyl stress product; receptor;
XX DE diabetes; vascular lesion; excretory dysfunction.
XX DE
XX OS Unidentified.
XX XX
XX PN WO200118060-A1.
XX XX
XX PD 15-MAR-2001.
XX XX
XX PF 08-SEP-2000; 2000MO-JP06172.
XX XX
XX PR 08-SEP-1999; 99JP-0254463.
XX XX
XX PA (TORA ) TORAY IND INC.
XX XX
XX PI Shimizu S, Kubota M, Akiyama H, Usui M;
XX DR WPI; 2001-290314/30.
XX XX
XX PT Material for extracorporeal circulation, applicable in selective
XX PT elimination of diabetic complication factors such as carbonyl stress
XX PT products caused by abnormally promoted carbonyl stress from excretory
XX PT dysfunction in vascular lesions
XX PS
XX PS Claim 1; Page 31-32; 36pp; Japanese.
XX XX
XX CC The present invention describes a material for extracorporeal circulation
XX CC which is made from a water-insoluble carrier immobilized with a protein
XX CC having the sequence shown here. The materials of the invention, including
XX CC adsorbents, are for extracorporeal circulation, which are applicable in
XX CC the selective elimination of diabetic complication factors from a body
XX CC fluid, and are therefore useful in treating vascular lesions like
XX CC arteriosclerosis due to carbonyl stress products caused by abnormally
XX CC promoted carbonyl stress from excretory dysfunction.
XX CC
XX SQ Sequence 404 AA;

Query Match 100.0%; Score 162; DB 22; Length 404;
Best Local Similarity 100.0%; Pred. No. 3.4e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGEPLVLCCKGAPKKPPORLEWK 30
   ||||||||||||||||||||||||||||
Db 23 agnitarigeplvlckgappkppqrlwkw 52

RESULT 9
AAV09350
ID AAV09350 standard; peptide: 30 AA.
XX
XX AAV09350;
XX
XX 09-JUL-1999 (first entry)
XX DT
XX DE Mouse RAGE V-domain peptide SEQ ID NO:2.
XX XX
XX RAGE: V-domain; receptor for advanced glycation endproduct;
XX ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;
XX senility; renal failure; hyperlipidaemic atherosclerosis; dementia;
XX neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;
XX multiple sclerosis; amyloidosis; autoimmune disease; inflammation;
XX tumour; cancer; male impotence; wound healing; periodontal disease;
XX neuropathy; retinopathy; nephropathy; neuronal degeneration.
XX OS Mus sp.

```

```

XX PN WO9918987-A1.
XX XX
XX PD 22-APR-1999.
XX XX
XX PF 09-OCT-1998; 98WO-US21346.
XX XX
XX PR 09-OCT-1997; 97US-0948131.
XX XX
XX PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX XX
XX PI Lamster I, Schmidt AM, Stern D, Yan SD;
XX DR WPI; 1999-277439/23.
XX XX
XX PT New peptides based on an advanced glycation end product receptor are
XX PT useful for treating Alzheimer's disease and Down's syndrome
XX PS
XX PS Claim 3; Page 78; 101pp; English.
XX XX
XX CC The present invention describes novel isolated peptides (1) having an
XX CC amino acid sequence corresponding to an amino acid sequence of a
XX CC V-domain of a receptor for an advanced glycation end product (RAGE).
XX CC Also described are methods for: (1) inhibiting an amyloid-beta peptide
XX CC (ABP) interaction with a receptor for RAGE when the receptor is on the
XX CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)
XX CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting
XX CC extracellular assembly of an ABP into a fibril; (5) inhibiting
XX CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration
XX CC of a microglial cell into senile plaques; (7) inhibiting activation of a
XX CC microglial cell by an ABP; (8) treating a subject with a condition
XX CC associated with an interaction of an ABP with a receptor for RAGE on a
XX CC cell; (9) evaluating the ability of an agent to inhibit binding of an
XX CC ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)
XX CC inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting
XX CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction
XX CC with a receptor for RAGE when the receptor is on the surface of a cell;
XX CC and (13) treating a subject with a condition associated with an
XX CC interaction of an RAGE with a receptor for RAGE on a cell. The methods
XX CC can be used for treating conditions associated with an interaction of an
XX CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's
XX CC disease, senility, renal failure, hyperlipidaemic atherosclerosis,
XX CC neuronal cytotoxicity, Down's syndrome, dementia associated with head
XX CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,
XX CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,
XX CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy
XX CC or neuronal degeneration.
XX CC
XX SQ Sequence 30 AA;

Query Match 92.0%; Score 149; DB 20; Length 30;
Best Local Similarity 93.1%; Pred. No. 1.5e-13;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 ONTARIGEPLVLCCKGAPKKPPORLEWK 30
   |||||||||||||:|||||
Db 2 qnitarigeplvlscxgappkppqglewk 30

RESULT 10
AAV09352
ID AAV09352 standard; peptide: 30 AA.
XX
XX AAV09352;
XX
XX 09-JUL-1999 (first entry)
XX DT
XX DE Bovine RAGE V-domain peptide SEQ ID NO:4.
XX XX
XX RAGE: V-domain; receptor for advanced glycation endproduct;
XX ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;
XX senility; renal failure; hyperlipidaemic atherosclerosis; dementia;

```

KM neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;  
 KM multiple sclerosis; amyloidosis; autoimmune disease; inflammation;  
 KM tumour; cancer; male impotence; wound healing; periodontal disease;  
 KM neuropathy; retinopathy; nephropathy; neuronal degeneration.  
 OS Bos sp.  
 PN W09918987-A1.  
 PD 22-APR-1999.  
 XX 09-OCT-1998; 98WO-US21346.  
 XX 09-OCT-1997; 97US-0948131.  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 PI Lamster I, Schmidt AM, Stern D, Yan SD;  
 DR WPI; 1999-277439/23.  
 XX New peptides based on an advanced glycation end product receptor are  
 PT useful for treating Alzheimer's disease and Down's syndrome  
 XX Claim 5; Page 78; 101pp; English.  
 PS The present invention describes novel isolated peptides (1) having an  
 CC amino acid sequence corresponding to an amino acid sequence of a  
 CC V-domain of a receptor for an advanced glycation end product (RAGE).  
 CC Also described are methods for: (1) inhibiting an amyloid-beta peptide  
 CC (ABP) interaction with a receptor for RAGE when the receptor is on the  
 CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)  
 CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting  
 CC extracellular assembly of an ABP into a fibril; (5) inhibiting  
 CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration  
 CC of a microglial cell into senile plaques; (7) inhibiting activation of a  
 CC microglial cell by an ABP; (8) treating a subject with a condition  
 CC associated with an interaction of an ABP with a receptor for RAGE on a  
 CC cell; (9) evaluating the ability of an agent to inhibit binding of an  
 CC ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)  
 CC inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting  
 CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction  
 CC with a receptor for RAGE when the receptor is on the surface of a cell;  
 CC and (13) treating a subject with a condition associated with an  
 CC interaction of an RAGE with a receptor for RAGE on a cell. The methods  
 CC can be used for treating conditions associated with an interaction of an  
 CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's  
 CC disease, senility, renal failure, hyperlipidemic atherosclerosis,  
 CC neuronal cytotoxicity, Down's syndrome, dementia associated with head  
 CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,  
 CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,  
 CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy  
 CC or neuronal degeneration.  
 XX Sequence 30 AA;  
 SO

Query Match 89.5%; Score 145; DB 20; Length 30;  
 Best Local Similarity 89.7%; Pred. No. 5.2e-13;  
 Matches 26; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 QNTTARIGEPVLKCKGAPKPPQRLKWK 30  
 DB 2 qnttarigepvlkckgapkppqrlkewk 30

RESULT 11  
 AAAY09351  
 ID AAAY09351 standard; peptide; 30 AA.  
 AC AAAY09351;  
 XX  
 DT 09-JUL-1999 (first entry)

XX Rat RAGE V-domain peptide SEQ ID NO:3.  
 DE  
 XX RAGE; V-domain; receptor for advanced glycation endproduct;  
 KM ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;  
 KM senility; renal failure; hyperlipidemic atherosclerosis; dementia;  
 KM neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;  
 KM multiple sclerosis; amyloidosis; autoimmune disease; inflammation;  
 KM tumour; cancer; male impotence; wound healing; periodontal disease;  
 KM neuropathy; retinopathy; nephropathy; neuronal degeneration.  
 XX Ratus sp.  
 OS W09918987-A1.  
 PN 22-APR-1999.  
 PD 09-OCT-1998; 98WO-US21346.  
 XX 09-OCT-1997; 97US-0948131.  
 XX (UYCO ) UNIV COLUMBIA NEW YORK.  
 PI Lamster I, Schmidt AM, Stern D, Yan SD;  
 DR WPI; 1999-277439/23.  
 XX New peptides based on an advanced glycation end product receptor are  
 PT useful for treating Alzheimer's disease and Down's syndrome  
 XX Claim 4; Page 78; 101pp; English.  
 PS The present invention describes novel isolated peptides (1) having an  
 CC amino acid sequence corresponding to an amino acid sequence of a  
 CC V-domain of a receptor for an advanced glycation end product (RAGE).  
 CC Also described are methods for: (1) inhibiting an amyloid-beta peptide  
 CC (ABP) interaction with a receptor for RAGE when the receptor is on the  
 CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)  
 CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting  
 CC extracellular assembly of an ABP into a fibril; (5) inhibiting  
 CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration  
 CC of a microglial cell into senile plaques; (7) inhibiting activation of a  
 CC microglial cell by an ABP; (8) treating a subject with a condition  
 CC associated with an interaction of an ABP with a receptor for RAGE on a  
 CC cell; (9) evaluating the ability of an agent to inhibit binding of an  
 CC ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)  
 CC inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting  
 CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction  
 CC with a receptor for RAGE when the receptor is on the surface of a cell;  
 CC and (13) treating a subject with a condition associated with an  
 CC interaction of an RAGE with a receptor for RAGE on a cell. The methods  
 CC can be used for treating conditions associated with an interaction of an  
 CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's  
 CC disease, senility, renal failure, hyperlipidemic atherosclerosis,  
 CC neuronal cytotoxicity, Down's syndrome, dementia associated with head  
 CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,  
 CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,  
 CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy  
 CC or neuronal degeneration.  
 XX Sequence 30 AA;  
 SO

Query Match 82.1%; Score 133; DB 20; Length 30;  
 Best Local Similarity 82.8%; Pred. No. 2.2e-11;  
 Matches 24; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 QNTTARIGEPVLKCKGAPKPPQRLKWK 30  
 DB 2 qnttarigepvlkckgapkppqrlkewk 30

RESULT 12



AAW23337  
ID AAW23337 standard; peptide; 30 AA.  
XX  
AC AAW23337;  
XX  
DT 12-MAR-1998 (first entry)  
XX  
DE N-terminal sequence of a protein which binds the amyloid beta peptide.  
XX  
KW Amyloid beta peptide; extracellular deposit; Alzheimer's disease;  
KW neurite outgrowth; microglial activation; neuronal cell degeneration;  
KW receptor for advanced glycosylation end product;  
KW Amyloid beta peptide fibril.  
XX  
OS Rattus sp.  
XX  
PN WO9726913-A1.  
XX  
PD 31-JUL-1997.  
XX  
PF 21-JAN-1997; 97WO-US00857.  
XX  
PR 26-JAN-1996; 96US-0592070.  
XX  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
PI Schmidt AM, Stern D, Yan SD;  
XX  
DR WPI: 1997-393374/36.  
XX  
PT Inhibiting damage to cells in e.g. Alzheimer's disease - using an  
PT agent which inhibits interaction of an amyloid-beta peptide with a  
PT receptor for advanced glycosylation end product  
XX  
PS Disclosure: Page 27; 91pp; English.  
XX  
CC The present sequence represents the amino acid sequence of the  
CC N-terminal of a 50 kDa cell-associated protein which binds the amyloid  
CC beta peptide. This peptide is the principal component of extracellular  
CC deposits in Alzheimer's disease. It has been shown to promote neurite  
CC outgrowth, generate reactive oxygen intermediates, induce cellular  
CC oxidant stress, lead to neuronal cytotoxicity, and promote microglial  
CC activation. The 50 kDa protein was purified from rat epithelial cells and  
CC is shown to be virtually identical to a bovine receptor for the advanced  
CC glycosylation end product. Peptides derived from the amyloid beta  
CC peptide are used in a pharmaceutical composition. This composition  
CC comprises an agent capable of inhibiting interaction of an amyloid-beta  
CC peptide with a receptor for advanced glycosylation end product and a  
CC carrier. A method for inhibiting interaction of amyloid beta peptide  
CC with a receptor for advanced glycosylation on the surface of a cell  
CC comprises contacting the cell with e.g. present peptide. Depending on  
CC the type of cell, inhibiting the interaction between the amyloid beta  
CC peptide and the receptor for advanced glycosylation can be used for  
CC inhibiting degeneration of a neuronal cell, inhibiting formation of an  
CC amyloid beta peptide fibril on a cell, inhibiting extracellular assembly  
CC of amyloid beta peptide into a fibril, inhibiting aggregation of amyloid  
CC beta peptide on the surface of a cell, inhibiting infiltration of a  
CC microglial cell into senile plaques, and inhibiting activation of a  
CC microglial cells by amyloid beta peptide. The methods can be used for  
CC treating e.g. diabetes, Alzheimer's Disease, senility, renal failure,  
CC hyperlipidemic atherosclerosis, neuronal cytotoxicity, Down's syndrome,  
CC dementia associated with head trauma, amyotrophic lateral sclerosis,  
CC multiple sclerosis or neuronal degeneration.  
XX  
SQ Sequence 30 AA:

Query Match 78.4%; Score 127; DB 18; Length 30;  
Best Local Similarity 82.8%; Pred. No. 1.5e-10;  
Matches 24; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 2 QNITARIGEPVLVKCGAPKPPQRLWK 30  
I |||||||:|||| ||||||||:||||

DB 2 qxlitarigkplylnxkgapkppqjlew 30  
RESULT 13  
ID AAW44214  
XX  
AC AAW44214 standard; peptide; 16 AA.  
XX  
DT 14-MAY-1998 (first entry)  
XX  
DE Human soluble RAGE immunologically active fragment SEQ ID NO:18.  
XX  
KW Human; soluble receptor; advanced glycosylation end product; RAGE;  
KW AGE; antibody; vascular permeability; immunologically active fragment;  
KW diabetes mellitus.  
XX  
OS Homo sapiens.  
XX  
PN WO9739125-A1.  
XX  
PD 23-OCT-1997.  
XX  
PF 11-APR-1997; 97WO-EP01834.  
XX  
PR 16-APR-1996; 96US-0633148.  
XX  
PA (SCHD ) SCHERING PATENTE AG.  
XX  
PI Hollander DA, Morser MJ, Nagashima M;  
XX  
DR WPI: 1997-558580/51.  
XX  
PT Anti-advanced glycosylation end product polypeptide antibody -  
PT prevents receptor binding and therefore reduces vascular  
PT permeability, useful to treat diabetes mellitus  
XX  
PS Claim 2: Page 49; 90pp; English.  
XX  
CC The present sequence represents an immunologically active fragment  
CC of a soluble human receptor to an advanced glycosylation end  
CC product (RAGE) polypeptide. The present invention describes  
CC an isolated antibody (Ab), specifically immunoreactive with  
CC RAGE. Advanced glycosylation end products (AGE) of proteins are  
CC non-enzymatically glycosylated proteins, which accumulate in vascular  
CC tissue in ageing, and at an accelerated rate in individuals with  
CC diabetes. The Ab, which prevents the interaction between an AGE and it's  
CC receptor (RAGE), reduces vascular permeability. The Ab can be used to  
CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive  
CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis  
CC associated amyloidosis or atherosclerosis. The Ab can also be used for  
CC the isolation and purification of human RAGE polypeptide.  
XX  
SQ Sequence 16 AA:

Query Match 50.0%; Score 81; DB 18; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00015;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AQNITARIGEPVLVKC 16  
|||||||:|||||  
DB 1 agnitarigepylvlkc 16

RESULT 14  
ID AAW33768  
XX  
AC AAW33768 standard; peptide; 16 AA.  
XX  
DT 08-MAY-1998 (first entry)  
XX  
XX

|  |   |                                     |
|--|---|-------------------------------------|
| DE   |   | Human RAGE polypeptide fragment 14. |
| XX   |   |                                     |
| KW   | Advanced glycosylation end-product receptor; RAGE; screening; AGE;        |                                     |
| KM   | vascular permeability; diabetes mellitus; treatment; atherosclerosis;     |                                     |
| XX   | Alzheimer's disease.  |                                     |
| OS   | Homo sapiens.   |                                     |
| XX   |   |                                     |
| PN   | MO9739121-A1.   |                                     |
| PD   | 23-OCT-1997.  |                                     |
| XX   |   |                                     |
| PF   | 11-APR-1997; 97WO-EP01832.  |                                     |
| XX   |   |                                     |
| PR   | 16-APR-1996; 96US-0633147.  |                                     |
| PA   | (SCHD ) SCHERING AG.  |                                     |
| XX   |   |                                     |
| PI   | Morser MJ, Nagashima M;   |                                     |
| XX   |   |                                     |
| DR   | WPI: 1997-526458/48.  |                                     |
| XX   |   |                                     |
| PT   | New soluble advanced glycosylation end-product receptor polypeptide       |                                     |
| PT   | - used for reducing vascular permeability, complications of diabetes      |                                     |
| PT   | etc., also for purification and to screen for modulators                  |                                     |
| PS   | Disclosure: Page 9; 91pp; English.  |                                     |
| XX   |   |                                     |
| CC   | This is a peptide fragment of a human advanced glycosylation end-product  |                                     |
| CC   | receptor (RAGE) polypeptide. The RAGE polypeptides and its active         |                                     |
| CC   | fragments or their mimetics can inhibit interaction between advanced      |                                     |
| CC   | glycosylation end-products (AGE) and a receptor (specifically RAGE). They |                                     |
| CC   | are used to treat diseases associated with AGE/RAGE interaction, such as  |                                     |
| CC   | increased vascular permeability, diabetes mellitus (particularly          |                                     |
| CC   | complications such as micro- or macro- vasculopathy or occlusive vascular |                                     |
| CC   | disorders such as neuropathy, nephropathy, atherosclerosis or             |                                     |
| CC   | retinopathy) or haemodialysis-associated amyloidosis, also activation     |                                     |
| CC   | of microglial cells by beta-amyloid peptides in Alzheimer's disease or    |                                     |
| CC   | age-related disorders such as oxidative stress. These RAGE polypeptides   |                                     |
| CC   | are also used, when immobilised, to purify AGE from a protein mixture and |                                     |
| CC   | to screen for compounds that are agonists and antagonists of AGE/RAGE     |                                     |
| CC   | interaction. They can also be used diagnostically to detect abnormal      |                                     |
| CC   | levels of AGE. Antibodies against RAGE polypeptides are useful as         |                                     |
| CC   | immunoassay reagents for measurement of RAGE levels, and as inhibitors of |                                     |
| CC   | interaction between AGE and RAGE or other receptors and for purification  |                                     |
| CC   | and quantification of RAGE polypeptides. The encoding nucleic acids are   |                                     |
| CC   | used to express recombinant RAGE and as probes for isolating related      |                                     |
| CC   | genes.  |                                     |
| XX   |   |                                     |
| SQ   | Sequence 16 AA:   |                                     |
| XX   |   |                                     |
| Query Match  | 50.0%; Score 81; DB 18; Length 16;  |                                     |
| Best Local Similarity                                      | 100.0%; Pred. No. 0.00015;  |                                     |
| Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0 |   |                                     |
| QY   | 1 AONTARIGEPLEVKC 16  |                                     |
| DB   |   |                                     |
|  | 1 agntarigepvlvkc 16  |                                     |
| RESULT 15  |   |                                     |
| AAM44208   |   |                                     |
| ID   | AAM44208 standard; peptide; 15 AA.  |                                     |
| XX   |   |                                     |
| AC   | AAM44208;   |                                     |
| XX   |   |                                     |
| DT   | 14-MAY-1998 (first entry)   |                                     |
| XX   |   |                                     |
| DE   | Human soluble RAGE immunologically active fragment SEQ ID NO:12.          |                                     |
| XX   |   |                                     |
| KW   | Human; soluble receptor; advanced glycosylation end product; RAGE;        |                                     |
| KM   | AGE; antibody; vascular permeability; immunologically active fragment;    |                                     |

|    |  |
|----|--|
| KM | diabetes mellitus.   |
| XX |  |
| OS | Homo sapiens.  |
| XX |  |
| PN | MO9739125-A1.  |
| XX |  |
| PD | 23-OCT-1997.   |
| XX |  |
| PF | 11-APR-1997; 97WO-EP01834.   |
| XX |  |
| PR | 16-APR-1996; 96US-0633148.   |
| XX |  |
| PA | (SCHD ) SCHERING PATENTE AG.   |
| XX |  |
| PI | Hollander DA, Morser MJ, Nagashima M;  |
| XX |  |
| DR | WPI; 1997-558580/51.   |
| XX |  |
| PT | Anti-advanced glycosylation end product polypeptide antibody -   |
| PT | prevents receptor binding and therefore reduces vascular   |
| PT | permeability, useful to treat diabetes mellitus  |
| XX |  |
| PS | Claim 2; Page 46; 90pp; English.   |
| XX |  |
| XX | The present sequence represents an immunologically active fragment   |
| CC | of a soluble human receptor to an advanced glycosylation end   |
| CC | product (RAGE) polypeptide. The present invention describes  |
| CC | an isolated antibody (Ab), specifically immunoreactive with  |
| CC | RAGE. Advanced glycosylation end products (AGE) of proteins are  |
| CC | non-enzymatically glycosylated proteins, which accumulate in vascular  |
| CC | tissue in ageing, and at an accelerated rate in individuals with   |
| CC | diabetes. The Ab, which prevents the interaction between an AGE and it's   |
| CC | receptor (RAGE), reduces vascular permeability. The Ab can be used to  |
| CC | treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive  |
| CC | vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis  |
| CC | associated amyloidosis or atherosclerosis. The Ab can also be used for   |
| CC | the isolation and purification of human RAGE polypeptide.  |
| XX |  |
| SQ | Sequence 15 AA:  |
| OY | Query Match 44.4%; Score 72; DB 18; Length 15;<br>Best Local Similarity 100.0%; Pred. No. 0.0023;<br>Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| db | 1 AONTARIGEPLYEK 15<br>     <br>1 agntarigeplyvk 15  |

Search completed: April 24, 2002, 09:17:37  
Job time: 141 sec



**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:24:54 ; Search time 21.46 Seconds  
(without alignments)  
51.256 Million cell updates/sec

Title: US-09-689-469-5  
Perfect score: 30  
Sequence: 1 AONTATIGEPLVLKCKGAPKKPPQRLKWK 30

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 100059 seqs, 36664827 residues  
Word size: 0

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 30    | 100.0       | 404    | 1  | Q15109 homo sapien |
| 2          | 13    | 43.3        | 403    | 1  | RAGE_MOUSE         |
| 3          | 11    | 36.7        | 402    | 1  | RAGE_RAT           |
| 4          | 10    | 33.3        | 416    | 1  | RAGE_BOVIN         |
| 5          | 7     | 23.3        | 223    | 1  | MUTH_HAEIN         |
| 6          | 7     | 23.3        | 537    | 1  | VGIF_PVM           |
| 7          | 6     | 20.0        | 110    | 1  | YG4L_YEAST         |
| 8          | 6     | 20.0        | 181    | 1  | YCF4_GUTTH         |
| 9          | 6     | 20.0        | 210    | 1  | YA79_HAEIN         |
| 10         | 6     | 20.0        | 234    | 1  | VGP8_EBV           |
| 11         | 6     | 20.0        | 259    | 1  | E434_ADECT         |
| 12         | 6     | 20.0        | 265    | 1  | E434_ADECT         |
| 13         | 6     | 20.0        | 265    | 1  | E434_ADECR         |
| 14         | 6     | 20.0        | 269    | 1  | MIND_GUTTH         |
| 15         | 6     | 20.0        | 278    | 1  | PROC_CHYAL         |
| 16         | 6     | 20.0        | 282    | 1  | MIND_CHLYU         |
| 17         | 6     | 20.0        | 401    | 1  | ENO_THEAC          |
| 18         | 6     | 20.0        | 429    | 1  | RM4_CABEL          |
| 19         | 6     | 20.0        | 468    | 1  | ARLY_METTH         |
| 20         | 6     | 20.0        | 481    | 1  | SH2B_HUMAN         |
| 21         | 6     | 20.0        | 504    | 1  | SH2B_MOUSE         |
| 22         | 6     | 20.0        | 513    | 1  | SPRL_HUMAN         |
| 23         | 6     | 20.0        | 607    | 1  | TVRC_PSEPL         |
| 24         | 6     | 20.0        | 635    | 1  | STY_RICPR          |
| 25         | 6     | 20.0        | 714    | 1  | EFEL_MCTU          |
| 26         | 6     | 20.0        | 754    | 1  | ASPH_BOVIN         |
| 27         | 6     | 20.0        | 757    | 1  | ASPH_HUMAN         |
| 28         | 6     | 20.0        | 788    | 1  | REC2_HAEIN         |
| 29         | 6     | 20.0        | 837    | 1  | HFC2_HAEIN         |
| 30         | 6     | 20.0        | 837    | 1  | HFC2_HAEIN         |
| 31         | 6     | 20.0        | 837    | 1  | HFC3_HAEIN         |
| 32         | 6     | 20.0        | 850    | 1  | DEXT_STRMU         |
| 33         | 6     | 20.0        | 879    | 1  | YN65_YEAST         |

## ALIGNMENTS

| RESULT | ID  | SEQUENCE | STANDARD | PRT    | AA  | DESCRIPTION         |
|--------|---|----------|----------|--------|-----|---------------------|
| 34     | RAGE_HUMAN  | Q15109   | Q913R3   | Q9H2X7 | 404 | 035787 ratu         |
| 35     | 01-NOV-1997 (Rel. 35, Created)  |          |          |        |     | 043896 homo sapien  |
| 36     | 01-NOV-1997 (Rel. 35, Last sequence update)                           |          |          |        |     | P3485 pseudorabie   |
| 37     | 20-AUG-2001 (Rel. 40, Last annotation update)                         |          |          |        |     | P48634 homo sapien  |
| 38     | ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR        |          |          |        |     | P20430 tacaribde v1 |
| 39     | (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS)                    |          |          |        |     | P09542 mus musculu  |
| 40     | AGER OR RAGE.   |          |          |        |     | P26548 human papil  |
| 41     | Homo sapiens (Human).   |          |          |        |     | 092712 chlamydia p  |
| 42     | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;               |          |          |        |     | Q06943 drosophila   |
| 43     | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.             |          |          |        |     | P05871 human immun  |
| 44     | NCBI_TaxID=9606;  |          |          |        |     | P28814 hordeum vul  |
| 45     | SEQUENCE FROM N.A. (ISOFORM 1).                                       |          |          |        |     | P39468 sulfolobus   |
| RP     | TISSUE=Lung;  |          |          |        |     |                     |
| RC     | MEDLINE=92340547; PubMed=1378843;                                     |          |          |        |     |                     |
| RA     | Nepper M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,       |          |          |        |     |                     |
| RA     | Elliston K., Stern D., Shaw A.;                                       |          |          |        |     |                     |
| RT     | "Cloning and expression of a cell surface receptor for advanced       |          |          |        |     |                     |
| RT     | glycosylation end products of proteins.";                             |          |          |        |     |                     |
| RL     | J. Biol. Chem. 267:14998-15004(1992).                                 |          |          |        |     |                     |
| RN     | [2]   |          |          |        |     |                     |
| RP     | SEQUENCE FROM N.A. (ISOFORM 1).                                       |          |          |        |     |                     |
| RA     | MEDLINE=95137587; PubMed=7835890;                                     |          |          |        |     |                     |
| RA     | Sugata K., Fukagawa T., Matsumoto K., Mita K., Takahashi E., Ando A., |          |          |        |     |                     |
| RT     | Inoko H., Ikemura T.;   |          |          |        |     |                     |
| RT     | "Three genes in the human MHC class III region near the junction with |          |          |        |     |                     |
| RT     | the class II: gene for receptor of advanced glycosylation end         |          |          |        |     |                     |
| RT     | products, PBX2 homeobox gene and a notch homolog, human counterpart   |          |          |        |     |                     |
| RT     | of mouse mammary tumor gene int-3.";                                  |          |          |        |     |                     |
| RL     | Genomics 23:408-419(1994).  |          |          |        |     |                     |
| RN     | [3]   |          |          |        |     |                     |
| RP     | SEQUENCE FROM N.A. (ISOFORM 1).                                       |          |          |        |     |                     |
| RA     | Rosen L., Dankers C., Baskin D., Faust J., Loretz C., Ahearn M.E.,    |          |          |        |     |                     |
| RA     | Banta A., Spies T., Hood L.;  |          |          |        |     |                     |
| RT     | Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.               |          |          |        |     |                     |
| RN     | [4]   |          |          |        |     |                     |
| RP     | SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-100.                  |          |          |        |     |                     |
| RA     | Abedin M.J., Yonekura H., Migita H., Karasawa J., Yamamoto Y.,        |          |          |        |     |                     |
| RA     | Yamamoto H.;  |          |          |        |     |                     |
| RT     | "Molecular heterogeneity of the receptor for advanced glycation       |          |          |        |     |                     |
| RT     | endproducts.";  |          |          |        |     |                     |
| RL     | Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.               |          |          |        |     |                     |
| RN     | [5]   |          |          |        |     |                     |
| RP     | SEQUENCE FROM N.A. (ISOFORM 2).                                       |          |          |        |     |                     |
| RA     | Malherbe P., Richards J., Galliard H., Thompson A., Diener C.,        |          |          |        |     |                     |
| RA     | Schuler A., Huber G.;   |          |          |        |     |                     |
| RT     | "CDNA cloning of a novel secreted isoform of the human Receptor for   |          |          |        |     |                     |
| RT     | advanced Glycation End products (RAGE) and characterization of cells  |          |          |        |     |                     |
| RT     | co-expressing cell-surface scavenger receptors and Swedish mutant     |          |          |        |     |                     |
| RL     | amyloid precursor protein.";  |          |          |        |     |                     |
| RL     | Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.               |          |          |        |     |                     |
| RN     | [6]   |          |          |        |     |                     |
| RP     | SEQUENCE OF 1-12 FROM N.A.  |          |          |        |     |                     |

| Query Match   | Best Local Similarity | Score 30; DB 1; Length 404; |
|---|-----------------------|-----------------------------|
| Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                       |                             |
| 1 ANONTARIGEPVLVCKGAPKPPQRLMK 30                            |                       |                             |

| DB                    | 23   | AMNTARIGEPVLKCKGAPKPPORLEWK       | 52                |
|-----------------------|--|-----------------------------------|-------------------|
| RESULT                | 2  |                                   |                   |
| AGE_MOUSE             |  |                                   |                   |
| DT                    | 01-NOV-1997  | (Rel. 35, Created)                |                   |
| DT                    | 01-NOV-1997  | (Rel. 35, Last sequence update)   |                   |
| DT                    | 15-JUL-1998  | (Rel. 36, Last annotation update) |                   |
| DE                    | ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR   |                                   |                   |
| DE                    | (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).  |                                   |                   |
| OS                    | AGER OR RAGE.  |                                   |                   |
| OS                    | Mus musculus (Mouse).  |                                   |                   |
| OC                    | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  |                                   |                   |
| OC                    | Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  |                                   |                   |
| OX                    | NCBI_Taxid=10090;  |                                   |                   |
| RP                    | SEQUENCE FROM N.A.   |                                   |                   |
| RC                    | STRAIN=BAIB/C; TISSUE=Lung;  |                                   |                   |
| RX                    | MEDLINE=97368045; PubMed=9224812;  |                                   |                   |
| RA                    | Renard C., Chappey O., Mautier M.P., Nagashima M., Louth E.,   |                                   |                   |
| RA                    | Morser J., Zhao L., Schmidt A.M., Scherrmann J.M., Mautier J.L.;   |                                   |                   |
| RT                    | "Recombinant advanced glycation end product receptor pharmacokinetics  |                                   |                   |
| RL                    | in normal and diabetic rats."  |                                   |                   |
| MoI                   | Pharmacol. 52:54-62(1997).   |                                   |                   |
| CC                    | -I- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END  |                                   |                   |
| CC                    | PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS   |                                   |                   |
| CC                    | WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED   |                                   |                   |
| CC                    | RATE IN DIABETES.  |                                   |                   |
| CC                    | -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.   |                                   |                   |
| CC                    | -I- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.   |                                   |                   |
| CC                    | -I- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS  |                                   |                   |
| CC                    | 2 C2-LIKE AND ONE V-LIKE DOMAINS.  |                                   |                   |
| CC                    | -----  |                                   |                   |
| CC                    | This SWISS-PROT entry is copyright. It is produced through a collaboration   |                                   |                   |
| CC                    | between the Swiss Institute of Bioinformatics and the EMBL outstation -  |                                   |                   |
| CC                    | the European Bioinformatics Institute. There are no restrictions on the  |                                   |                   |
| CC                    | use by non-profit institutions as long as its content is in no way   |                                   |                   |
| CC                    | modified and this statement is not removed. Usage by and for commercial  |                                   |                   |
| CC                    | entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> |                                   |                   |
| CC                    | or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).  |                                   |                   |
| CC                    | -----  |                                   |                   |
| DR                    | EMBL, L3412; AAA4004.1; .  |                                   |                   |
| DR                    | MGD; MG1:893592; Ager.   |                                   |                   |
| DR                    | InterPro: IPR003006; IG_MHC.   |                                   |                   |
| DR                    | InterPro: IPR003598; IG_C2.  |                                   |                   |
| DR                    | InterPro: IPR003600; IG_Like.  |                                   |                   |
| DR                    | Pfam: PF00047; Ig: 3.  |                                   |                   |
| DR                    | SMART: SM00408; IGC2: 1.   |                                   |                   |
| DR                    | SMART: SM00410; IG_Like: 1.  |                                   |                   |
| DR                    | PROSITE: PS00290; IG_MHC: 1.   |                                   |                   |
| DR                    | Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.  |                                   |                   |
| FT                    | SIGNAL   | 1                                 | 22                |
| FT                    | CHAIN  | 23                                | 403               |
| FT                    | DOMAIN   | 23                                | 341               |
| FT                    | TRANSMEM   | 342                               | 362               |
| FT                    | DOMAIN   | 363                               | 403               |
| FT                    | DOMAIN   | 31                                | 105               |
| FT                    | DOMAIN   | 136                               | 213               |
| FT                    | DISULFID   | 251                               | 307               |
| FT                    | DISULFID   | 38                                | 98                |
| FT                    | DISULFID   | 143                               | 207               |
| FT                    | DISULFID   | 258                               | 300               |
| FT                    | CARBOHYD   | 25                                | 25                |
| FT                    | CARBOHYD   | 80                                | 80                |
| FT                    | SEQUENCE   | 403 AA;                           | 42668 MW;         |
| Query Match           | 43.3%;   | Score 13;                         | DB 1; Length 403; |
| Best Local Similarity | 100.0%;  | Pred No. 7.3e-07;                 |                   |

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 2 QNTARIGEPLV 14  
 |||||  
 Db 24 QNTARIGEPLV 36

## RESULT 3

RAGE\_RAT  
 ID RAGE\_RAT STANDARD: PRT: 402 AA.

AC 063495;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR

DE (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).

GN AGER OR RAGE.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Lung;

RA MEDLINE=97368045; PubMed=9224812;

RA Renard C., Chappey O., Wautier M.P., Nagashima M., Lunth E.,

RA Morser J., Zhao L., Schmidt A.M., Scherrenmann J.M., Wautier J.L.;

RT "Recombinant advanced glycation end product receptor pharmacokinetics

in normal and diabetic rats";

Mol. Pharmacol. 52:54-62(1997).

RL -1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END

PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS

WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED

RATE IN DIABETES.

-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.

-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS

2 C2-LIKE AND ONE V-LIKE DOMAINS.

-----

CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation-

Query Match 36.7%; Score 11; DB 1; Length 402;  
 Best Local Similarity 100.0%; Pred. No. 0.00011;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 4

RAGE\_BOVIN  
 ID RAGE\_BOVIN STANDARD: PRT: 416 AA.

AC 028173;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR

DE (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).

GN AGER OR RAGE.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE=Lung;

RA MEDLINE=92360547; PubMed=13708843;

RA Nepper M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,

RA Ellington K., Stern D., Shaw A.;

RT "Cloning and expression of a cell surface receptor for advanced

glycosylation end products of proteins";

J. Biol. Chem. 267:14998-15004(1992).

RL -1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END

PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS

WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED

RATE IN DIABETES.

-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.

-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS

2 C2-LIKE AND ONE V-LIKE DOMAINS.

-----

CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation-

the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial

entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

-----

CC EMBL: M91212; AAA03575.1; -

DR InterPro: IPR003006; Iq\_MHC.

DR InterPro: IPR003598; Iq\_C2.

DR InterPro: IPR003600; Iq\_Like.

DR Pfam: PF00047; Iq; 2.

DR SMART: SM00408; IqC2; 1.

DR SMART: SM00410; Iq\_Like; 1.

DR PROSITE: PS00290; Iq\_MHC; 1.

KW Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 22

FT CHAIN 23 416

FT DOMAIN 23 352

FT TRANSMEM 353 373

FT DOMAIN 374 416

FT DOMAIN 31 105

FT DOMAIN 136 213

FT DOMAIN 262 318

FT DISULFID 38 98

FT DISULFID 143 207

FT CARBOHYD 25 25

FT CARBOHYD 80 80

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT DOMAIN 391 396 POLY-GLU.  
SQ SEQUENCE 416 AA: 44182 MW: B703815573E767AE CRC64;

Query Match 33.3%; Score 10; DB 1; Length 416;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 CKGAPKPPQ 25  
|1111111111|  
DB 38 CKGAPKPPQ 47

RESULT 5  
MUTN\_HAEIN.  
ID MUTN\_HAEIN STANDARD: PRT; 223 AA.  
AC P44688;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE DNA MISMATCH REPAIR PROTEIN MUTN.  
GN MUTN OR H10403.  
OS Haemophilus influenzae.  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
OC Haemophilus.  
OX NCBI\_TaxID=727;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-RD / KW20 / ATCC 51907;  
RX MEDLINE=95350630; Pubmed=7542800;  
RA Fleischiemann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
RA Kerlavage A.R., Bult C.J., Tomb J.F., Dougherty B.A., Merrick J.M.,  
RA McKenney K., Shitton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
RA Scott J.D., Shirley R., Liu L.-I., Glodet A., Kelley J.M.,  
RA Weidman J.F., Phillips C.A., Spriggs T., Heddlom E., Cotton M.D.,  
RA Fine L.D., Fritchman J.L., Fuhrman D.T., Saudek D.M., Brandon R.C.,  
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
RA Venter J.C.;  
RT "Whole-genome random sequencing and assembly of Haemophilus  
influenzae Rd.";  
RL Science 269:496-512(1995).  
CC -1- FUNCTION: SEQUENCE-SPECIFIC ENDONUCLEASE THAT CLEAVES UNMETHYLATED  
GATC SEQUENCES. IT IS INVOLVED IN DNA MISMATCH REPAIR (BY  
SIMILARITY).  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
CC DR EMBL: U32723; AAC22062.1; -.  
DR HSSP: P06722; ZAZO.  
DR TIGR: H10403; -.  
KM DNA repair: Hydrolyase; Endonuclease: Complete proteome.  
SQ SEQUENCE 223 AA: 24906 MW: 339A4EF9DA0E622A CRC64;

Query Match 23.3%; Score 7; DB 1; Length 223;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ITARIGE 10  
|1111111111|  
DB 165 ITARIGE 171

RESULT 6  
VGLF\_PVM STANDARD: PRT; 537 AA.  
ID VGLF\_PVM

AC P35949;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE FUSION GLYCOPROTEIN PRECURSOR [CONTAINS: FUSION GLYCOPROTEIN F2;  
DE FUSION GLYCOPROTEIN F1].  
GN F.  
OS Pneumonia virus of mice (PVM).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
OX NCBI\_TaxID=11263;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92333256; Pubmed=1629698;  
RA Chambers P., Pringle C.R., Easton A.J.;  
RT "Sequence analysis of the gene encoding the fusion glycoprotein of  
RT pneumonia virus of mice suggests possible conserved secondary  
RT structure elements in paramyxovirus fusion glycoproteins.";  
RL J. Gen. Virol. 73:1717-1724(1992).  
CC -1- FUNCTION: THIS PROTEIN DIRECTS FUSION OF VIRAL AND CELLULAR  
CC MEMBRANES, RESULTING IN VIRAL PENETRATION, & CAN DIRECT FUSION OF  
CC INFECTED CELLS WITH ADJOINING CELLS, RESULTING IN THE FORMATION OF  
CC SYNCYTIA.  
CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2  
CC LINKED BY A DISULFIDE BOND.  
CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES FUSION GLYCOPROTEIN  
CC FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
CC DR EMBL: D11128; BAA01902.1; -.  
DR PIR: J01619; J01619.  
DR InterPro: IPR000776; Fusion\_gly.  
DR Pfam: PF00523; fusion\_gly; 1.  
KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.  
FT SIGNAL 1 22  
FT CHAIN 23 537  
FT CHAIN 23 537  
FT CHAIN 102 537  
FT CHAIN 102 537  
FT TRANSMEM 491 514  
FT CARBOHYD 463 463  
FT CARBOHYD 488 488  
SQ SEQUENCE 537 AA: 59366 MW: BA6116E2FABE702 CRC64;

Query Match 23.3%; Score 7; DB 1; Length 537;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GEPLVTK 15  
|1111111111|  
DB 434 GEPLVTK 440

RESULT 7  
YGAL\_YEAST STANDARD: PRT; 110 AA.  
ID YGAL\_YEAST  
AC P53305;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE HYPOTHETICAL 12.4 KDA PROTEIN IN NAB1A-GP11 INTERGENIC REGION.  
GN YGR215W.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;



RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288C;  
 RA MEDLINE=97435481; PubMed=9290212;  
 RT Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.;  
 "Sequence analysis of 203 kilobases from *Saccharomyces cerevisiae*  
 chromosome VII.";  
 RL Yeast 13:1077-1090(1997).  
 CC -1- SIMILARITY: TO S.POMBE SPBC30D10.12C.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: 273000; CAA97242.1; -  
 DR SGD: S0003447; YGR215W.  
 KW Hypothetical protein.  
 SO SEQUENCE 110 AA; 12393 MW; 05008CA4F5D09004 CRC64;

Query Match 20.0%; Score 6; DB 1; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 8.7;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 KGAPK 22  
 ID 111111  
 DB 88 KGAPK 93

RESULT 8  
 YCF4\_GUTH STANDARD; PRT; 181 AA.  
 ID YCF4\_GUTH  
 AC 078467;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE PHOTOSYSTEM I ASSEMBLY PROTEIN YCF4.  
 GN YCF4.  
 OS Guillardia theta (Cryptomonas ph1).  
 OC Chloroplast.  
 OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.  
 RX NCBI\_TaxID=55529;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99128221; PubMed=9929392;  
 RA Douglas S.E., Penny S.L.;  
 "The plastid genome of the cryptophyte alga, *Guillardia theta*:  
 RT complete sequence and conserved syteny groups confirm its common  
 RT ancestry with red algae.";  
 RL J. Mol. Evol. 48:236-244(1999).  
 CC -1- FUNCTION: SEEMS TO BE REQUIRED FOR THE ASSEMBLY OF THE PHOTOSYSTEM  
 CC I COMPLEX (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: THYLAKOID MEMBRANE-ASSOCIATED (BY  
 CC SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE YCF4 FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AF041468; AAC35658.1; -  
 DR InterPro: IPR003359; Ycf4.  
 DR Pfam: PF02392; Ycf4; 1.  
 KW Photosynthesis; Thylakoid; Transmembrane; Chloroplast.  
 FT TRANSMEM 19 41 POTENTIAL.

FT TRANSMEM 61 83 POTENTIAL.  
 SQ SEQUENCE 181 AA; 20921 MW; 9B74EC86AEECF48 CRC64;

Query Match 20.0%; Score 6; DB 1; Length 181;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RISEPL 12  
 ID 111111  
 DB 153 RISEPL 158

RESULT 9  
 YA79\_HAEIN STANDARD; PRT; 210 AA.  
 ID YA79\_HAEIN  
 AC P45023;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE HYPOTHETICAL AMINO-ACID ABC TRANSPORTER PERMEASE PROTEIN HI0179.  
 GN HI0179.  
 OS Haemophilus influenzae.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
 OC Haemophilus.  
 OX NCBI\_TaxID=727;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RD / KW20 / ATCC 51907;  
 RX MEDLINE=9530630; PubMed=7542800;  
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
 RA Scott J.D., Shirley R., Liu L.-T., Glodek A., Kelley J.M.,  
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,  
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
 RA Venter J.C.;  
 RT "Whole-genome random sequencing and assembly of *Haemophilus*  
 RT *influenzae* Rd.";  
 RL Science 269:496-512(1995).  
 RN [2]  
 RP REVISIONS.  
 RA White O., Clayton R.A., Kerlavage A.R., Fleischmann R.D.;  
 RL Submitted (SEP-1996) to the EMBL/Genbank/DBD databases.  
 CC -1- FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT  
 CC SYSTEM FOR AN AMINO-ACID. PROBABLY RESPONSIBLE FOR THE  
 CC TRANSLLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE  
 CC (POTENTIAL).  
 CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-  
 CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE HISMQ  
 CC SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: U32788; AAC22735.1; -  
 DR TIGR: H11079; -  
 DR InterPro: IPR00515; BPD\_transp.  
 DR Pfam: PF00528; BPD\_transp; 1.  
 DR PROSITE: PS00402; BPD\_TRANSPP\_INN\_MEMBR; 1.  
 KW Hypothetical protein; Transport; Amino-acid transport; Transmembrane;  
 KW Inner membrane; Complete proteome.  
 FT TRANSMEM 10 30 POTENTIAL.  
 FT TRANSMEM 57 77 POTENTIAL.  
 FT TRANSMEM 79 99 POTENTIAL.

FT TRANSMEM 177 197 POTENTIAL.  
SQ SEQUENCE 210 AA; 23393 MW; 662C7C590DC4FDCD CRC64;

Query Match 20.0%; Score 6; DB 1; Length 210;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITA 6  
Db 167 AONITA 172

RESULT 10  
VCP8\_EBV  
ID VCP8\_EBV STANDARD; PRT; 234 AA.  
AC P03224;

DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-DEC-1992 (Rel. 24, Last annotation update)  
DE PROBABLE MEMBRANE ANTIGEN GP85.

GN EDLP3.  
OS Epstein-Barr virus (strain B95-8) (Human herpesvirus 4).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Gammaherpesvirinae; Lymphocryptovirus.

OX NCBI\_TaxID=10377;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=84270667; PubMed=6087149;  
RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,  
RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,  
RA Tufnell P.S., Barrett B.G.;  
RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";  
RL Nature 310:207-211(1984).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; V01555; CA24835.1; -  
DR PIR; A03787; Q0BEA3.  
DR PIR; S33040; S33040.  
KW Membrane: Glycoprotein; Late protein.  
SQ SEQUENCE 234 AA; 23791 MW; 48DECED0931119E CRC64;

Query Match 20.0%; Score 6; DB 1; Length 234;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITA 6  
Db 108 AONITA 113

RESULT 11  
E434\_ADECT  
ID E434\_ADECT STANDARD; PRT; 259 AA.  
AC P87568;

DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE EARLY E4 30 KDA PROTEIN.

OS Canine adenovirus type 2 (strain Toronto A 26-61).  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

OX NCBI\_TaxID=69152;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Campbell J.B., Zhao Y.;

RT "Complete DNA sequence and genomic organization of canine  
RT adenovirus type 2.";  
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE ADENOVIRUS E4 30 TO 34 KDA PROTEIN  
CC FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; U77082; AAB38735.1; -  
KW Early protein.  
SQ SEQUENCE 259 AA; 30014 MW; 9C966CA011C2A745 CRC64;

Query Match 20.0%; Score 6; DB 1; Length 259;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 LVLKCK 17  
Db 178 LVLKCK 183

RESULT 12  
E434\_ADECC  
ID E434\_ADECC STANDARD; PRT; 265 AA.  
AC O65962;

DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE EARLY E4 31 KDA PROTEIN.

OS Canine adenovirus type 1 (strain CUL).  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

OX NCBI\_TaxID=69150;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Campbell J.B., Zhao Y.;

RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.  
RN [12]

RP SEQUENCE OF 248-265 FROM N.A.  
RX MEDLINE=91272490; PubMed=1828920;  
RA Dragulev B.P., Sira S., Abounaidar M.G., Campbell J.B.;

RT "Sequence analysis of putative E3 and fiber genomic regions of two  
RT strains of canine adenovirus type 1.";

RL Virology 183:298-305(1991).  
CC -1- SIMILARITY: BELONGS TO THE ADENOVIRUS E4 30 TO 34 KDA PROTEIN  
CC FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; U55001; AAB05452.1; -  
KW Early protein.  
SQ SEQUENCE 265 AA; 30822 MW; 92606E5E30134103 CRC64;

Query Match 20.0%; Score 6; DB 1; Length 265;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 LVLKCK 17  
Db 184 LVLKCK 189

```
RESULT 13
E434_ADECR STANDARD: PRT: 265 AA.
AC 096690.
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE EARLY E4 31 KDA PROTEIN.
OS Canine adenovirus type 1 (strain RI261).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=69151.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97275900; PubMed=9129661;
RA Morrison M.D., Onions D.E., Nicolson L.;
RL "Complete DNA sequence of canine adenovirus type 1.";
J. Gen. Virol. 78:873-878(1997).
CC -I SIMILARITY: BELONGS TO THE ADENOVIRUS E4 31 TO 34 KDA PROTEIN
FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Y07760; CAA69046.1; -.
KM Early protein.
SQ SEQUENCE 265 AA; 30737 MW; 14B3DC9CD9D2E15 CRC64;

Query Match 20.0%; Score 6; DB 1; Length 265;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 LVLKCK 17
DB 184 LVLKCK 189

RESULT 14
MIND_GUTH STANDARD: PRT: 269 AA.
AC 078436.
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PUTATIVE SEPTUM SITE-DETERMINING PROTEIN MIND.
GN MIND.
OS Gullardia theta (Cryptomonas phl).
OG Chloroplast.
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Gullardia.
OX NCBI_TaxID=55529;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99128221; PubMed=9929392;
RA Douglas S.E., Penny S.L.;
RT "The plastid genome of the cryptophyte alga, gullardia theta:
RT complete sequence and conserved syteny groups confirm its common
RT ancestry with red algae.";
RL J. Mol. Evol. 48:236-244(1999).
CC -I FUNCTION: ATPASE REQUIRED FOR THE CORRECT PLACEMENT OF THE
CC DIVISION SITE (BY SIMILARITY).
CC -I SIMILARITY: BELONGS TO THE PARA FAMILY. MIND SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
```

```
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF041468; AAC35621.1; -.
DR InterPro: IPR000707; Para.
DR Pfam: PF00991; Para; 1.
KW Cell division; Septation; ATP-Binding; Chloroplast.
FT NP BIND 10 17 ATP (POTENTIAL).
SQ SEQUENCE 269 AA; 29455 MW; BC363B954E689EAA2 CRC64;
```

```
Query Match 20.0%; Score 6; DB 1; Length 269;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GEPLVL 14
DB 215 GEPLVL 220
```

```
RESULT 15
PROC_VIBAL STANDARD: PRT: 278 AA.
AC P52053;
ID 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).
GN PROC.
OS Vibrio alginolyticus.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrrio.
OX NCBI_TaxID=663;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=138-2;
MEDLINE=97137009; PubMed=8982386;
RA Nakamura T., Katoh Y., Shimizu Y., Matsuba Y., Umemoto T.;
RT "Cloning and sequencing of novel genes from Vibrio alginolyticus that
RT support the growth of K+ uptake-deficient mutant of Escherichia
RT coli.";
RL Blochim. Biophys. Acta 1277:201-208(1996).
CC -I CATALYTIC ACTIVITY: L-PROLINE + NAD(P)(+) = L-PYRROLINE-5-
CC CARBOXYLATE + NAD(P)H.
CC -I PATHWAY: TERMINAL (THIRD) STEP IN PROLINE BIOSYNTHESIS.
CC -I SIMILARITY: BELONGS TO THE PYRROLINE-5-CARBOXYLATE REDUCTASE
CC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D50472; BAA09063.1; -.
DR InterPro: IPR000304; P5CR.
DR Pfam: PF01089; P5CR; 1.
DR PROSITE: PS00521; P5CR; 1.
KW Oxidoreductase; Proline biosynthesis; NADP.
SQ SEQUENCE 278 AA; 29815 MW; 50359E5EF97CD68B CRC64;
```

```
Query Match 20.0%; Score 6; DB 1; Length 278;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 AONITA 6
DB 35 AONITA 40
```

Wed Apr 24 09:48:09 2002

us-09-689-469-5.oli.rsp

Page 8

Search completed: April 24, 2002, 09:24:54  
Job time: 247 sec

---

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:24:25 ; Search time 63.44 Seconds  
(without alignments)  
69.170 Million cell updates/sec

Title: US-09-689-469-5  
Perfect score: 30  
Sequence: 1 AONITARIGEPVLKCKGAPKPPQRLKWK 30

Scoring table:  
Gapop 60.0 , Gapext 60.0

Searched: 473505 seqs, 146272329 residues

Word size : 0

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL\_17:\*  
1: sp-archaea:\*  
2: sp-bacteria:\*  
3: sp-fungi:\*  
4: sp-human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|-------|-------------|-----------|----|-------------|
| 1          | 30    | 100.0       | 342       | 4  | 09Y3R3      |
| 2          | 13    | 43.3        | 402       | 11 | 035444      |
| 3          | 9     | 30.0        | 32        | 6  | 09Y3R3      |
| 4          | 7     | 23.3        | 237       | 5  | 09Y5N7      |
| 5          | 7     | 23.3        | 330       | 2  | 09Y1E6      |
| 6          | 7     | 23.3        | 330       | 2  | 09Y1E6      |
| 7          | 7     | 23.3        | 330       | 2  | 09Y1E6      |
| 8          | 7     | 23.3        | 330       | 2  | 09Y1E6      |
| 9          | 6     | 20.0        | 61        | 5  | 09Y5N7      |
| 10         | 6     | 20.0        | 71        | 5  | 09Y5N7      |
| 11         | 6     | 20.0        | 76        | 5  | 09Y5N7      |
| 12         | 6     | 20.0        | 96        | 10 | 080389      |
| 13         | 6     | 20.0        | 99        | 10 | 09Y5N7      |
| 14         | 6     | 20.0        | 101       | 12 | 09Y1E6      |
| 15         | 6     | 20.0        | 127       | 12 | 09Y5N7      |
| 16         | 6     | 20.0        | 155       | 10 | 09Y5N7      |
| 17         | 6     | 20.0        | 209       | 2  | 006630      |
| 18         | 6     | 20.0        | 230       | 2  | 09Y5N7      |
| 19         | 6     | 20.0        | 257       | 2  | 006157      |

|    |   |      |     |    |        |                      |
|----|---|------|-----|----|--------|----------------------|
| 20 | 6 | 20.0 | 259 | 2  | 09CCU3 | 09ccu3 mycobacteri   |
| 21 | 6 | 20.0 | 261 | 2  | 007711 | 007711 mycobacteri   |
| 22 | 6 | 20.0 | 271 | 2  | 067348 | 067348 aquifex aeo   |
| 23 | 6 | 20.0 | 298 | 2  | 09A7U8 | 09a7u8 caulobacter   |
| 24 | 6 | 20.0 | 298 | 10 | 09ZS04 | 09zs04 arabidopsis   |
| 25 | 6 | 20.0 | 326 | 2  | 09HXX1 | 09hxx1 pseudomonas   |
| 26 | 6 | 20.0 | 334 | 2  | 09HXX1 | 09hxx1 pseudomonas   |
| 27 | 6 | 20.0 | 334 | 5  | 09Y6W0 | 09y6w0 drosophila    |
| 28 | 6 | 20.0 | 339 | 11 | 062708 | 062708 rattus norv   |
| 29 | 6 | 20.0 | 339 | 11 | 09QYV4 | 09qyv4 rattus norv   |
| 30 | 6 | 20.0 | 359 | 2  | 088036 | 088036 streptomyce   |
| 31 | 6 | 20.0 | 359 | 8  | 09YUR6 | 09yur6 protobact     |
| 32 | 6 | 20.0 | 387 | 10 | 09YXSO | 09yxso arabidopsis   |
| 33 | 6 | 20.0 | 389 | 9  | 038644 | 038644 bacteriophage |
| 34 | 6 | 20.0 | 392 | 2  | 09FCL0 | 09fcl0 streptomyce   |
| 35 | 6 | 20.0 | 411 | 10 | 09M3H9 | 09m3h9 cicer arict   |
| 36 | 6 | 20.0 | 426 | 5  | 09Y1W7 | 09y1w7 drosophila    |
| 37 | 6 | 20.0 | 433 | 2  | 052912 | 052912 rhizobium m   |
| 38 | 6 | 20.0 | 452 | 10 | 09YLR5 | 09ylr5 arabidopsis   |
| 39 | 6 | 20.0 | 471 | 1  | 004928 | 004928 methanobact   |
| 40 | 6 | 20.0 | 474 | 2  | 09KSM2 | 09ksm2 vibrio chol   |
| 41 | 6 | 20.0 | 479 | 10 | 09Y1T1 | 09y1t1 arabidopsis   |
| 42 | 6 | 20.0 | 479 | 11 | 09QWS2 | 09qws2 mus musculi   |
| 43 | 6 | 20.0 | 482 | 4  | 09Y6W6 | 09y6w6 mus musculi   |
| 44 | 6 | 20.0 | 483 | 11 | 09ESS0 | 09ess0 mus musculi   |
| 45 | 6 | 20.0 | 483 | 11 | 09CZY9 | 09czy9 mus musculi   |

#### ALIGNMENTS

| RESULT | 1  | PRELIMINARY | PRT | 342 AA. |
|--------|--|-------------|-----|---------|
| 09Y3R3 | AC   | 09Y3R3      |     |         |
| DT     | 01-NOV-1999 (TREMBLrel. 12, Created)                                   |             |     |         |
| DT     | 01-NOV-1999 (TREMBLrel. 12, Last sequence update)                      |             |     |         |
| DT     | 01-JUN-2001 (TREMBLrel. 17, Last annotation update)                    |             |     |         |
| DE     | RECEPTOR FOR ADVANCED GLYCATION END PRODUCTS PRECURSOR.                |             |     |         |
| GN     | RAGESEC.   |             |     |         |
| OS     | Homo sapiens (Human).  |             |     |         |
| OC     | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;                |             |     |         |
| OC     | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.              |             |     |         |
| OX     | NCBI_TaxId=9606;   |             |     |         |
| RN     | [1]  |             |     |         |
| RA     | SEQUENCE FROM N.A.   |             |     |         |
| RA     | Malherbe P., Richards J., Galliard H., Thompson A., Diener C.,         |             |     |         |
| RA     | Schuler A., Huber G.;  |             |     |         |
| RT     | "CDNA cloning of a novel secreted isoform of the human Receptor for    |             |     |         |
| RT     | Advanced Glycation End products (RAGE) and characterization of cells   |             |     |         |
| RT     | co-expressing cell-surface scavenger receptors and Swedish mutant      |             |     |         |
| RT     | amyloid precursor protein."  |             |     |         |
| RL     | Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.                |             |     |         |
| CC     | -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX |             |     |         |
| CC     | DOMAIN.  |             |     |         |
| DR     | EMBL: A1133822; CAB43108.1; "  |             |     |         |
| DR     | InterPro: IPR003598; Ig_C2.  |             |     |         |
| DR     | InterPro: IPR003600; Ig_Like.  |             |     |         |
| DR     | InterPro: IPR003006; Ig_MHC.   |             |     |         |
| DR     | Pfam: PF00047; Ig_2.   |             |     |         |
| DR     | SMART: SM00408; IgC2; 1.   |             |     |         |
| DR     | SMART: SM00410; Ig_Like; 1.  |             |     |         |
| KW     | Signal; Receptor.  |             |     |         |
| FT     | SIGNAL 1 22  |             |     |         |
| FT     | CHAIN 23 342   |             |     |         |
| FT     | POTENTIAL RECEPTOR FOR ADVANCED GLYCATION END                          |             |     |         |
| FT     | PRODUCTS.  |             |     |         |
| SO     | SEQUENCE 342 AA; 36193 MW; 35DDF66A13B39B38 CRC64;                     |             |     |         |

Query Match 100.0%; Score 30; DB 4; Length 342;  
Best Local Similarity 100.0%; Pred. No. 6e-24;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGEPLVKCKGAPKPPORLEWK 30  
 ||||||||||||||||||||  
 DB 23 AONTARIGEPLVKCKGAPKPPORLEWK 52

RESULT 2  
 ID 035444 PRELIMINARY; PRT; 402 AA.  
 AC 035444;  
 DT 01-JAN-1998 (TReMBLrel. 05, Created)  
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE RAGE.  
 GN RAGE.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Rowen L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,  
 RA Loretz C., Schmidt S., Tipton S., Tralcoff R., Zackrone K., Hood L.,  
 RL Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 DR EMBL: AF030001; AAB82007.1; -  
 DR InterPro: IPR003598; Ig\_C2.  
 DR InterPro: IPR003600; Ig\_Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig\_3.  
 DR SMART: SM00408; IgC2; 1.  
 DR SMART: SM00410; Ig\_Like; 1.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN.1.  
 DR SEQUENCE 402 AA: 42653 MW; DBFDC50A6C8CB902 CRC64;

Query Match 43.3%; Score 13; DB 11; Length 402;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-06;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 2 ONTARIGEPLVL 14  
 ||||||||||||  
 DB 24 ONTARIGEPLVL 36

RESULT 3  
 ID 09TR01 PRELIMINARY; PRT; 32 AA.  
 AC 09TR01;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)  
 DE 35 KRA ADVANCED GLYCOSYLATION END PRODUCT BINDING PROTEIN (FRAGMENT).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE=92340546; PubMed=1321822;  
 RA Schmidt A.M., Vianna M., Gerlach M., Brett J., Ryan J., Kao J.,  
 RA Esposito C., Hegarty H., Hurley W., Clausen M.,  
 RT Isolation and characterization of two binding proteins for advanced  
 RT glycosylation end products from bovine lung which are present on the  
 RT endothelial cell surface.  
 RL J. Biol. Chem. 267:14987-14997(1992).  
 SO SEQUENCE 32 AA: 3507 MW; AE4C3147CE5B3D91 CRC64;

Query Match 30.0%; Score 9; DB 6; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 0.011;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 KGAPKPPQ 25  
 |||||||||  
 DB 17 KGAPKPPQ 25

RESULT 4  
 ID 09V5N7 PRELIMINARY; PRT; 237 AA.  
 AC 09V5N7;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)  
 DE CG12934 PROTEIN.  
 GN CG12934.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephygroidae; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miles G.L.G.,  
 RA Abril J.F., Adayant A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman J.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burlis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferreira S., Ferreira S., Fleischmann W.,  
 RA Fester A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Gloder A., Gong F., Gottell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003828; AAF58764.1; -  
 DR FlyBase: FBgn0033541; CG12934.  
 SO SEQUENCE 237 AA: 27208 MW; C050101AD183FAF7 CRC64;

Query Match 23.3%; Score 7; DB 5; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 8.6;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 22 KPPORLE 28  
 ||||||||

Db 106 KPPORLE 112

RESULT 5

Q9K1F6 PRELIMINARY: PRT: 330 AA.

AC Q9K1F6; 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DE RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C.

GN NMB0196.

OS Neisseria meningitidis (serogroup B).

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI\_TaxID=491;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MC58 / SEROGROUP B;

RA MEDLINE=20175755; PubMed=10710307;

RT Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwin M.L., DeBoy R., Peterson J.D., Hickey E.K., Hatt D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cifton H., Clark E.B., Cotton M.D., Ulterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Maignani V., Pizzi M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.; "Complete genome sequence of Neisseria meningitidis serogroup B strain MC58." Science 287:1809-1815(2000).

RL EMBL: AE002377; AAF0655.1; -.

DR TIGR: NMB0198; -.

DR InterPro: IPR000613; Pseudou\_synth.

DR InterPro: IPR002990; PSI\_RLU.

DR InterPro: IPR002942; S4.

DR Pfam: PF00849; Pseudou\_synth\_2; 1.

DR Pfam: PF01479; S4; 1.

DR ProDom: PD001819; Pseudou\_synth; 1.

DR SMART: SM00363; S4; 1.

DR PROSITE: PS01129; PSI\_RLU; 1.

KW Complete proteome.

SO SEQUENCE 330 AA; 36682 MW; F2058C52ACE443EC CRC64;

Query Match 23.3%; Score 7; DB 2; Length 330;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GEPLVVK 15

DB 304 GEPLVVK 310

RESULT 6

Q9JX44 PRELIMINARY: PRT: 330 AA.

AC Q9JX44; 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DE RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C (EC 4.2.1.70).

GN RLUC OR NMA0070.

OS Neisseria meningitidis (serogroup A).

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI\_TaxID=65699;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;

RA MEDLINE=20222556; PubMed=10761919;

RT Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,

RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491." Nature 404:502-506(2000).

RL EMBL: AL162752; CAB83386.1; -.

DR InterPro: IPR000613; Pseudou\_synth.

DR InterPro: IPR002990; PSI\_RLU.

DR InterPro: IPR002942; S4.

DR Pfam: PF00849; Pseudou\_synth\_2; 1.

DR Pfam: PF01479; S4; 1.

DR ProDom: PD001819; Pseudou\_synth; 1.

DR SMART: SM00363; S4; 1.

DR PROSITE: PS01129; PSI\_RLU; 1.

KW Lyase; Complete proteome.

SO SEQUENCE 330 AA; 36768 MW; 9B1AB94890F675EA CRC64;

Query Match 23.3%; Score 7; DB 2; Length 330;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GEPLVVK 15

DB 304 GEPLVVK 310

RESULT 7

Q9LOP6 PRELIMINARY: PRT: 595 AA.

AC Q9LOP6; 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DE F24B9.20.

GN Arabidopsis thaliana (Mouse-ear cress).

OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI\_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. COLUMBIA;

RA Liu S., Yu G., Sakano H., Jhaveri A., Lee J., Lenz C., Pham P., Toriumi M., Chin C., Choi E., Chiod J., Gonzalez A., Chung M., RA Hwang B., Koo T., Li J., Liu A., Vaysberg M., Altati H., Brooks S., RA Buehler E., Chao Q., Conn L., Conway A.B., Hansen N., RA Johnson-Hopson C., Khan S., Kim C., Lam B., Nguyen M., Palm C., RA Shin P., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.; "The sequence of BAC F24B9 from Arabidopsis thaliana chromosome 1." Submitted (May-1999) to the EMBL/Genbank/DBJ databases.

RL Submitted (May-1999) to the EMBL/Genbank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. COLUMBIA;

RA Theologis A.; Submitted (May-1999) to the EMBL/Genbank/DBJ databases.

RL Submitted (May-1999) to the EMBL/Genbank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. COLUMBIA;

RA Theologis A.; Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.

RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. COLUMBIA;

RA Theologis A.; Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: AC007583; AAF75084.1; -.

SO SEQUENCE 595 AA; 63982 MW; FF5B15F9BB28B87E CRC64;

Query Match 23.3%; Score 7; DB 10; Length 595;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RICEPLV 13  
 Db 550 RICEPLV 556

RESULT 8  
 ID Q9W322 PRELIMINARY; PRT; 742 AA.  
 AC Q9W322;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE CG3106 PROTEIN.  
 GN CG3106.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxId=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,  
 RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hootin D., Houston K.A., Howland T.J., Wei M.-H., Ibegam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Modyarty C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleib J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Maassamman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003448; AAF46515.1; -;  
 DR FlyBase: FBgn0030148; CG3106.  
 DR InterPro: IPR003862; UPF0063.  
 DR Pfam: PF02712; UPF0063; 1.  
 SQ SEQUENCE 742 AA; 84476 MW; EFF31DF7DC6DE02D CRC64;

QY 17 KGAPKP 23  
 Db 254 KGAPKP 260

RESULT 9  
 ID Q9NFJ5 PRELIMINARY; PRT; 61 AA.  
 AC Q9NFJ5;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE HISTONE H1.  
 GN H1A61.  
 OS Trypanosoma brucei brucei.  
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
 OC NCBI\_TaxId=5702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-TREU 927/4;  
 RA Grueter E.;  
 RL Thesis (2000), Department of Parasitology, Institute of Zoology,  
 RL SWITZERLAND.  
 DR EMBL: AJ287603; CAB76188.1; -;  
 SQ SEQUENCE 61 AA; 6012 MW; 7B66DA10A7D33B93 CRC64;

Query Match 20.0%; Score 6; DB 5; Length 61;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 KGAPKP 22  
 Db 30 KGAPKP 35

RESULT 10  
 ID Q9N6K0 PRELIMINARY; PRT; 71 AA.  
 AC Q9N6K0;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE HISTONE H1.  
 GN H1E71 OR H1A71.  
 OS Trypanosoma brucei brucei.  
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
 OC NCBI\_TaxId=5702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-TREU 927/4;  
 RA Grueter E.;  
 RL Thesis (2000), Department of Parasitology, Institute of Zoology,  
 DR EMBL: AJ400881; CAB90839.1; -;  
 DR EMBL: AJ287600; CAB76185.1; -;  
 SQ SEQUENCE 71 AA; 7005 MW; 478C7B6994847C80 CRC64;

Query Match 20.0%; Score 6; DB 5; Length 71;  
 Best Local Similarity 100.0%; Pred. No. 34;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 KGAPKP 22  
 Db 30 KGAPKP 35

RESULT 11  
 ID Q9N6I0 PRELIMINARY; PRT; 76 AA.  
 AC Q9N6I0;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)

Query Match 23.3%; Score 7; DB 5; Length 742;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)  
 DE HISTONE H1.  
 GN H1E76 OR H1E76.  
 OS Trypanosoma brucei brucei.  
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
 OX NCBI\_TaxId=5702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TREU 927/4;  
 RA Grueter E.;  
 RL Theiss (2000), Department of Parasitology, Institute of Zoology,  
 RL SWITZERLAND.  
 DR EMBL; AJ287605; CAB76190.1; -  
 DR EMBL; AJ287601; CAB76186.1; -  
 DR InterPro: IPR001386; linker\_histone.  
 DR PRINTS: PR00624; HISTONEH5.  
 SQ SEQUENCE 76 AA; 7573 MW; 6079EF4982B50767 CRC64;

Query Match 20.0%; Score 6; DB 5; Length 76;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 KGAPKK 22  
 |||||  
 Db 30 KGAPKK 35

RESULT 12  
 ID 080389 PRELIMINARY; PRT; 96 AA.  
 AC 080389;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)  
 DE CYSTEIN PROTEINASE INHIBITOR.  
 OS Cucumis sativus (Cucumber).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.  
 OX NCBI\_TaxId=3659;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yamakawa S.;  
 RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB014760; BAA28867.1; -  
 DR InterPro: IPR000010; Cystatin.  
 DR InterPro: IPR003243; Cystatin\_C\_M.  
 DR Pfam: PF00031; Cystatin\_1.  
 DR ProDom: PD001231; Cystatin\_C\_M; 1.  
 DR ProSITE: PS00287; CYSTATIN; UNKNOWN\_1.  
 DR SMART; SM00043; CY; 1.  
 SQ SEQUENCE 96 AA; 10973 MW; 027252E14B6C4F4 CRC64;

Query Match 20.0%; Score 6; DB 10; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 44;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 LVLKCK 17  
 |||||  
 Db 59 LVLKCK 64

RESULT 13  
 ID 09FR57 PRELIMINARY; PRT; 99 AA.  
 AC 09FR57;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)

DE SELF-PRUNING INTERACTING PROTEIN 1.  
 OS Lycopersicon esculentum (Tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxId=4081;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. VENT;  
 RA Pnueli L., Lifschitz E.;  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF175963; AAG43410.1; -  
 SQ SEQUENCE 99 AA; 11408 MW; E55F6975B7BA97A3 CRC64;

Query Match 20.0%; Score 6; DB 10; Length 99;  
 Best Local Similarity 100.0%; Pred. No. 45;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GAPKKP 23  
 |||||  
 Db 45 GAPKKP 50

RESULT 14  
 ID 09JH47 PRELIMINARY; PRT; 101 AA.  
 AC 09JH47;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)  
 DE START CODON IS NOT IDENTIFIED (FRAGMENT).  
 GN E4.  
 OS Human papillomavirus type 69.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxId=37121;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Matsukura T., Sata T.;  
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20087389; PubMed=10618284;  
 RA Kino N., Sata T., Sato Y., Sugase M., Matsukura T.;  
 RT "Molecular cloning and nucleotide sequence analysis of a novel human  
 RT papillomavirus (type 82) associated with vaginal intraepithelial  
 RT neoplasia."  
 RL Clin. Diagn. Lab. Immunol. 7:91-95(2000).  
 DR EMBL; AB027020; BAA90731.1; -  
 DR InterPro: IPR003861; Papilloma\_E4.  
 DR Pfam: PF02711; Pap\_E4; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 101 AA; 11267 MW; 328999BE169CAC792 CRC64;

Query Match 20.0%; Score 6; DB 12; Length 101;  
 Best Local Similarity 100.0%; Pred. No. 46;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GAPKKP 23  
 |||||  
 Db 39 GAPKKP 44

RESULT 15  
 ID 09EAJ5 PRELIMINARY; PRT; 127 AA.  
 AC 09EAJ5;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)  
 DE PROTEASE (FRAGMENT).

GN POL.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NBL\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=99-117635;  
 RA Barlow K.L., Tatt I.D., Cane P.A., Pillay D., Clewley J.P.;  
 RT "Detection of simple and complex recombinant strains of HIV-1 in the  
 UK."  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO  
 KNOWN AS THE RETROPEPSIN FAMILY.  
 DR EMBL: AJ296662; CAC03693.1; -  
 DR InterPro: IPR001969; Asp\_protease.  
 DR InterPro: IPR001995; Asp\_prot\_retrov.  
 DR Pfam: PF00077; rvp; 1.  
 DR PROSITE: PS00141; ASP\_PROTEASE; 1.  
 DR PROSITE: PS50175; ASP\_PROT\_RETROV; 1.  
 KM Aspartyl protease; Hydrolase.  
 FT NON\_TER 1 1  
 FT 127 127  
 SQ SEQUENCE 127 AA; 13648 MW; CEAF2745863D5F4 CRC64;

Query Match 20.0%; Score 6; DB 12; Length 127;  
 Best Local Similarity 100.0%; Pred. No. 56;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 4 ITARIG 9  
 |||||  
 Db 39 ITARIG 44

Search completed: April 24, 2002, 09:24:27  
 Job time: 251 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:19:01 ; Search time 38.71 Seconds  
(without alignments)  
59.035 Million cell updates/sec

Title: US-09-689-469-5  
Perfect score: 162  
Sequence: 1 AONITARIGEPLVLKCKGAPKPPORLEWK 30

Scoring table: BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 162   | 100.0       | 404    | 1     | advanced glycosyla |
| 2          | 149   | 92.0        | 402    | 2     | probable advanced  |
| 3          | 145   | 89.5        | 416    | 1     | advanced glycosyla |
| 4          | 64    | 39.5        | 3375   | 2     | hypothetical prote |
| 5          | 54    | 33.3        | 1344   | 2     | rig-1 protein - mo |
| 6          | 53.5  | 33.0        | 483    | 2     | hypothetical prote |
| 7          | 53    | 32.7        | 587    | 2     | DM-GRASP precursor |
| 8          | 53    | 32.7        | 588    | 2     | adhesion molecule  |
| 9          | 53    | 32.7        | 588    | 2     | surface glycoprote |
| 10         | 53    | 32.7        | 602    | 2     | acetylcholine rece |
| 11         | 53    | 32.7        | 1612   | 2     | dufil protein - mo |
| 12         | 53    | 32.7        | 1651   | 2     | transmembrane rece |
| 13         | 52.5  | 32.4        | 7962   | 2     | elastic titin - hu |
| 14         | 51    | 31.5        | 757    | 1     | secretory componen |
| 15         | 51    | 31.5        | 757    | 1     | polymetric immunog |
| 16         | 51    | 31.5        | 1260   | 1     | neural cell adhesi |
| 17         | 51    | 31.5        | 1356   | 2     | protein-tyrosine k |
| 18         | 51    | 31.5        | 1442   | 2     | transcription acti |
| 19         | 50    | 30.9        | 284    | 2     | probable 3-mercapt |
| 20         | 50    | 30.9        | 372    | 2     | ig v-region-like B |
| 21         | 50    | 30.9        | 386    | 2     | hypothetical prote |
| 22         | 50    | 30.9        | 392    | 2     | acetyl-CoA acetyl  |
| 23         | 50    | 30.9        | 1154   | 2     | related to SRBP c  |
| 24         | 50    | 30.9        | 1257   | 1     | neural cell adhesi |
| 25         | 50    | 30.9        | 1259   | 2     | neural cell adhesi |
| 26         | 50    | 30.9        | 1487   | 1     | immediate-early pr |
| 27         | 50    | 30.9        | 1487   | 1     | 155K transcription |
| 28         | 49.5  | 30.6        | 478    | 1     | formate-dependent  |
| 29         | 49.5  | 30.6        | 478    | 2     | hypothetical prote |

|    |      |      |      |   |        |                    |
|----|------|------|------|---|--------|--------------------|
| 30 | 49.5 | 30.6 | 1048 | 2 | T30815 | platelet-derived g |
| 31 | 49   | 30.2 | 102  | 2 | PH1238 | ig heavy chain v r |
| 32 | 49   | 30.2 | 223  | 2 | H64065 | mutator muH - Hae  |
| 33 | 49   | 30.2 | 430  | 2 | T28143 | tapasin I homology |
| 34 | 49   | 30.2 | 850  | 2 | JC5700 | ErB kinase activa  |
| 35 | 49   | 30.2 | 1239 | 1 | A32579 | neuroglian - fruit |
| 36 | 49   | 30.2 | 6642 | 2 | T29757 | protein UNC-89 - C |
| 37 | 48.5 | 29.9 | 438  | 2 | C86244 | DnaJ homolog, 4706 |
| 38 | 48.5 | 29.9 | 525  | 1 | A58674 | neurotrophin-3 rec |
| 39 | 48.5 | 29.9 | 803  | 1 | S35695 | neurotrophin-3 rec |
| 40 | 48.5 | 29.9 | 852  | 2 | T51259 | tyrosine kinase C  |
| 41 | 48.5 | 29.9 | 937  | 2 | A45082 | neurotrophic recep |
| 42 | 48   | 29.6 | 337  | 2 | B83246 | probable transcrip |
| 43 | 48   | 29.6 | 441  | 2 | B70773 | probable thra prot |
| 44 | 48   | 29.6 | 448  | 2 | S15018 | transcription fact |
| 45 | 48   | 29.6 | 508  | 2 | A31637 | transcription fact |

## ALIGNMENTS

RESULT 1  
I61596  
advanced glycosylation end-products receptor precursor - human  
N:Alternate names: advanced glycosylation end product-binding protein, 35k; glycoprot  
C:Species: Homo sapiens (man)  
C>Date: 24-May-1996 #sequence, revision 07-Feb-1997 #text\_change 16-Jul-1999  
C:Accession: I61596; B42879; S27968  
R:Sugaya, K.; Fukagawa, T.; Matsunoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko,  
Genomics 23, 408-419, 1994  
A:Title: Three genes in the human MHC class III region near the junction with the cla  
nterpart of mouse mammary tumor gene int-3.  
A:Reference number: A55562; MUID:95137587  
A:Accession: I61596  
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
A:Molecule type: DNA  
A:Residues: 1-404 <RES>  
A:Cross-references: GB:D28769; NID:9561657; PIDN:BA05958.1; PID:9561659  
R:Nepper, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.;  
J. Biol. Chem. 267, 14998-15004, 1992  
A:Title: Cloning and expression of a cell surface receptor for advanced glycosylation  
A:Reference number: A42879; MUID:92340547  
A:Accession: B42879  
A:Molecule type: mRNA  
A:Residues: 'G', '2-99', 'R', '101-404' <NE>  
A:Cross-references: EMBL:M91211; NID:9190845; PIDN:AAA03574.1; PID:9190846  
A:Experimental source: Lung  
A:Note: sequence extracted from NCBI backbone (NCBIP:109438)  
C:Comment: Advanced glycosylation end products are heterogeneous nonenzymatically gly  
cellular function, thus contributing to tissue lesions in diabetes.  
C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide  
ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.  
A:Gene: GDB:ACER  
A:Cross-references: GDB:306354; OMIM:600214  
A:Map position: 6p21.3-6p21.3  
A:Intons: 18/1; 53/3; 119/1; 140/3; 170/1; 231/1; 274/3; 322/1; 331/1; 373/2  
C:Function:  
A:Description: neuronal receptor for amphoterin, a DNA-binding protein involved in ne  
C:Superfamily: advanced glycosylation end products receptor; immunoglobulin homology  
C:Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-404/Product: advanced glycosylation end products receptor #status predicted <MAT  
F:23-344/Domain: extracellular #status predicted <EXT>  
F:31-101/Domain: immunoglobulin homology <IM1>  
F:137-210/Domain: immunoglobulin homology <IM2>  
F:252-303/Domain: immunoglobulin homology <IM3>  
F:345-362/Domain: transmembrane #status predicted <TMW>  
F:363-404/Domain: intracellular #status predicted <INT>  
F:25/81/Binding site: carbonyl (Asn) (covalent) #status predicted  
F:38-99,144-208,259-301/Disulfide bonds: #status predicted

```

Query Match      100.0%; Score 162; DB 1; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGEPVLVCKGAPKPPQOLEWK 30
Db 23 AONTARIGEPVLVCKGAPKPPQOLEWK 52

RESULT 2
T09062
probable advanced glycosylation end-products receptor precursor - mouse
N:Alternate names: RAGE
C:Species: Mus musculus (house mouse)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000
R:Rowen, L.; Mahairas, G.; Qin, S.; Ahern, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sc
submitted to the EMBL Data Library, October 1997
A:Description: Sequence of the mouse major histocompatibility locus class III region.
A:Reference number: Z16543
A:Accession: T09062
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-402 <ROW>
A:Cross-references: EMBL:AF030001; NID:g2564945; PID:g2564950
A:Genetics:
A:Gene: RAGE
A:Map position: 17
A:Hitons: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1; 272/3; 320/1; 329/1; 371/2
C:Superfamily: advanced glycosylation end products receptor; immunoglobulin homology
C:Keywords: receptor; transmembrane protein
F:31-100/Domain: immunoglobulin homology <IMM>

Query Match      92.0%; Score 149; DB 2; Length 402;
Best Local Similarity 93.1%; Pred. No. 1.1e-13;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QNTARIGEPVLVCKGAPKPPQOLEWK 30
Db 24 QNTARIGEPVLVCKGAPKPPQOLEWK 52

RESULT 3
A42879
advanced glycosylation end-products receptor precursor - bovine
N:Alternate names: advanced glycosylation end product-binding protein, 35K; glycoprotein
C:Species: Bos primigenius taurus (cattle)
C>Date: 04-Mar-1993 #sequence_revision 07-Feb-1997 #text_change 16-Jul-1999
C:Accession: A42879; A42878; S27949
R:Neeger, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; St
J. Biol. Chem. 267, 14998-15004, 1992
A>Title: Cloning and expression of a cell surface receptor for advanced glycosylation en
A:Reference number: A42879; MUID:92340547
A:Accession: A42879
A:Molecule type: mRNA
A:Residues: 1-416 <NEE>
A:Cross-references: GB:M91212; NID:g163650; PIDN:AAA03575.1; PID:g163651
A:Experimental source: Lung
A>Note: sequence extracted from NCBI backbone (NCBI:P109436)
A>Note: Parts of this sequence, including the amino end of the mature protein, were dete
R.Schmidt, A.M.; Viana, M.; Gerlach, M.; Brett, J.; Ryan, J.; Kao, J.; Esposito, C.; He
J. Biol. Chem. 267, 14987-14997, 1992
A>Title: Isolation and characterization of two binding proteins for advanced glycosylati
A:Reference number: A42878; MUID:92340546
A:Accession: A42878
A:Molecule type: protein
A:Residues: 23-24, 'X', 26-37, 'X', 39-49, 'XX', 52-54 <SCH>
A:Experimental source: endothelial cells
A>Note: sequence extracted from NCBI backbone (NCBI:P109434)
C:Comment: Advanced glycosylation end products are heterogeneous nonenzymatically glycos
cellular function, thus contributing to tissue lesions in diabetes.
C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide on

```

```

ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.
A:Function:
C:Description: neuronal receptor for amphoterin, a DNA-binding protein involved in ne
C:Superfamily: advanced glycosylation end products receptor; immunoglobulin homology
C:Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-416/Product: advanced glycosylation end-products receptor RAGE #status predicted
F:23-354/Domain: extracellular #status predicted <EXT>
F:31-100/Domain: immunoglobulin homology <IM1>
F:136-209/Domain: immunoglobulin homology <IM2>
F:262-313/Domain: immunoglobulin homology <IM3>
F:335-372/Domain: transmembrane #status predicted <TMW>
F:373-416/Domain: intracellular #status predicted <INT>
F:25,80/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:38-98,143-207,269-311/Disulfide bonds: #status predicted

Query Match      89.5%; Score 145; DB 1; Length 416;
Best Local Similarity 89.7%; Pred. No. 4.3e-13;
Matches 26; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QNTARIGEPVLVCKGAPKPPQOLEWK 30
Db 24 QNTARIGEPVLVCKGAPKPPQOLEWK 52

RESULT 4
T19821
hypothetical protein ZC101.2e - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000
C:Accession: T19821; T19819; T19820; T27490; T27488; T27489; A47648; B47648;
R:Baynes, C.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19182
A:Accession: T19821
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-3375 <WIL>
A:Cross-references: EMBL:Z93375; PIDN:CAB07569.1; GSPDB:GN00020; CESP:ZC101.2e
A:Experimental source: clone C38C6
A:Accession: T19819
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2441, 'R', 'KRKH', 3369, 'GN', 3372-3373, 'G', 3375, 'RLRHRNRNONGPLSKRTTTTTLF
A:Cross-references: EMBL:Z93375; PIDN:CAB07567.1; GSPDB:GN00020; CESP:ZC101.2a
A:Experimental source: clone C38C6
A:Accession: T19820
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1694, 'H', 1883-2441, 'R', 'KRKH', 3369, 'GN', 3372-3373, 'G', 3375, 'RLRHRNRNONG
A:Cross-references: EMBL:Z93375; PIDN:CAB07568.1; GSPDB:GN00020; CESP:ZC101.2c
A:Experimental source: clone C38C6
R:Percy, C.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z20375
A:Accession: T27490
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-3375 <M12>
A:Cross-references: EMBL:Z93395; PIDN:CAB07708.1; GSPDB:GN00020; CESP:ZC101.2e
A:Experimental source: clone ZC101
A:Accession: T27488
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2441, 'R', 'KRKH', 3369, 'GN', 3372-3373, 'G', 3375, 'RLRHRNRNONGPLSKRTTTTTLF
A:Cross-references: EMBL:Z93395; PIDN:CAB07706.1; GSPDB:GN00020; CESP:ZC101.2a
A:Experimental source: clone ZC101
A:Accession: T27489
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1694, 'H', 1883-2441, 'R', 'KRKH', 3369, 'GN', 3372-3373, 'G', 3375, 'RLRHRNRNONG
A:Cross-references: EMBL:Z93395; PIDN:CAB07707.1; GSPDB:GN00020; CESP:ZC101.2c

```

A:Experimental source: clone ZC101  
 A:Accession: T27487  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1128, 1290, 'DFARNSPS', 1299, 'NSS', 1303-1304, 'R', 'RHR', 1544-1545, 'RINVR', 155  
 A:Cross-references: EMBL:293395; PIDN:CAR07704.1; GSPDB:GN00020; CESP:ZC101.2b  
 A:Experimental source: clone ZC101  
 R:Kogalski, T.M.; Williams, B.D.; Mullen, G.P.; Moerman, D.G.  
 Genes Dev. 7, 1471-1484, 1993  
 A:Title: Products of the unc-52 gene in *Caenorhabditis elegans* are homologous to the coo  
 A:Reference number: A47648; MID:93339574  
 A:Accession: A47648  
 A:Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 1-546, 'P', 548-2441, 'R', 'KRKH', 3369, 'GN', 3372-3373, 'G', 3375, 'RLRHRRNAQNGPLSR  
 A:Cross-references: GB:L13458  
 A:Accession: B47648  
 A:Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 1-546, 'P', 548-2198, 'D', 2290, 'NAR', 2294, 'L', 2296, 'WHATE', 2302-2303, 'V', 2305, '1', 'ANIV', 2516-2517, 'LQOG', 2522, 'IDG', 2526, 'S', 2528, 'SRGFHV', 2535, 'F', <R02>  
 A:Cross-references: GB:L13458  
 A:Accession: C47648  
 A:Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 1-546, 'P', 548-1128, 1290, 'DFARNSPS', 1299, 'NSS', 1303-1304, 'R', 'RHR', 1544-1545, 'C:Genetics:  
 A:Gene: CESP:ZC101.2e; CESP:ZC101.2a; CESP:ZC101.2c; CESP:ZC101.2b  
 A:Map position: 2  
 A:Introns: 32/1; 134/1; 225/1; 335/2; 450/3; 739/3; 830/3; 860/2; 1064/2; 1129/1; 1158/3  
 2: 2613/1; 2684/1; 2673/1; 2813/1; 2863/1; 2900/3; 3084/1; 3176/1; 3250/2  
 C:Superfamily: LDL receptor ligand-binding repeat homology; laminin-type EGF-like homolo  
 C:Keywords: extracellular matrix  
 F:149-183/Domain: LDL receptor ligand-binding repeat homology <LDL1>  
 F:190-224/Domain: LDL receptor ligand-binding repeat homology <LDL2>  
 F:233-268/Domain: LDL receptor ligand-binding repeat homology <LDL3>  
 F:955-1002/Domain: laminin-type EGF-like homology <LEG1>  
 F:1011-1058/Domain: laminin-type EGF-like homology <LEG2>

Query Match 39.5%; Score 64; DB 2; Length 3375;  
 Best Local Similarity 50.0%; Pred. No. 1.5;  
 Matches 12; Conservative 4; Mismatches 6; Indels 2; Gaps 1;  
 QY 8 IGEPLVLCCK-GAPKKPPORLEW 29  
 Db 1990 VGEPLQVLCCKGAPGAPDPEPEVM 2013  
 RESULT 5  
 T14316  
 T19-1 protein - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C:Accession: T14316  
 R:Yuan, S.S.F.; Cox, L.A.; Dasika, G.K.; Lee, E.Y.H.P.  
 submitted to the EMBL Data Library, April 1998  
 A:Reference number: Z17975  
 A:Accession: T14316  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1344 <YUA>  
 A:Cross-references: EMBL:AF060570; NID:94206385; PID:94206386; PIDN:AAD11628.1

Query Match 33.3%; Score 54; DB 2; Length 1344;  
 Best Local Similarity 32.1%; Pred. No. 16;  
 Matches 9; Conservative 5; Mismatches 14; Indels 0; Gaps 0;  
 QY 3 NITARIGEPLVLCCKGAPKKPPORLEW 30  
 Db 152 NVVAVGEPLVLCCKGAPKKPPORLEW 179

RESULT 6  
 T17346  
 hypothetical protein DKFZp58601624.1 - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T17346  
 R:Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
 Submitted to the Protein Sequence Database, September 1999  
 A:Reference number: Z18727  
 A:Accession: T17346  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-483 <DUE>  
 A:Cross-references: EMBL:AL117666  
 A:Experimental source: adult uterus; clone DKFZp58601624  
 C:Genetics:  
 A:Note: DKFZp58601624.1

Query Match 33.0%; Score 53.5; DB 2; Length 483;  
 Best Local Similarity 45.5%; Pred. No. 6.8;  
 Matches 10; Conservative 4; Mismatches 7; Indels 1; Gaps 1;  
 QY 8 IGEPLVLCCKGAPKKPPORLEW 29  
 Db 96 VGEPLVLCCK-ATGNNPPRIW 116

RESULT 7  
 JH0464  
 DM-GRASP precursor - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 02-Sep-2000  
 C:Accession: JH0464  
 R:Burns, F.R.; von Kannen, S.; Guy, L.; Raper, J.A.; Kamholz, J.; Chang, S.  
 Neuron 7, 209-220, 1991  
 A:Title: DM-GRASP, a novel immunoglobulin superfamily axonal surface protein that sup  
 A:Reference number: JH0464; MID:91337449  
 A:Accession: JH0464  
 A:Molecule type: mRNA  
 A:Residues: 1-587 <BUR>  
 A:Experimental source: brain  
 C:Comment: This is a cell surface glycoprotein.  
 C:Comment: This protein is localized to axons in the dorsal funiculus and ventral mid  
 C:Keywords: glycoprotein  
 F:1-32/Domain: signal sequence #status predicted <SIG>  
 F:33-587/Product: DM-GRASP #status predicted <DMG>  
 F:67,198,270,311,365,461,484,503/Binding site: carbohydrate (Asn) (covalent) #status

Query Match 32.7%; Score 53; DB 2; Length 587;  
 Best Local Similarity 40.0%; Pred. No. 9.8;  
 Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;  
 QY 1 AONTARIGEPLVLCCKGAPKKPPQ 25  
 Db 260 SOSTIKEDNYTLCKSGNGNPPQ 284

RESULT 8  
 JH0506  
 adhesion molecule SCL precursor - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 21-Jul-2000  
 C:Accession: JH0506; PS0270  
 R:Tanaka, H.; Matsui, T.; Agata, A.; Tomura, M.; Kubota, I.; McFarland, K.C.; Kohr, B.  
 Neuron 7, 535-545, 1991  
 A:Title: Molecular cloning and expression of a novel adhesion molecule, SCL.  
 A:Reference number: JH0506; MID:92030150  
 A:Accession: JH0506  
 A:Molecule type: mRNA

A:Residues: 1-588 <TRAN>  
 A:Cross-references: GB:S63276; NID:g238000; PIDN:AAB20170.1; PID:g238001  
 A:Experimental source: embryo  
 A:Accession: PS0270  
 A:Molecule type: protein  
 A:Residues: 34-48 <TRAN>  
 C:Comment: This protein is uniquely and transiently expressed on spinal cord motoneurons  
 C:Keywords: glycoprotein; transmembrane protein  
 F:1-33/Domain: signal sequence #status predicted <Sig>  
 F:34-588/Product: adhesion molecule SCI #status predicted <ADH>  
 F:500-523/Domain: transmembrane #status predicted <TRA>  
 F:101,173,199,271,312,366,462,485,504/Binding site: carbohydrate (Asn) (covalent) #statu

Query Match 32.7%; Score 53; DB 2; Length 588;  
 Best Local Similarity 40.0%; Pred. No. 9.8;  
 Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

OY 1 AONTARIGEPVLKCKGAPKRPQ 25  
 DB 261 SQSSTIKESGDNVTLKCSGNGNPPQ 285

RESULT 9  
 A45254  
 surface glycoprotein BEN precursor - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 21-Jul-2000  
 C:Accession: A45254; S19202  
 R:Bouquie, O.; Corbel, C.; Le Caer, J.P.; Rossier, J.; Le Douarin, N.M.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 5261-5265, 1992  
 A:Title: BEN, a surface glycoprotein of the immunoglobulin superfamily, is expressed in  
 A:Reference number: A45254; MUID:92302224  
 A:Accession: A45254  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-588 <POU>  
 A:Cross-references: EMBL:X64301; NID:g63087; PIDN:CAA45579.1; PID:g63088  
 C:Keywords: glycoprotein

Query Match 32.7%; Score 53; DB 2; Length 588;  
 Best Local Similarity 40.0%; Pred. No. 9.8;  
 Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

OY 1 AONTARIGEPVLKCKGAPKRPQ 25  
 DB 261 SQSSTIKESGDNVTLKCSGNGNPPQ 285

RESULT 10  
 A45769  
 acetylcholine receptor synthesis stimulator ARIA-1 precursor - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jul-2000  
 C:Accession: A45769  
 R:Fallis, D.L.; Rosen, K.M.; Corfas, G.; Lane, W.S.; Fischbach, G.D.  
 Cell 72, 801-815, 1993  
 A:Title: ARIA, a protein that stimulates acetylcholine receptor synthesis, is a member of  
 A:Reference number: A45769; MUID:93201602  
 A:Accession: A45769  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-602 <PAL>  
 A:Cross-references: GB:LI1264; NID:g212603; PIDN:AAA49037.1; PID:g212604  
 A:Experimental source: brain  
 A:Note: sequence extracted from NCBI backbone (NCBIN:127787, NCBIP:127788)  
 C:Superfamily: unassigned EGF-related proteins; EGF homology

Query Match 32.7%; Score 53; DB 2; Length 602;  
 Best Local Similarity 32.1%; Pred. No. 10;  
 Matches 9; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

OY 2 ONITARIGEPVLKCKGAPKRPQRLFW 29  
 DB 35 KNOEVAVGOKVLKRCETTSPPALRFKW 62

RESULT 11  
 T30805  
 dut1 protein - mouse  
 M:Alternate names: Transmembrane receptor protein Robol homolog  
 C:Species: Mus musculus (house mouse)  
 C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 22-Oct-1999  
 C:Accession: T30805  
 R:Wu, M.C.; Lowe, N.; Fortham, R.; Rabbits, P.  
 submitted to the EMBL data library, July 1998  
 A:Description: The mouse homologue of human DUT1/H-robol gene: protein sequence and  
 A:Reference number: Z20879  
 A:Accession: T30805  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1612 <MUN>  
 A:Cross-references: EMBL:Y17793; NID:e1329712; PID:e1329713; PIDN:CAA76850.1  
 A:Experimental source: brain  
 C:Genetics:  
 A:Gene: dut1  
 A:Map position: 16

Query Match 32.7%; Score 53; DB 2; Length 1612;  
 Best Local Similarity 28.6%; Pred. No. 27;  
 Matches 8; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

OY 3 NITARIGEPVLKCKGAPKRPQRLFW 30  
 DB 139 DVAVAVGEPAVMCCQPPRGHPPTISWK 166

RESULT 12  
 T14160  
 transmembrane receptor protein Robol - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C:Accession: T14160  
 R:Kidd, T.; Brose, K.; Mitchell, K.J.; Fetter, R.D.; Tessier-Lavigne, M.; Goodman, C.  
 Cell 92, 205-215, 1998  
 A:Title: Roundabout controls axon crossing of the CNS midline and defines a novel sub  
 A:Reference number: Z17897; MUID:98117249  
 A:Accession: T14160  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1651 <KID>  
 A:Cross-references: EMBL:AF041082; NID:g2811215; PID:g2811216; PIDN:ACC39960.1  
 A:Function:  
 A:Description: appears to function as the gatekeeper controlling midline crossing  
 C:Keywords: transmembrane protein

Query Match 32.7%; Score 53; DB 2; Length 1651;  
 Best Local Similarity 28.6%; Pred. No. 27;  
 Matches 8; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

OY 3 NITARIGEPVLKCKGAPKRPQRLFW 30  
 DB 178 DVAVAVGEPAVMCCQPPRGHPPTISWK 205

RESULT 13  
 I38346  
 elastic titin - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 21-Jul-2000  
 C:Accession: I38346  
 R:Labell, S.; Kolmerer, B.

Science 270,293-296, 1995  
 A:Title: Titrins: giant proteins in charge of muscle ultrastructure and elasticity  
 A:Reference number: A57450; MUID:96026330  
 A:Accession: J138346  
 A:Status: Preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-7962 <RES>  
 A:Cross-references: EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g1017427  
 C:Genetics:  
 A:Gene: GDB:TTN  
 A:Cross-references: GDB:I27867; OMIM:188840  
 A:Map position: 2q31-2q31





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:18:15 ; Search time 32.34 Seconds  
(without alignments)  
20.875 Million cell updates/sec

Title: US-09-689-469-5  
Perfect score: 162  
Sequence: 1 AONTTARIGEPVLKCKGAPKPPORLEWK 30

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: Issued\_Patents\_AA.\*
- 2: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/1aa/6CTUS.COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
|------------|-------|-------------|--------|----|-------------------|
| 1          | 162   | 100.0       | 318    | 2  | US-08-633-148-4   |
| 2          | 162   | 100.0       | 340    | 2  | US-08-633-148-2   |
| 3          | 129   | 79.6        | 278    | 2  | US-08-432-016-5   |
| 4          | 129   | 79.6        | 278    | 2  | US-08-684-594-5   |
| 5          | 81    | 50.0        | 16     | 2  | US-08-633-148-18  |
| 6          | 72    | 44.4        | 15     | 2  | US-08-633-148-12  |
| 7          | 60    | 37.0        | 10     | 2  | US-08-633-148-5   |
| 8          | 60    | 37.0        | 10     | 2  | US-08-633-148-13  |
| 9          | 54    | 33.3        | 602    | 1  | US-08-168-091A-2  |
| 10         | 53.5  | 33.0        | 1101   | 3  | US-08-986-485-2   |
| 11         | 53    | 32.7        | 477    | 2  | US-08-432-016-3   |
| 12         | 53    | 32.7        | 477    | 2  | US-08-684-594-3   |
| 13         | 53    | 32.7        | 602    | 1  | US-08-428-926-5   |
| 14         | 53    | 32.7        | 602    | 1  | US-08-428-927-5   |
| 15         | 53    | 32.7        | 602    | 1  | US-08-428-298-5   |
| 16         | 53    | 32.7        | 602    | 1  | US-08-339-517-5   |
| 17         | 53    | 32.7        | 1651   | 4  | US-09-540-245A-18 |
| 18         | 51    | 31.5        | 106    | 2  | US-08-341-843B-5  |
| 19         | 51    | 31.5        | 106    | 2  | US-08-427-497E-10 |
| 20         | 51    | 31.5        | 757    | 3  | US-08-434-000A-6  |
| 21         | 51    | 31.5        | 757    | 4  | US-09-312-157-6   |
| 22         | 51    | 31.5        | 767    | 4  | US-08-874-678-2   |
| 23         | 51    | 31.5        | 767    | 3  | US-08-643-839-2   |
| 24         | 51    | 31.5        | 788    | 1  | US-08-232-538-15  |
| 25         | 51    | 31.5        | 788    | 2  | US-08-786-164-15  |
| 26         | 51    | 31.5        | 1356   | 2  | US-08-810-116-8   |
| 27         | 51    | 31.5        | 1356   | 2  | US-07-930-548A-8  |

|    |      |      |      |   |                    |                    |
|----|------|------|------|---|--------------------|--------------------|
| 28 | 51   | 31.5 | 1356 | 4 | US-09-098-707A-2   | Sequence 2, Appl1  |
| 29 | 50   | 30.9 | 106  | 2 | US-08-341-843B-17  | Sequence 17, Appl1 |
| 30 | 50   | 30.9 | 106  | 2 | US-08-427-497E-22  | Sequence 22, Appl1 |
| 31 | 50   | 30.9 | 611  | 2 | US-08-752-307B-10  | Sequence 10, Appl1 |
| 32 | 49   | 30.2 | 388  | 1 | US-08-429-742-4    | Sequence 4, Appl1  |
| 33 | 49   | 30.2 | 407  | 3 | US-08-753-007A-6   | Sequence 6, Appl1  |
| 34 | 49   | 30.2 | 421  | 2 | US-09-398-496-6    | Sequence 6, Appl1  |
| 35 | 49   | 30.2 | 421  | 2 | US-08-659-984A-1   | Sequence 1, Appl1  |
| 36 | 49   | 30.2 | 444  | 2 | US-08-660-531-1    | Sequence 1, Appl1  |
| 37 | 49   | 30.2 | 444  | 4 | US-08-659-984A-5   | Sequence 5, Appl1  |
| 38 | 49   | 30.2 | 444  | 4 | US-08-660-531-5    | Sequence 5, Appl1  |
| 39 | 49   | 30.2 | 469  | 3 | US-08-753-007A-8   | Sequence 8, Appl1  |
| 40 | 49   | 30.2 | 469  | 4 | US-09-398-496-8    | Sequence 8, Appl1  |
| 41 | 49   | 30.2 | 615  | 2 | US-08-752-307B-9   | Sequence 9, Appl1  |
| 42 | 49   | 30.2 | 647  | 3 | US-08-753-007A-32  | Sequence 32, Appl1 |
| 43 | 49   | 30.2 | 647  | 4 | US-09-398-496-32   | Sequence 32, Appl1 |
| 44 | 48.5 | 29.9 | 601  | 2 | US-08-795-868-16   | Sequence 16, Appl1 |
| 45 | 48.5 | 29.9 | 937  | 2 | US-08-469-537A-105 | Sequence 105, App  |

ALIGNMENTS

RESULT 1  
US-08-633-148-4  
; Sequence 4, Application US/08633148  
; Patent No. 5864018  
GENERAL INFORMATION:  
APPLICANT: MORSE, MICHAEL J.  
APPLICANT: NAGASHIMA, MARIKO  
APPLICANT: HOLANDER, DORIS A.  
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION  
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP  
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: U.S.A.  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/633,148  
FILING DATE: 16-Apr-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MORPHY ESO., MATTHEW B.  
REGISTRATION NUMBER: 39,787  
REFERENCE/DOCKET NUMBER: 014618-005600US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 318 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-633-148-4  
Query Match 100.0%; Score 162; DB 2; Length 318;  
Best Local Similarity 100.0%; Pred. No. 2.1e-15;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 AONTTARIGEPVLKCKGAPKPPORLEWK 30  
|||||

Db 1 AONITARIGEPVLKCKGAPKPPQRLMK 30

## RESULT 2

US-08-633-148-2

Sequence 2, Application US/08633148

Patent No. 5864018

## GENERAL INFORMATION:

APPLICANT: MORSE, MICHAEL J.

APPLICANT: MAGASHIMA, MARIKO

APPLICANT: HOLLANDER, DORIS A.

TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION

TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR

NUMBER OF SEQUENCES: 23

## CORRESPONDENCE ADDRESSES:

ADDRESSEE: TOWNSEND &amp; TOWNSENT &amp; CREW LLP

STREET: TWO EMBARCADERO CENTER, 8TH FLOOR

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: U.S.A.

ZIP: 94111

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/633,148

FILING DATE: 16-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURPHY ESO., MATTHEW B.

REGISTRATION NUMBER: 39,787

REFERENCE/DOCKET NUMBER: 014618-005600US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 340 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-633-148-2

## Query Match

Best Local Similarity 100.0%; Score 162; DB 2; Length 340;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONITARIGEPVLKCKGAPKPPQRLMK 30

Db 23 AONITARIGEPVLKCKGAPKPPQRLMK 52

## RESULT 3

US-08-432-016-5

Sequence 5, Application US/08432016

Patent No. 5968768

## GENERAL INFORMATION:

APPLICANT: HAYNES, BARTON F.

APPLICANT: ARUEFO, ALEJANDRO

APPLICANT: PATEL, DHAVALKUMAR

APPLICANT: BOWEN, MICHAEL A.

APPLICANT: MARQUARDT, HANS

TITLE OF INVENTION: CD6 LIGAND

NUMBER OF SEQUENCES: 9

## CORRESPONDENCE ADDRESSES:

ADDRESSEE: NIXON &amp; VANDERHYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/432,016

FILING DATE: 01-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/333,350

FILING DATE: 02-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/143,903

FILING DATE: 02-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955

REFERENCE/DOCKET NUMBER: 1579-95

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 278 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-432-016-5

## Query Match

Best Local Similarity 79.6%; Score 129; DB 2; Length 278;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 IGEPLVLKCKGAPKPPQRLMK 30

Db 1 IGEPLVLKCKGAPKPPQRLMK 23

## RESULT 4

US-08-684-594-5

Sequence 5, Application US/08684594

Patent No. 5998172

## GENERAL INFORMATION:

APPLICANT: HAYNES, BARTON F.

APPLICANT: ARUEFO, ALEJANDRO

APPLICANT: PATEL, DHAVALKUMAR

APPLICANT: BOWEN, MICHAEL A.

APPLICANT: MARQUARDT, HANS

TITLE OF INVENTION: CD6 LIGAND

NUMBER OF SEQUENCES: 14

## CORRESPONDENCE ADDRESSES:

ADDRESSEE: NIXON &amp; VANDERHYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/684,594

FILING DATE: 18-JUL-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/432,016

FILING DATE: 01-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/333,350  
FILING DATE: 02-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/143,903  
FILING DATE: 02-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 1579-112  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 278 amino acids  
TYPE: amino acid  
STRANDEDNESS: linear  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-684-594-5

Query Match 79.6%; Score 129; DB 2; Length 278;  
Best Local Similarity 100.0%; Pred. No. 8.5e-11;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 IGEPLVLCGAPKPPORLEWK 30  
DB 1 IGEPLVLCGAPKPPORLEWK 23

RESULT 5  
US-08-633-148-18  
Sequence 18, Application US/08633148  
Patent No. 5864018  
GENERAL INFORMATION:  
APPLICANT: MORSE, MICHAEL J.  
APPLICANT: NAGASHIMA, MARIKO  
APPLICANT: HOLLANDER, DORIS A.  
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION  
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP  
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: U.S.A.  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/633,148  
FILING DATE: 16-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY ESO., MATTHEW B.  
REGISTRATION NUMBER: 39,787  
REFERENCE/DOCKET NUMBER: 014618-005600US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
US-08-633-148-18

Query Match 50.0%; Score 81; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.2e-05;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGEPVLKC 16  
DB 1 AONTARIGEPVLKC 16

RESULT 6  
US-08-633-148-12  
Sequence 12, Application US/08633148  
Patent No. 5864018  
GENERAL INFORMATION:  
APPLICANT: MORSE, MICHAEL J.  
APPLICANT: NAGASHIMA, MARIKO  
APPLICANT: HOLLANDER, DORIS A.  
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION  
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP  
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: U.S.A.  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/633,148  
FILING DATE: 16-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY ESO., MATTHEW B.  
REGISTRATION NUMBER: 39,787  
REFERENCE/DOCKET NUMBER: 014618-005600US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-633-148-12

Query Match 44.4%; Score 72; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.00039;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGEPVLK 15  
DB 1 AONTARIGEPVLK 15

RESULT 7  
US-08-633-148-5  
Sequence 5, Application US/08633148  
Patent No. 5864018  
GENERAL INFORMATION:  
APPLICANT: MORSE, MICHAEL J.  
APPLICANT: NAGASHIMA, MARIKO

APPLICANT: HOLLANDER, DORIS A.  
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP  
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: U.S.A.  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/633,148  
FILING DATE: 16-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY ESO., MATTHEW B.  
REGISTRATION NUMBER: 39,787  
REFERENCE/DOCKET NUMBER: 014618-005600US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-633-148-5

Query Match 37.0%; Score 60; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CKGAPKKRPQ 25  
Db 1 CKGAPKKRPQ 10

RESULT 8  
US-08-633-148-13  
Sequence 13, Application US/08633148  
Patent No. 5864018  
GENERAL INFORMATION:  
APPLICANT: MORSE, MICHAEL J.  
APPLICANT: NAGASHIMA, MARIKO  
APPLICANT: HOLLANDER, DORIS A.  
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION  
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USRS THEREFOR  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP  
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: U.S.A.  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/633,148  
FILING DATE: 16-APR-1996  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY ESO., MATTHEW B.  
REGISTRATION NUMBER: 39,787  
REFERENCE/DOCKET NUMBER: 014618-005600US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-633-148-13

Query Match 37.0%; Score 60; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CKGAPKKRPQ 25  
Db 1 CKGAPKKRPQ 10

RESULT 9  
US-08-168-091A-2  
Sequence 2, Application US/08168091A  
Patent No. 5665862  
GENERAL INFORMATION:  
APPLICANT: Fischbach, Gerald.  
APPLICANT: Falls, Douglas R.  
APPLICANT: Rosen, Kenneth M.  
APPLICANT: Corfas, Gabriel  
TITLE OF INVENTION: Neurotrophic Factor  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHYE AND COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/168,091A  
FILING DATE: 15-DEC-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/953,742  
FILING DATE: 29-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: HMI-002CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 602 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-168-091A-2

Query Match 33.3%; Score 54; DB 1; Length 602;



OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/684,594  
FILING DATE: 18-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/432,016  
FILING DATE: 01-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/333,350  
FILING DATE: 02-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/143,903  
FILING DATE: 02-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 1579-112  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 477 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-684-594-3

Query Match 32.7%; Score 53; DB 2; Length 477;  
Best local Similarity 40.0%; Pred. No. 8.5;  
Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

OY 1 AONTARIGEPLVLCGAPKPPQ 25  
DB 221 SOSSTIEGDNVTLKSGNGNPPQ 245

RESULT 13  
US-08-428-926-5  
Sequence 5, Application US/08428926  
Patent No. 5667780  
GENERAL INFORMATION:  
APPLICANT: HO, Wei-Hsien  
APPLICANT: Osheroff, Phyllis L.  
TITLE OF INVENTION: SENSOR AND MOTOR NEURON DERIVED FACTOR (SMDF)  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: palin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/428,926  
FILING DATE: 25-APR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/339517  
FILING DATE: 14-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 00,000  
REFERENCE/DOCKET NUMBER: 853D4

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 602 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-428-926-5

Query Match 32.7%; Score 53; DB 1; Length 602;  
Best local Similarity 32.1%; Pred. No. 11;  
Matches 9; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

OY 2 QNTARIGEPLVLCGAPKPPQRLW 29  
DB 35 KNDVAVGOKLVLCRTTSEYPALRFK 62

RESULT 14  
US-08-428-927-5  
Sequence 5, Application US/08428927  
Patent No. 5756456  
GENERAL INFORMATION:  
APPLICANT: HO, Wei-Hsien  
APPLICANT: Osheroff, Phyllis L.  
TITLE OF INVENTION: SENSOR AND MOTOR NEURON DERIVED FACTOR (SMDF)  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: palin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/428,927  
FILING DATE: 25-APR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/339517  
FILING DATE: 14-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 00,000  
REFERENCE/DOCKET NUMBER: 853D3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 602 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-428-927-5

Query Match 32.7%; Score 53; DB 1; Length 602;  
Best local Similarity 32.1%; Pred. No. 11;  
Matches 9; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

OY 2 QNTARIGEPLVLCGAPKPPQRLW 29  
DB 35 KNDVAVGOKLVLCRTTSEYPALRFK 62

## RESULT 15

US-08-428-298-5

; Sequence 5, Application US/08428298

; Patent No. 5763213

; GENERAL INFORMATION:

; APPLICANT: Ho, Wei-Hsien

; APPLICANT: Osheroff, Phyllis L.

; TITLE OF INVENTION: SENSORY AND MOTOR NEURON DERIVED FACTOR (SMDF)

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/428,298

; FILING DATE: 25-APR-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/339517

; FILING DATE: 14-NOV-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 00,000

; REFERENCE/DOCKET NUMBER: 853D2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 602 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

US-08-428-298-5

Query Match 32.7%; Score 53; DB 1; Length 602;

Best Local Similarity 32.1%; Pred. No. 11;

Matches 9; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 2 ONITARIGEPYVKCKGAPKPPORLEW 29

DB 35 KNOEVAVGOKLVLCETTSEYPALRFRW 62

Search completed: April 24, 2002, 09:18:16  
Job time: 175 sec

**THIS PAGE BLANK (USPTO)**



**THIS PAGE BLANK (USPTO)**

RX MEDLINE-98112489; PubMed-9452110;  
 RA Vils L., Chitayat D., van Camp G., Holden J.J.A., Fransen E.,  
 RA Willems P.J.;  
 RT "Evidence for somatic and germline mosaicism in CRASH syndrome.";  
 RL Hum. Mutat. Suppl. 1:S284-S287(1998).  
 RN [20]  
 RP VARIANTS HSAS/MASA THR-219; ARG-335; CYS-386; CYS-473 AND LEU-1224.  
 RX MEDLINE-98415726; PubMed-9744477;  
 RA Saugier-Veber P., Martin C., le Meur N., Lyonnet S., Munnich A.,  
 RA David A., Henocq A., Heron D., Jouveaux P., Odent S., Manouvrier S.,  
 RA Moncla A., Morichon N., Philip N., Sauge D., Tost M., Frebourg T.;  
 RT "Identification of novel L1CAM mutations using fluorescence-assisted  
 mismatch analysis."; RT  
 RL Hum. Mutat. 12:259-266(1998).  
 CC -1- FUNCTION: CELL ADHESION MOLECULE WITH AN IMPORTANT ROLE IN THE  
 CC DEVELOPMENT OF THE NERVOUS SYSTEM. INVOLVED IN NEURON-NEURON  
 CC ADHESION, NEURITE FASCICULATION, OUTGROWTH OF NEURITES, ETC. BINDS  
 CC TO AXONIN ON NEURONS.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS IN THE CYTOPLASMIC REGION ARE  
 CC PRODUCED BY DIFFERENTIAL SPLICING.  
 CC -1- DISEASE: DEFECTS IN L1CAM ARE THE CAUSE OF THREE X-LINKED  
 CC SYNDROMES. 1: HYDROCEPHALUS OWING TO STENOSIS OF THE AQUEDUCT OF  
 CC SYLVIUS (HSAS) CHARACTERIZED BY MENTAL RETARDATION AND ENLARGED  
 CC BRAIN VENTRICLES. 2: MASA SYNDROME WHICH IS CHARACTERIZED BY  
 CC MENTAL RETARDATION, APHASIA, SHUFFLING GAIT, AND ADDUCTED THUMBS.  
 CC HAS AN OVERLAPPING PROFILE OF CLINICAL SIGNS WITH HSAS, BUT WITH A  
 CC Milder presentation and a longer life expectancy. 3: SPASTIC  
 CC PARAPLEGIA TYPE 1 (SPG1). COLLECTIVELY THESE SYNDROMES ARE ALSO  
 CC KNOWN AS CRASH SYNDROME, AN ACRONYM WHICH STANDS FOR CORPUS  
 CC CALLOSUM HYPOPLASIA, PSYCHOMOTOR RETARDATION, ADDUCTED THUMBS,  
 CC SPASTIC PARAPARESIS, AND HYDROCEPHALUS.  
 CC -1- DISEASE: DEFECTS IN L1CAM ARE THE CAUSE OF HIRSCHSPRUNG DISEASE  
 CC (HSCR).  
 CC -1- SIMILARITY: CONTAINS 6 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- DATABASE: NAME-L1CAM; NOTE-L1CAM mutation web Page:  
 CC WWW="http://hgins.uia.ac.be/dnlab/11".  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; X59847; CAA42508.1; -;  
 DR EMBL; Z29373; CAA82564.1; -;  
 DR EMBL; W74387; AAA59476.1; -;

Query Match 30.9%; Score 50; DB 1; Length 1257;  
 Best Local Similarity 42.9%; Pred. No. 29;  
 Matches 9; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 9 GEPVLCKGAPKPPORLEW 29  
 |||||  
 DB 151 GESVVLPCNPPPSAEPLRIYW 171

Search completed: April 24, 2002, 09:20:40  
 Job time: 254 sec

DT 20-AUG-2001 (rel. 40, Last annotation update)  
 DE NEURAL CELL ADHESION MOLECULE L1 PRECURSOR (N-CAM L1).  
 GN L1CAM OR CAM1 OR MIC5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92031698; PubMed=1932117;  
 RA Kobayashi M., Miura M., Asou H., Uyemura K.;  
 RT "Molecular cloning of cell adhesion molecule L1 from human nervous  
 RT tissue: a comparison of the primary sequences of L1 molecules of  
 RT different origin."  
 RL Biochim. Biophys. Acta 1090:238-240(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Rosenthal A., Coutelle O., Drescher B.;  
 RL Submitted (Apr-1994) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92329299; PubMed=1627459;  
 RA Reid R.A., Hemperly J.J.;  
 RT "Variants of human L1 cell adhesion molecule arise through alternate  
 RT splicing of RNA."  
 RL J. Mol. Neurosci. 3:127-135(1992).  
 RN [4]  
 RP SEQUENCE OF 353-1176 FROM N.A.  
 RX MEDLINE=92020233; PubMed=1923824;  
 RA Rosenthal A., Mackinnon R.N., Jones D.S.C.;  
 RT "PCR walking from microdissection clone M54 identifies three exons  
 RT from the human gene for the neural cell adhesion molecule L1  
 RT (CAM-L1)."  
 RL Nucleic Acids Res. 19:5395-5401(1991).  
 RN [5]  
 RP SEQUENCE OF 332-371 FROM N.A.  
 RX MEDLINE=90353957; PubMed=2387585;  
 RA Djafarzadeh M., Mattei M.-G., Nguyen C., Roux D., Demengeot J.,  
 RA Denizot F., Moos M., Schachner M., Goridis C., Jordan B.R.;  
 RT "The gene encoding L1, a neural adhesion molecule of the  
 RT immunoglobulin family, is located on the X chromosome in mouse and  
 RT man."  
 RL Genomics 7:587-593(1990).  
 RN [6]  
 RP SEQUENCE OF 1030-1257 FROM N.A.  
 RX MEDLINE=91132183; PubMed=1993895;  
 RA Harper J.R., Prince J.T., Healy P.A., Stuart J.K., Nauman S.J.,  
 RA Stallcup W.B.;  
 RT "Isolation and sequence of partial cDNA clones of human L1: homology  
 RT of human and rodent L1 in the cytoplasmic region."  
 RL J. Neurochem. 56:797-804(1991).  
 RN [7]  
 RP SEQUENCE OF 20-36.  
 RX MEDLINE=88298676; PubMed=3136168;  
 RA Wolff J.M., Frank R., Mujoo K., Spiro R.C., Reisfeld R.A.,  
 RA Ratjen F.G.;  
 RT "A human brain glycoprotein related to the mouse cell adhesion  
 RT molecule L1."  
 RL J. Biol. Chem. 263:11943-11947(1988).  
 RN [8]  
 RP VARIANT HSAS TYR-264.  
 RX MEDLINE=94004956; PubMed=8401576;  
 RA Jouet M., Rosenthal A., Macfarlane J., Kenwrick S., Donnai D.;  
 RT "A missense mutation confirms the L1 defect in X-linked hydrocephalus  
 RT (HSAS)."  
 RL Nat. Genet. 4:331-331(1993).  
 RN [9]  
 RP VARIANT HSAS/MASA LEU-1194.  
 RX MEDLINE=95187172; PubMed=781431;  
 RA Fransen E., Schrander-Stumpel C., Vits L., Coucke P., van Camp G.,  
 RA Willems P.J.;  
 RT "X-linked hydrocephalus and MASA syndrome present in one family are  
 RT due to a single missense mutation in exon 28 of the L1CAM gene."

RL Hum. Mol. Genet. 3:2255-2256(1994).  
 RN [10]  
 RP VARIANTS HSAS GLN-184 AND ARG-452, AND VARIANT MASA GLN-210.  
 RX MEDLINE=95004608; PubMed=7920659;  
 RA Jouet M., Rosenthal A., Armstrong G., Macfarlane J., Stevenson R.,  
 RA Paterson J., Metzberg A., Ionescu V., Temple K., Kenwrick S.;  
 RT "X-linked spastic paraplegia (SPG1), MASA syndrome and X-linked  
 RT hydrocephalus result from mutations in the L1 gene."  
 RL Nat. Genet. 7:402-407(1994).  
 RN [11]  
 RP VARIANTS MASA GLN-210 AND ASN-598.  
 RX MEDLINE=95004609; PubMed=7920660;  
 RA Vits L., van Camp G., Coucke P., Fransen E., de Boule K.,  
 RA Reyniers E., Korn B., Poustka A., Wilson G., Schrander-Stumpel C.,  
 RA Winter R.M., Schwartz C., Willems P.J.;  
 RT "MASA syndrome is due to mutations in the neural cell adhesion gene  
 RT L1CAM."  
 RL Nat. Genet. 7:408-413(1994).  
 RN [12]  
 RP VARIANTS HSAS/MASA S-9; S-121; K-309; F-768; L-941 AND C-1070.  
 RX MEDLINE=95282776; PubMed=7765552;  
 RA Jouet M., Moncla A., Paterson J., McKeown C., Fryer A., Carpenter N.,  
 RA Holmberg E., Madellus C., Kenwrick S.;  
 RT "New domains of neural cell-adhesion molecule L1 implicated in  
 RT X-linked hydrocephalus and MASA syndrome."  
 RL Am. J. Hum. Genet. 56:1304-1314(1995).  
 RN [13]  
 RP VARIANTS HSAS/MASA Q-184; Q-210; Y-264; R-452; N-598 AND L-1194.  
 RX MEDLINE=96153146; PubMed=8556302;  
 RA Fransen E., Lemmon V., van Camp G., Vits L., Coucke P., Willems P.J.;  
 RT "CRASH syndrome: clinical spectrum of corpus callosum hypoplasia,  
 RT retardation, adducted thumbs, spastic paraparesis and hydrocephalus  
 RT due to mutations in one single gene, L1."  
 RL Eur. J. Hum. Genet. 3:273-284(1995).  
 RN [14]  
 RP ERRATUM.  
 RA Fransen E., Lemmon V., van Camp G., Vits L., Coucke P., Willems P.J.;  
 RL Eur. J. Hum. Genet. 4:126-126(1996).  
 RN [15]  
 RP VARIANTS HSAS/MASA/SPG1 SER-179 AND ARG-370.  
 RX MEDLINE=96057511; PubMed=7562969;  
 RA Ruiz J.C., Cuppens H., Legius E., Fryns J.-P., Glover T., Marynen P.,  
 RA Cassiman J.-J.;  
 RT "Mutations in L1-CAM in two families with X linked complicated  
 RT spastic paraplegia, MASA syndrome, and HSAS."  
 RL J. Med. Genet. 32:549-552(1995).  
 RN [16]  
 RP VARIANTS HSAS CYS-194 AND LEU-240.  
 RX MEDLINE=97083370; PubMed=8929944;  
 RA Gu S.-M., Orth U., Veeke A., Enders H., Riuender K., Schloesser M.,  
 RA Engel W., Schwinger E., Gal A.;  
 RT "Five novel mutations in the L1CAM gene in families with X linked  
 RT hydrocephalus."  
 RL J. Med. Genet. 33:103-106(1996).  
 RN [17]  
 RP VARIANTS HSAS Q-184; V-439; T-443 DEL; C-784 AND L-936--L-948 DEL.  
 RX MEDLINE=97338664; PubMed=9195224;  
 RA Macfarlane J.R., Du J.-S., Peys M.E., Ramsden S., Donnai D.,  
 RA Charlton R., Garrett C., Toimle J., Yates J.R.W., Berry C., Goudie D.,  
 RA Moncla A., Lunt P., Hodgson S., Jouet M., Kenwrick S.;  
 RT "Nine novel L1 CAM mutations in families with X-linked  
 RT hydrocephalus."  
 RL Hum. Mutat. 9:512-518(1997).  
 RN [18]  
 RP VARIANTS HSAS/MASA ASP-691; ARG-698 AND PRO-935.  
 RX MEDLINE=98180721; PubMed=9521424;  
 RA Du Y.-Z., Srivastava A.K., Schwartz C.E.;  
 RT "Multiple exon screening using restriction endonuclease  
 RT fingerprinting (REF) detection of six novel mutations in the L1 cell  
 RT adhesion molecule (L1CAM) gene."  
 RL Hum. Mutat. 11:222-230(1998).  
 RN [19]  
 RP VARIANT CRASH PRO-632.

```

FT DOMAIN 564 649 IG-LIKE C2-TYPE DOMAIN 6.
FT DOMAIN 681 744 IG-LIKE C2-TYPE DOMAIN 7.
FT DOMAIN 834 1162 PROTEIN KINASE.
FT NP_BIND 840 848 ATP (BY SIMILARITY).
FT BINDING 868 868 ATP (BY SIMILARITY).
FT ACT_SITE 1028 1028 ATP (BY SIMILARITY).
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 245 245 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 318 318 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 374 374 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 511 511 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 580 580 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 619 619 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 631 631 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 675 675 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 704 704 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 721 721 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 1059 1059 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CONFLICT 2 2 O -> E (IN REF. 2).
FT CONFLICT 772 772 A -> T (IN REF. 3).
FT CONFLICT 787 787 R -> G (IN REF. 3).
FT CONFLICT 835 835 K -> N (IN REF. 3).
FT CONFLICT 848 848 V -> E (IN REF. 3).
FT CONFLICT 1347 1347 S -> T (IN REF. 3).
SQ SEQUENCE 1356 AA; 151526 MW; 59E7C44B05CEB83 CRC64;

```

Query Match 31.5%; Score 51; DB 1; Length 1356;  
 Best Local Similarity 34.5%; Pred. No. 22;  
 Matches 10; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

2 ONTARIGEPVLKCKGAPKPPORLEWK 30  
 674 ENOTTISIGSEVSCIASGNPPQIMWFK 702

```

RESULT 14
ID NAH2_HUMAN STANDARD; PRT; 812 AA.
AC Q9UBX0.
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SODIUM/HYDROGEN EXCHANGER 2 (NA(+)/H(+) EXCHANGER 2) (NHE-2).
GN SLC9A2 OR NHE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=99375108; PubMed=10444453;
RA Malakocli J., Dandaj R.Y., Schmidt L., Layden T.J., Dudeja P.K.,
RA Ramaswamy K.;
RT "Molecular cloning, tissue distribution, and functional expression of
RT the human Na(+)/H(+) exchanger NHE2."
RL Am. J. Physiol. 277:G383-G390(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Hou S., Wohldmann P.;
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
CC SODIUM ION CHEMICAL GRADIENT. SEEMS TO PLAY AN IMPORTANT ROLE IN

```

```

CC COLONIC SODIUM ABSORPTION.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- TISSUE SPECIFICITY: EXPRESSED IN SKELETAL MUSCLE, COLON AND
CC KIDNEY. LOWER LEVELS IN THE TESTIS, PROSTATE, OVARY, AND SMALL
CC INTESTINE.
CC -I- PTM: PHOSPHORYLATED (POSSIBLE).
CC -I- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CC -I- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF073299; AAD41635.1; -.
CC EMBL; AC007239; AAF19248.1; -.
CC MIM; 600530; -.
CC DR InterPro: IPR000676; NaH_Exchange.
CC DR Pfam; PF00999; Na_H_Exchange; 1.
CC DR PRINTS; PR01084; NAHEXCHNGR.
CC DR PRINTS; PR01086; NAHEXCHNGR2.
CC DR Transmembrane; Glycoprotein; Sodium transport; Transport; Symport;
CC Multigene family; Phosphorylation.
CC FT DOMAIN 1 13
CC FT DOMAIN 14 33
CC FT DOMAIN 34 79
CC FT DOMAIN 80 100
CC FT DOMAIN 101 106
CC FT TRANSMEM 107 127
CC FT TRANSMEM 128 138
CC FT TRANSMEM 139 159
CC FT TRANSMEM 160 168
CC FT TRANSMEM 169 189
CC FT TRANSMEM 190 208
CC FT TRANSMEM 209 229
CC FT TRANSMEM 230 236
CC FT TRANSMEM 237 257
CC FT TRANSMEM 258 277
CC FT TRANSMEM 278 298
CC FT TRANSMEM 299 307
CC FT TRANSMEM 308 328
CC FT TRANSMEM 329 360
CC FT TRANSMEM 361 381
CC FT TRANSMEM 382 391
CC FT TRANSMEM 392 412
CC FT TRANSMEM 413 429
CC FT TRANSMEM 430 450
CC FT TRANSMEM 451 458
CC FT TRANSMEM 459 479
CC FT TRANSMEM 480 812
CC FT CARBOHYD 350 350
CC FT SEQUENCE 812 AA; 91519 MW; 17EE177DC3830D0A CRC64;

```

Query Match 31.2%; Score 50.5; DB 1; Length 812;  
 Best Local Similarity 34.4%; Pred. No. 16;  
 Matches 11; Conservative 4; Mismatches 6; Indels 11; Gaps 1;

10 EPLVLR-----CKGAPKPPORLEWK 30  
 765 QPLSRDQSGSEREDSLTEGIPKPPRLWVR 796

```

RESULT 15
ID CAML_HUMAN STANDARD; PRT; 1257 AA.
AC P32004;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)

```

|                       |  |           |                         |                         |                                      |
|-----------------------|--|-----------|-------------------------|-------------------------|--------------------------------------|
| FT                    | DOMAIN   | 440       | 503                     |                         | IG-LIKE C2-TYPE DOMAIN 5.            |
| FT                    | DOMAIN   | 531       | 599                     |                         | IG-LIKE C2-TYPE DOMAIN 6.            |
| FT                    | DOMAIN   | 827       | 896                     |                         | FIBRONECTIN TYPE-III 1.              |
| FT                    | DOMAIN   | 932       | 994                     |                         | FIBRONECTIN TYPE-III 2.              |
| FT                    | DOMAIN   | 1032      | 1094                    |                         | FIBRONECTIN TYPE-III 3.              |
| FT                    | SITE   | 553       | 555                     |                         | CELL ATTACHMENT SITE (POTENTIAL).    |
| FT                    | SITE   | 562       | 564                     |                         | CELL ATTACHMENT SITE (POTENTIAL).    |
| FT                    | CARBOHYD   | 100       | 100                     |                         | N-LINKED (GLCNAC . . .) (POTENTIAL). |
| FT                    | CARBOHYD   | 202       | 202                     |                         | N-LINKED (GLCNAC . . .) (POTENTIAL). |
| FT                    | CARBOHYD   | 246       | 246                     |                         | N-LINKED (GLCNAC . . .) (POTENTIAL). |
| FT                    | CARBOHYD   | 293       | 293                     |                         | N-LINKED (GLCNAC . . .) (POTENTIAL). |
| FT                    | CARBOHYD   | 432       | 432                     |                         | N-LINKED (GLCNAC . . .) (POTENTIAL). |
| FT                    | CARBOHYD   | 478       | 478                     |                         | N-LINKED (GLCNAC . . .) (POTENTIAL). |
| FT                    | CARBOHYD   | 489       | 489                     |                         | N-LINKED (GLCNAC . . .) (POTENTIAL). |
| FT                    | CARBOHYD   | 504       | 504                     |                         | N-LINKED (GLCNAC . . .) (POTENTIAL). |
| FT                    | CARBOHYD   | 587       | 587                     |                         | N-LINKED (GLCNAC . . .) (POTENTIAL). |
| FT                    | CARBOHYD   | 670       | 670                     |                         | N-LINKED (GLCNAC . . .) (POTENTIAL). |
| FT                    | CARBOHYD   | 725       | 725                     |                         | N-LINKED (GLCNAC . . .) (POTENTIAL). |
| FT                    | CARBOHYD   | 776       | 776                     |                         | N-LINKED (GLCNAC . . .) (POTENTIAL). |
| FT                    | CARBOHYD   | 824       | 824                     |                         | N-LINKED (GLCNAC . . .) (POTENTIAL). |
| FT                    | CARBOHYD   | 848       | 848                     |                         | N-LINKED (GLCNAC . . .) (POTENTIAL). |
| FT                    | CARBOHYD   | 875       | 875                     |                         | N-LINKED (GLCNAC . . .) (POTENTIAL). |
| FT                    | CARBOHYD   | 968       | 968                     |                         | N-LINKED (GLCNAC . . .) (POTENTIAL). |
| FT                    | CARBOHYD   | 978       | 978                     |                         | N-LINKED (GLCNAC . . .) (POTENTIAL). |
| FT                    | CARBOHYD   | 1022      | 1022                    |                         | N-LINKED (GLCNAC . . .) (POTENTIAL). |
| FT                    | CARBOHYD   | 1030      | 1030                    |                         | N-LINKED (GLCNAC . . .) (POTENTIAL). |
| FT                    | CARBOHYD   | 1073      | 1073                    |                         | N-LINKED (GLCNAC . . .) (POTENTIAL). |
| FT                    | CARBOHYD   | 1107      | 1107                    |                         | N-LINKED (GLCNAC . . .) (POTENTIAL). |
| FT                    | VARSPLIC   | 1180      | 1183                    |                         | MISSING (IN SHORT ISOFORM)           |
| SO                    | SEQUENCE   | 1260 AA;  | 140968 MM;              | 22BE57001CB2A538 CRC64; | (BY SIMILARITY).                     |
| <hr/>                 |  |           |                         |                         |                                      |
| Query Match           |  | 31.5%;    | Score 51;               | DB 1;                   | Length 1260;                         |
| Best Local Similarity |  | 42.9%;    | Pred. No. 21;           |                         |                                      |
| Matches               |  | 9;        | Conservative            | 2;                      | Mismatches 10; Indels 0; Gaps 0;     |
| Oy                    | 9 GEPLVLKCKGAPKKRPQRLW 29  |           |                         |                         |                                      |
|                       | :                  :   |           |                         |                         |                                      |
| Db                    | 150 GESVVLPCNPSPSAAPRIYW 170   |           |                         |                         |                                      |
| <hr/>                 |  |           |                         |                         |                                      |
| RESULT 13             |  |           |                         |                         |                                      |
| ID                    | VRG2_HUMAN   | STANDARD; | PRT:                    | 1356 AA.                |                                      |
| AC                    | P35968;  | O60723;   | Q14178;                 |                         |                                      |
| DT                    | 01-JUN-1994  | (Rel. 29, | Created)                |                         |                                      |
| DT                    | 20-AUG-2001  | (Rel. 40, | Last sequence update)   |                         |                                      |
| DT                    | 20-AUG-2001  | (Rel. 40, | Last annotation update) |                         |                                      |
| DE                    | VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 2 PRECURSOR (EC 2.7.1.112)       |           |                         |                         |                                      |
| DE                    | (VEGFR-2) (KINASE INSERT DOMAIN RECEPTOR) (FLK-1).                           |           |                         |                         |                                      |
| GN                    | KDR OR FLK1.   |           |                         |                         |                                      |
| OS                    | Homo sapiens (Human).  |           |                         |                         |                                      |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;            |           |                         |                         |                                      |
| OC                    | Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.                     |           |                         |                         |                                      |
| OX                    | NCBI_TaxID=9606;   |           |                         |                         |                                      |
| RN                    | [1]  |           |                         |                         |                                      |
| RN                    | SEQUENCE FROM N.A.   |           |                         |                         |                                      |
| RA                    | Yin L.Y., Wu Y., Patterson C.;   |           |                         |                         |                                      |
| RT                    | "Full length human KDR/Flk-1 sequence."                                      |           |                         |                         |                                      |
| RL                    | Submitted (Dec-1997) to the EMBL/GenBank/DBJ databases.                      |           |                         |                         |                                      |
| RP                    | SEQUENCE FROM N.A.   |           |                         |                         |                                      |
| RC                    | TISSUE=umbilical vein;   |           |                         |                         |                                      |
| RA                    | Yu Y., Whitney R.G., Sato J.D.;  |           |                         |                         |                                      |
| RT                    | "Coding region for human VEGF receptor KDR (VEGFR-2)."                       |           |                         |                         |                                      |
| RL                    | Submitted (May-1998) to the EMBL/GenBank/DBJ databases.                      |           |                         |                         |                                      |
| RN                    | [3]  |           |                         |                         |                                      |
| RP                    | SEQUENCE OF 3-1356 FROM N.A.   |           |                         |                         |                                      |
| RC                    | TISSUE=umbilical vein;   |           |                         |                         |                                      |
| RX                    | MEDLINE=92019839; PubMed=1656371;  |           |                         |                         |                                      |
| RA                    | Terman B.L., Carrion M.E., Kovacs E., Rasmussen B.A., Eddy R.L., Shows T.B.; |           |                         |                         |                                      |

```

RT      "Identification of a new endothelial cell growth factor receptor
RL      tyrosine kinase."
RN      Oncogene 6:1677-1683(1991).
RN      [4]
RN      SEQUENCE OF 1-22 FROM N.A.
RX      MEDLINE=96033749; PubMed=7559454;
RA      Patterson C., Perrella M.A., Hsieh C.M., Yoshizumi M., Lee M.E.,
RA      Harder E.;
RT      "Cloning and functional analysis of the promoter for KDR/flk-1, a
RT      receptor for vascular endothelial growth factor.";
RL      J. Biol. Chem. 270:23111-23118(1995).
RN      [5]
RP      FUNCTION
RX      MEDLINE=93038639; PubMed=1417831;
RA      Terman B.I., Dougher-Vermazen M., Carrion M.E., Dimitrov D.,
RA      Armellino D.C., Gospodarowicz D., Boehlen P.;
RT      "Identification of the KDR tyrosine kinase as a receptor for vascular
RT      endothelial cell growth factor.";
RL      Biochem. Biophys. Res. Commun. 187:1579-1586(1992).
CC      -1- FUNCTION: RECEPTOR FOR VEGF OR VEGF-C. HAS A TYROSINE-PROTEIN
CC      KINASE ACTIVITY. THE VEGF-KINASE LIGAND/RECEPTOR SIGNALING SYSTEM
CC      PLAYS A KEY ROLE IN VASCULAR DEVELOPMENT AND REGULATION OF
CC      VASCULAR PERMEABILITY.
CC      -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC      TYROSINE PHOSPHATE
CC      -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC      -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC      PROTEIN KINASES.
CC      -1- SIMILARITY: CONTAINS 7 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb.ch/announce/
CC      or send an email to license@isb.slb.ch).
CC      -----
DR      EMBL, AF035121; AAB88005.1; -
DR      EMBL, AF063658; AAC16450.1; -
DR      EMBL, X61656; CAA43837.1; -
DR      EMBL, L04947; AAA59459.1; -
DR      EMBL, X89776; CAA61916.1; -
DR      HSSP, P11362; IAGW.
DR      MIM, 191306; -
DR      InterPro: IPR000719; Euk_Pkinase.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003598; Ig_C2.
DR      InterPro: IPR003600; Ig_Like.
DR      InterPro: IPR001824; Rptor_Tyr_kin_III.
DR      InterPro: IPR001245; Tyr_kin.
DR      Pfam: PF00047; Ig_6.
DR      Pfam: PF00069; Pkinase_2.
DR      SMART: SM00408; IgC2_2.
DR      SMART: SM00410; Ig_Like; 4.
DR      SMART: SM00219; TyKc; 1.
DR      PROSITE: PS00107; PROTEIN_KINASE_ATP_FALSE_NEG.
DR      PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
DR      PROSITE: PS00240; RECEPTOR_TYR_KIN_III; 1.
DR      PROSITE: PS50011; PROTEIN_KINASE_DOM_1.
KW      Signal, transferase, tyrosine-protein kinase; Receptor; Transmembrane;
KW      Glycoprotein; Phosphorylation; ATP-binding; Immunoglobulin domain.
FT      SIGNAL 1 19
FT      CHAIN 20 1356
FT      VASCULAR ENDOTHELIAL GROWTH FACTOR
FT      RECEPTOR 2.
FT      DOMAIN 20 764
FT      TRANSMEM 765 789
FT      TRANSMEM POTENTIAL.
FT      CYTOPLASMIC (POTENTIAL).
FT      DOMAIN 790 1356
FT      IG-LIKE C2-TYPE DOMAIN 1.
FT      DOMAIN 141 207
FT      IG-LIKE C2-TYPE DOMAIN 2.
FT      DOMAIN 239 314
FT      IG-LIKE C2-TYPE DOMAIN 3.
FT      DOMAIN 345 400
FT      IG-LIKE C2-TYPE DOMAIN 4.
FT      DOMAIN 438 537
FT      IG-LIKE C2-TYPE DOMAIN 5.

```

|    |  |
|----|--|
| CC | TISSUE=Mammary gland;  |
| RX | MEDLINE=96069604; PubMed=7590352;  |
| RA | Verbeet M.P., Vermeer H., Wamestam G.C., de Boer H.A., Lee S.H.;           |
| RT | "Cloning and characterization of the bovine polymeric immunoglobulin       |
| RL | receptor-encoding cDNA.";  |
| CC | Gene 164:329-333(1995).  |
| CC | -1 FUNCTION: THIS RECEPTOR BINDS POLYMERIC IGA AND IGM AT THE              |
| CC | BASOLATERAL SURFACE OF EPITHELIAL CELLS. THE COMPLEX IS THEN               |
| CC | TRANSPORTED ACROSS THE CELL TO BE SECRETED AT THE APICAL SURFACE.          |
| CC | DURING THIS PROCESS A CLEAVAGE OCCURS THAT SEPARATE THE                    |
| CC | EXTRACELLULAR (KNOWN AS THE SECRETORY COMPONENT) FROM THE                  |
| CC | TRANSMEMBRANE SEGMENT.   |
| CC | -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALSO SECRETED.           |
| CC | -1 ALTERNATIVE PRODUCTS: 2 ISOFORMS. A LONG FORM (SHOWN HERE) AND A        |
| CC | SHORT FORM. ARE PRODUCED BY ALTERNATIVE SPLICING.                          |
| CC | -1 TISSUE SPECIFICITY: FOUND IN MAMMARY GLAND, JEJUNUM, LUNG,              |
| CC | KIDNEY AND SMALL INTESTINE.  |
| CC | -1 PTM: IN THE ABSENCE OF DIMERIC IGA, SER-727 IS PHOSPHORYLATED           |
| CC | WHICH ALLOWS PIGR TO FUNCTION NORMALLY.                                    |
| CC | -1 SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.              |
| CC | -----  |
| CC | This SWISS-PROT entry is copyright. It is produced through a collaboration |
| CC | between the Swiss Institute of Bioinformatics and the EMBL outstation -    |
| CC | the European Bioinformatics Institute. There are no restrictions on its    |
| CC | use by non-profit institutions as long as its content is in no way         |
| CC | modified and this statement is not removed. Usage by and for commercial    |
| CC | entities requires a license agreement (See http://www.isb-slb.ch/announce/ |
| CC | or send an email to license@isb-slb.ch)                                    |
| CC | -----  |
| DR | EMBL; L04797; AAC41620.1; -;   |
| DR | EMBL; X81371; CA57136.1; -;  |
| DR | InterPro; IPRO03599; Ig.   |
| DR | InterPro; IPRO03006; Ig_MHC.   |
| DR | InterPro; IPRO03600; Ig_Like.  |
| DR | Pfam; PF00047; Ig_5.   |
| DR | SMART; SM00409; Ig_4.  |
| DR | SMART; SM00410; IG_Like; 1.  |
| KW | Immunoglobulin domain; Repeat; Transmembrane; Glycoprotein; Signal;        |
| KW | Polymorphism; Phosphorylation; Alternative splicing.                       |
| FT | SIGNAL 1 18  |
| FT | CHAIN 19 757   |
| FT | CHAIN 19 599   |
| FT | DOMAIN 19 632  |
| FT | DOMAIN 633 653   |
| FT | TRANSMEM 654 757   |
| FT | DOMAIN 19 132  |
| FT | DOMAIN 133 238   |
| FT | DOMAIN 239 350   |
| FT | DOMAIN 351 462   |
| FT | DOMAIN 463 575   |
| FT | DISULFID 40 110  |
| FT | DISULFID 56 64   |
| FT | DISULFID 152 220   |
| FT | DISULFID 257 324   |
| FT | DISULFID 271 279   |
| FT | DISULFID 370 440   |
| FT | DISULFID 384 394   |
| FT | DISULFID 481 543   |
| FT | DISULFID 485 519   |
| FT | DISULFID 495 502   |
| FT | CARBOHYD 83 83   |
| FT | CARBOHYD 420 420   |
| FT | CARBOHYD 468 468   |
| FT | MOD_RES 727 727  |
| FT | VARSPLIC 129 346   |
| FT | VARIANT 29 29  |
| FT | VARIANT 142 142  |
| FT | VARIANT 404 404  |
| FT | VARIANT 413 413  |
| FT | VARIANT 435 435  |
| FT | VARIANT 435 435  |
| FO | SEQUENCE 757 AA: 82434 MW: DECD67FDD06A6E6C6 CRC64;                        |
|    | T -> A.  |

[illegible]



EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR FORM.

-1- PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTEOLYTIC CLEAVAGE (BY SIMILARITY).

-1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

-1- SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.

-----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC

DR EMBL: L11264; AAA49037.1; -

DR EMBL: AF045654; AAC05670.1; -

DR EMBL: AF045655; AAC05671.1; -

DR EMBL: AF045656; AAC05672.1; -

DR HSP: C02297; 1HRF.

DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR003006; Ig\_MHC.

DR InterPro: IPR003598; Ig\_C2.

DR Pfam: PF0047; Ig\_1.

DR Pfam: PF02158; Neuregulin; 1.

DR PRINTS: PR01089; NEUREGULIN.

DR SMART: SM00181; EGF; 1.

DR SMART: SM00408; IgC2; 1.

DR PROSITE: PS00022; EGF\_1; 1.

DR PROSITE: PS01186; EGF\_2; FALSE\_NEG.

KW Growth factor; EGF-like domain; Immunoglobulin domain; Glycoprotein; Transmembrane; Alternative splicing.

FT CHAIN 1 602

FT DOMAIN 1 205

FT TRANSMEM 207 229

FT DOMAIN 230 602

FT DOMAIN 425 442

FT DOMAIN 125 136

FT DOMAIN 137 181

FT DISULFID 49 105

FT DISULFID 141 155

FT DISULFID 149 169

FT DISULFID 171 180

FT CARBOHYD 21 21

FT CARBOHYD 113 113

FT CARBOHYD 126 126

FT VARSPLIC 1 127

PRO-NEUREGULIN-1, MEMBRANE-BOUND FORM.

NEUREGULIN-1.

EXTRACELLULAR (POTENTIAL).

INTERNAL SIGNAL SEQUENCE (POTENTIAL).

CYTOSOLASMIC (POTENTIAL).

IG-LIKE C2-TYPE DOMAIN.

SER/THR-RICH.

EGF-LIKE.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

MMATSEGLPGLYSLAPOTDVNSYNSYVPPKLNKMEKNOEYAV

GOKLVRCETSEYPLARKMLKNGKEITKKNRENVKIPK

KOKKXSELIYRATTLADAGEACRVSCKGNDSTKSVIT

DTNA -> MSEGTEFPSPSADSPDASIGGLPAENMG

PHREDSRVGVAGLSTCCVCEAEKLGKLNSEKICIAPI

LACLLSLICLIGLKWFDYDKIFEYSPHLDGRIQOPR

STVDPTALSAWPEYVAYPPIPSLESAEYVVDSSIV

PSRPELOPSLYNRILIDVGMASATPISPSLEPTASAO

ARETNLOTPKIS (IN ISOFORM BETA1A, ISOFORM

BETA2A AND ISOFORM BETA2B).

MISSING (IN ISOFORM BETA2A AND ISOFORM

BETA2B).

VASMTTPARMSPVDFHTP -> HTPPTSLLAGKVSILRVS

(IN ISOFORM BETA2B).

MISSING (IN ISOFORM BETA2B).

FT VARSPLIC 388 405

FT VARSPLIC 406 602

FT VARSPLIC 602 AA; 67453 MW; 4183056565346 CRC64;

FT SEQUENCE

Query Match 32.7%; Score 53; DB 1; Length 602;

Best Local Similarity 32.1%; Pred. No. 5.2; Mismatches 0; Gaps 0;

Matches 9; Conservative 7; Indels 0; Gaps 0;

2 ONTARIGEPLVLCCKGAPKPPORLEW 29

DB 35 KNOEAVGOKLVLCRCETTSXPALRFKW 62

RESULT 9

VEJA\_HUMAN STANDARD; PRT; 298 AA.

AC P57087;

DT 20-AUG-2001 (Rel. 40, Created)

DT 20-AUG-2001 (Rel. 40, Last sequence update)

DE 20-AUG-2001 (Rel. 40, Last annotation update)

DE VASCULAR ENDOTHELIAL JUNCTION-ASSOCIATED MOLECULE PRECURSOR (VE-JM).

GN C21ORF43.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eulalia; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxID=9606;

RP [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Vascular endothelial cells;

RX MEDLINE=20317114; PubMed=10779521;

RA Palmeri D., van Zante A., Huang C.C., Hemmerlich S., Rosen S.D.;

RT "Vascular endothelial junction-associated molecule, a novel member of the immunoglobulin superfamily, is localized to intercellular boundaries of endothelial cells."

RT J. Biol. Chem. 275:19139-19145(2000).

RL J. Biol. Chem. 275:19139-19145(2000).

CC -1- FUNCTION: MAY PLAY A ROLE IN THE PROCESSES OF LYMPHOCYTE HOMING TO SECONDARY LYMPHOID ORGANS.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).

CC -1- TISSUE SPECIFICITY: PROMINENTLY EXPRESSED ON HIGH ENDOTHELIAL VENULES BUT IS ALSO PRESENT ON THE ENDOTHELIA OF OTHER VESSELS.

CC LOCALIZED TO THE INTERCELLULAR BOUNDARIES OF HIGH ENDOTHELIAL CELLS.

CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

-----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC

DR EMBL: AF255910; AAF81223.1; -

DR InterPro: IPR003006; Ig\_MHC.

DR InterPro: IPR003598; Ig\_C2.

DR InterPro: IPR003600; Ig\_Like.

DR Pfam: PF0047; Ig; 2.

DR SMART: SM00408; IgC2; 1.

DR SMART: SM00410; Ig\_Like; 1.

KW Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 20

FT CHAIN 21 298

FT DOMAIN 21 238

FT TRANSMEM 239 259

FT DOMAIN 260 298

FT DOMAIN 43 116

FT DOMAIN 148 221

FT DISULFID 50 109

FT DISULFID 155 214

FT CARBOHYD 98 98

FT CARBOHYD 187 187

FT CARBOHYD 236 236

FT SEQUENCE 298 AA; 33207 MW; CA78518E22DCABE CRC64;

VASCULAR ENDOTHELIAL JUNCTION-ASSOCIATED MOLECULE.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOSOLASMIC (POTENTIAL).

IG-LIKE V-TYPE DOMAIN.

IG-LIKE C2-TYPE DOMAIN.

POTENTIAL.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 32.1%; Score 52; DB 1; Length 298;

Best Local Similarity 41.4%; Pred. No. 3.6; Mismatches 14; Indels 0; Gaps 0;

Matches 12; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

2 ONTARIGEPLVLCCKGAPKPPORLEW 30



[illegible]

```

FT CONFLICT 112 113 SD -> RH (IN REF. 3).
FT CONFLICT 329 329 A -> T (IN REF. 2).
FT CONFLICT 401 402 LQ -> HK (IN REF. 2).
SQ SEQUENCE 588 AA; 65726 MW; 2A28612D0164531E CRC64;

Query Match 32.7%, Score 53; DB 1; Length 588;
Best Local Similarity 40.0%; Pred. No. 5.1;
Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

OY 1 AONTARIGEPYLKCKGPKKPPQ 25
DB 261 SOSSTIKEDNVTLKCSGNGNPPQ 285

      1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25
RESULT 8
NRG1_CHICK STANDARD; PRT; 602 AA.
ID NRG1_CHICK
AC 005199; 073750; 073751; 073752;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PRO-NEUREGULIN-1 PRECURSOR (PRO-NRG1) [CONTAINS: NEUREGULIN-1
DE (ACETYLCHOLINE RECEPTOR INDUCING ACTIVITY) (ARIA)].
GN NRG1 OR ARIA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxId=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ARIA), AND PARTIAL SEQUENCE.
RC STRAIN=WHITE LECHORN; TISSUE=Brain;
RX MEDLINE=93201602; PubMed=8453670;
RA Falls D.L., Rosen K.M., Corfas G., Lane W.S., Fischbach G.D.;
RT "ARIA, a protein that stimulates acetylcholine receptor synthesis, is
RT a member of the neu ligand family.";
RL Cell 72:801-815(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS BETA1A; BETA2A AND BETA2B).
RC TISSUE=Brain, and Spinal cord;
RX MEDLINE=98150951; PubMed=9491987;
RA Yang X., Kuo Y., Deway P., Yu C., Role L.;
RT "A cysteine-rich isoform of neuroligin controls the level of
RT expression of neuronal nicotinic receptor channels during
RT synaptogenesis.";
RL Neuron 20:255-270(1998).
CC -I- FUNCTION: DIRECT LIGAND FOR THE ERBB TYROSINE KINASE RECEPTORS.
CC THE MULTIPLE ISOFORMS PERFORM DIVERSE FUNCTIONS: CYSTEINE-RICH
CC DOMAIN CONTAINING ISOFORMS (CRD-NRG) PROBABLY REGULATE THE
CC EXPRESSION OF NICOTINIC ACETYLCHOLINE RECEPTORS AT DEVELOPING
CC INTERNEURONAL SYNAPSES. THE IG-NRG ISOFORM IS REQUIRED FOR THE
CC INITIAL INDUCTION AND/OR MAINTENANCE OF THE MATURE LEVELS OF
CC ACETYLCHOLINE RECEPTORS AT NEUROMUSCULAR SYNAPSES.
CC -I- SUBCELLULAR LOCATION: EXISTS AS A TYPE I MEMBRANE PROTEIN AND AS A
CC PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE MEMBRANE-
CC BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).
CC -I- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS: ARIA/IG-NRG (SHOWN
CC HERE), CRD-NRG-BETA1A, CRD-NRG-BETA2A AND CRD-NRG-BETA2B; ARE
CC PRODUCED BY ALTERNATIVE SPLICING. ARIA CONTAINS AN IG-LIKE DOMAIN,
CC WHEREAS IN THE CRD-NRG (OR NARIA) ISOFORMS, THE EGF-LIKE DOMAIN IS
CC REPLACED BY A CYSTEINE-RICH DOMAIN (CRD).
CC -I- DEVELOPMENTAL STAGE: CRD-NRG ISOFORM IS DETECTED AT EMBRYONIC DAY
CC 4 (Ed4) IN BOTH VISCERAL AND SOMATIC MOTOR NEURONS OF SPINAL CORD
CC AND IS HIGHEST AT ED 6. IG-NRG ISOFORM IS NOT EXPRESSED UNTIL ED 6
CC IN SPINAL CORD. AT ED 11 BOTH ISOFORMS DISPLAY COMPARABLE LEVELS.
CC -I- DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION
CC OF TRAFFICKING AND PROTEOLYTIC PROCESSING. REGULATION OF THE
CC PROTEOLYTIC PROCESSING INVOLVES INITIAL INTRACELLULAR DOMAIN
CC DIMERIZATION (BY SIMILARITY).
CC -I- DOMAIN: ERBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE
CC DOMAIN.
CC -I- PTM: PROTEOLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE

```

FT DISULFID 1718 1766 BY SIMILARITY.  
 FT DISULFID 1813 1860 BY SIMILARITY.  
 FT DISULFID 1906 1953 BY SIMILARITY.  
 FT DISULFID 1997 2052 BY SIMILARITY.  
 FT DISULFID 2098 2146 BY SIMILARITY.  
 FT DISULFID 2194 2241 BY SIMILARITY.  
 FT DISULFID 2283 2328 BY SIMILARITY.  
 FT DISULFID 2373 2419 BY SIMILARITY.  
 FT CARBOHYD 1421 1421 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 2481 AA; 270812 MW; E47FBE2B310F5031 CRC64;

Query Match 39.5%; Score 64; DB 1; Length 2481;  
 Best Local Similarity 50.0%; Pred. No. 0.59;  
 Matches 12; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

OY 8 IGEPLVKCK--GAPKKPQRLM 29  
 Db 1989 VGEPLVKCEAFGAPDPEPEVM 2012

RESULT 6  
 FVB\_MOUSE STANDARD; PRT; 819 AA.  
 AC 035601; Q9Z2H3;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DE FYN-BINDING PROTEIN (FYN-T-BINDING PROTEIN) (FVB-120/130) (P120/P130)  
 DE (SLP-76 ASSOCIATED PHOSPHOPROTEIN) (SLAP-130).  
 GN FVB.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM FVB-120).  
 RC TISSUE=T-cell lymphoma;  
 RX MEDLINE=97352826; PubMed=9207119;  
 RA da Silva A.J., Li Z., de Vera C., Canto E., Findell P., Rudd C.E.;  
 RT "Cloning of a novel T-cell protein FVB that binds FYN and SH2 domain-  
 RT containing leukocyte protein 76 and modulates Interleukin 2  
 RT production.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 94:7493-7498(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM FVB-130).  
 RC TISSUE=Hybridoma;  
 RX MEDLINE=99428514; PubMed=10497204;  
 RA Veale M., Raab M., Li Z., da Silva A.J., Kraeft S.-K., Wieremowicz S.,  
 RA Morton C.C., Rudd C.E.;  
 RT "Novel isoform of lymphoid adaptor FYN-T-binding protein (FVB-130)  
 RT interacts with SLP-76 and up-regulates Interleukin 2 production.";  
 RT J. Biol. Chem. 274:28427-28435(1999).  
 CC -1- FUNCTION: ACTS AS A ADAPTER PROTEIN OF THE FYN AND SH2-DOMAIN-  
 CC CONTAINING LEUCOCYTE PROTEIN-76 (SLP76) SIGNALING CASCADES IN T  
 CC CELLS. MODULATES THE EXPRESSION OF INTERLEUKIN-2 (IL-2).  
 CC -1- SUBUNIT: INTERACTS WITH FYN AND SLP76.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, FVB-130 (SHOWN HERE) AND FVB-  
 CC 120. ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEMATOPOIETIC TISSUES SUCH AS  
 CC MYELOID AND T CELLS, SPLEEN AND THYMUS. NOT EXPRESSED IN B CELLS,  
 CC NOR IN NON-LYMPHOID TISSUES. FVB-130 IS PREFERENTIALLY EXPRESSED  
 CC IN MATURE T-CELLS COMPARED TO FVB-120. WHEREAS THYMOCYTES SHOWED A  
 CC GREATER RELATIVE AMOUNT OF FVB-120.  
 CC -1- PTM: T-CELL RECEPTOR LIGATION LEADS TO INCREASED TYROSINE  
 CC PHOSPHORYLATION.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb.ch/announce/>  
 CC or send an email to [license@isb.ch](mailto:license@isb.ch)).  
 CC -----  
 DR EMBL: AF001863; AAB62227.1; -  
 DR EMBL: AF061744; AAD03267.1; -  
 DR WGD; MG1:1346327; Fyb.  
 DR InterPro: IPR002965; P-rtch\_extensn.  
 DR InterPro: IPR001452; SH3.  
 DR Pfam: PF00018; SH3; 1.  
 DR PRINTS: PR01217; PRICEXTENSN.  
 DR SMART: SM00326; SH3; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW SH3 domain; Phosphorylation; Nuclear protein; Coiled coil;  
 KW Alternative splicing.  
 FT DOMAIN 343 348 POLY-PRO.  
 FT DOMAIN 381 385 POLY-PRO.  
 FT DOMAIN 448 495 COILED COIL (POTENTIAL).  
 FT DOMAIN 479 493 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT DOMAIN 584 587 SH2-BINDING (TO SLP-76).  
 FT DOMAIN 606 609 POLY-PRO.  
 FT DOMAIN 615 618 SH2-BINDING (TO FYN).  
 FT DOMAIN 622 625 POLY-ASP.  
 FT DOMAIN 696 699 POLY-PRO.  
 FT DOMAIN 699 756 SH3.  
 FT DOMAIN 710 736 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
 FT DOMAIN 739 805 SH3-LIKE.  
 FT VARSPLIC 627 672 MISSING (IN ISOFORM FVB-120).  
 SQ SEQUENCE 819 AA; 90055 MW; 6222CC7E1CA2BBD CRC64;

Query Match 34.6%; Score 56; DB 1; Length 819;  
 Best Local Similarity 44.4%; Pred. No. 2.6;  
 Matches 12; Conservative 6; Mismatches 7; Indels 2; Gaps 1;

OY 1 AQNTARIGEPLVL--KCKGAPKKRPQ 25  
 Db 213 SKNPVQKSPVQKAGSKGAPFKPK 239

RESULT 7  
 C166\_CHICK STANDARD; PRT; 588 AA.  
 ID C166\_CHICK  
 AC P42292;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE C166 ANTIGEN PRECURSOR (SCI GLYCOPROTEIN) (BEN GLYCOPROTEIN) (DM-  
 DE GRASP PROTEIN) (JC7 PROTEIN).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 34-53.  
 RC TISSUE=Embryo;  
 RX MEDLINE=92030150; PubMed=1931049;  
 RA Tanaka H., Matsui T., Agata A., Tomura M., Kubota I.,  
 RA McFarland K.C., Kohr B., Lee A., Phillips H.S., Shelton D.L.;  
 RT "Molecular cloning and expression of a novel adhesion molecule, SCI.";  
 RT Neuron 7:535-545(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91337449; PubMed=1873027;  
 RA Burns F.R., von Kannen S., Guy L., Raper J.A., Kamholz J.,  
 RA Chang S.;  
 RT "DM-GRASP, a novel immunoglobulin superfamily axonal surface protein  
 RT that supports neurite extension.";  
 RT Neuron 7:209-220(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 34-52; 87-93; 504-512 AND 569-582.  
 RC TISSUE=Bursa of fabricius;



Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 QNTARIGELVLCCKGAPKPPQPLEWK 30  
 |||||  
 DB 24 QNTARIGELVLCCKGAPKPPQPLEWK 52

RESULT 3  
 RAGE\_BOVIN  
 ID RAGE\_BOVIN STANDARD; PRT; 416 AA.  
 AC 028173;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR  
 DE (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).  
 GN AGER OR RAGE.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Lung;  
 RX MEDLINE=92340547; PubMed=1378843;  
 RA Neepser M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,  
 RA Elliston K., Stern D., Shaw A.;  
 RT "Cloning and expression of a cell surface receptor for advanced  
 RT glycosylation end products of proteins."  
 RL J. Biol. Chem. 267:14998-15004(1992).  
 CC -1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END  
 CC PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS  
 CC WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED  
 CC RATE IN DIABETES.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.  
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS  
 CC 2 C2-LIKE AND ONE V-LIKE DOMAINS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: M91212; AAA03575.1; -  
 CC InterPro: IPR003006; Iq\_MHC.  
 CC InterPro: IPR003598; Iq\_C2.  
 CC InterPro: IPR003600; Iq\_Like.  
 CC Pfam: PF00047; Iq\_2.  
 CC SMART: SM00408; IqC2; 1.  
 CC SMART: SM00410; Iq\_Like; 1.  
 CC PROSITE: PS00290; Iq\_MHC; 1.  
 CC Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.  
 FT SIGNAL 1 22  
 FT CHAIN 23 416  
 FT DOMAIN 23 352 ADVANCED GLYCOSYLATION END PRODUCT-  
 FT TRANSMEM SPECIFIC RECEPTOR.  
 FT TRASMEM 353 373 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 374 416 POTENTIAL.  
 FT DOMAIN 31 105 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 136 213 IG-LIKE V-TYPE DOMAIN 1.  
 FT DOMAIN 262 318 IG-LIKE C2-TYPE DOMAIN 1.  
 FT DISULFID 38 98 IG-LIKE C2-TYPE DOMAIN 2.  
 FT DISULFID 143 207 POTENTIAL.  
 FT DISULFID 269 311 POTENTIAL.  
 FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT DOMAIN 391 396 POLY-GLU.  
 FT SEQUENCE 416 AA; 44182 MW; B70381573E767AE CRC64;

Query Match 89.5%; Score 145; DB 1; Length 416;  
 Best Local Similarity 89.7%; Pred: No. 3.5e-13;  
 Matches 26; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 QNTARIGELVLCCKGAPKPPQPLEWK 30  
 |||||  
 DB 24 QNTARIGELVLCCKGAPKPPQPLEWK 52

RESULT 4  
 RAGE\_RAT  
 ID RAGE\_RAT STANDARD; PRT; 402 AA.  
 AC 063495;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR  
 DE (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).  
 GN AGER OR RAGE.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Lung;  
 RX MEDLINE=97368045; PubMed=9224812;  
 RA Renard C., Chappey O., Wautier M.P., Nagashima M., Lunsh E.,  
 RA Morser J., Zhao L., Schmidt A.M., Schermann J.M., Wautier J.L.;  
 RT "Recombinant advanced glycation end product receptor pharmacokinetics  
 RT in normal and diabetic rats."  
 RL Mol. Pharmacol. 52:54-62(1997).  
 CC -1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END  
 CC PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS  
 CC WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED  
 CC RATE IN DIABETES.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.  
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS  
 CC 2 C2-LIKE AND ONE V-LIKE DOMAINS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: L33413; AAA42027.1; -  
 CC InterPro: IPR003006; Iq\_MHC.  
 CC InterPro: IPR003598; Iq\_C2.  
 CC InterPro: IPR003600; Iq\_Like.  
 CC Pfam: PF00047; Iq\_3.  
 CC SMART: SM00408; IqC2; 1.  
 CC SMART: SM00410; Iq\_Like; 1.  
 CC PROSITE: PS00290; Iq\_MHC; 1.  
 CC Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.  
 FT SIGNAL 1 22  
 FT CHAIN 23 402  
 FT DOMAIN 23 341 POTENTIAL.  
 FT TRANSMEM 342 362 ADVANCED GLYCOSYLATION END PRODUCT-  
 FT TRASMEM 363 402 SPECIFIC RECEPTOR.  
 FT DOMAIN 31 105 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 136 213 POTENTIAL.  
 FT DISULFID 250 306 IG-LIKE V-TYPE DOMAIN 1.  
 FT DISULFID 38 98 IG-LIKE C2-TYPE DOMAIN 1.  
 FT DISULFID 143 206 IG-LIKE C2-TYPE DOMAIN 2.  
 FT CARBOHYD 257 299 POTENTIAL.  
 FT SEQUENCE 402 AA; 44182 MW; B70381573E767AE CRC64;

RA Hudson B.I., Puters T.S.;  
 RT "Novel polymorphisms in the receptor for advanced glycation  
 end-products (RAGE) gene."  
 RL Submitted (NOV-1999) to the EMBL/Genbank/DBS databases.  
 CC - FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END  
 CC PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS  
 CC WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED  
 CC RATE IN DIABETES.  
 CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1) AND  
 CC SECRETED (ISOFORM 2).  
 CC - ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2/RAGESEC;  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC - TISSUE SPECIFICITY: ENDOTHELIAL CELLS.  
 CC - SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS  
 CC 2 C2-LIKE AND ONE V-LIKE DOMAINS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: M91211; AAA03574.1; -  
 CC EMBL: D28769; BAA05958.1; -  
 CC EMBL: U89336; BAA7491.1; -  
 CC EMBL: AB036432; BAA89369.1; -  
 CC EMBL: AJ133822; CAB43108.1; -  
 CC EMBL: AF208289; AAG35728.1; -  
 CC MIM: 600214; -  
 CC InterPro: IPR003006; Ig\_MHC.  
 CC InterPro: IPR003598; Ig\_C2.  
 CC InterPro: IPR003600; Ig\_Like.  
 CC Pfam: PF00047; Ig\_2.  
 CC SMART: SM00408; IgC2; 1.  
 CC SMART: SM00410; Ig\_Like; 1.  
 CC DR Immunoglobulin domain; Glycoprotein; Transmembrane; Signal;  
 CC KW Alternative splicing; Polymorphism.  
 CC FT SIGNAL 1 22  
 CC CHAIN 23 404  
 CC FT DOMAIN 23 342  
 CC FT TRANSMEM 343 363  
 CC FT DOMAIN 364 404  
 CC FT DOMAIN 31 106  
 CC FT DOMAIN 137 214  
 CC FT DOMAIN 252 308  
 CC FT DISULFID 38 99  
 CC FT DISULFID 144 208  
 CC FT DISULFID 259 301  
 CC FT CARBOHYD 25 25  
 CC FT CARBOHYD 81 81  
 CC FT DOMAIN 384 384  
 CC FT VARSPLIC 54 67  
 CC VARSPLIC 275 404  
 CC FT VARIANT 100 100  
 CC FT CONFLICT 1 1  
 CC SEQUENCE 404 AA; 42802 MW; 0D584C436C30CE7 CRC64;  
 CC  
 CC Query Match 100.0%; Score 162; DB 1; Length 404;  
 CC Best Local Similarity 100.0%; Pred. No. 1.3e-15;  
 CC Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC 1 AONTARIGEPVLVKCKGAPKPPORLEWK 30

DB 23 AONTARIGEPVLVKCKGAPKPPORLEWK 52  
 RESULT 2  
 RAGE\_MOUSE  
 ID RAGE\_MOUSE STANDARD; PRT; 403 AA.  
 AC 062151;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR  
 DE (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).  
 GN AGER OR RAGE.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C; TISSUE=Lung;  
 RX MEDLINE=97368045; PubMed=9224812;  
 RA Renard C., Chappey O., Mautier M.P., Nagashima M., Lunn E.,  
 RA Morser J., Zhao L., Schmidt A.M., Scherrmann J.M., Mautier J.L.;  
 RT "Recombinant advanced glycation end product receptor pharmacokinetics  
 RL in normal and diabetic rats."  
 RL Mol. Pharmacol. 52:54-62(1997).  
 CC - FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END  
 CC PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS  
 CC WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED  
 CC RATE IN DIABETES.  
 CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC - TISSUE SPECIFICITY: ENDOTHELIAL CELLS.  
 CC - SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS  
 CC 2 C2-LIKE AND ONE V-LIKE DOMAINS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: L33412; AAA00040.1; -  
 CC MGD: MGI:893592; Ager.  
 CC DR InterPro: IPR003006; Ig\_MHC.  
 CC DR InterPro: IPR003598; Ig\_C2.  
 CC DR InterPro: IPR003600; Ig\_Like.  
 CC Pfam: PF00047; Ig\_2.  
 CC SMART: SM00408; IgC2; 1.  
 CC SMART: SM00410; Ig\_Like; 1.  
 CC DR PROSITE: PS00290; Ig\_MHC; 1.  
 CC KW Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.  
 CC FT SIGNAL 1 22  
 CC CHAIN 23 403  
 CC FT DOMAIN 23 341  
 CC FT TRANSMEM 342 362  
 CC FT DOMAIN 363 403  
 CC FT DOMAIN 31 105  
 CC FT DOMAIN 136 213  
 CC FT DOMAIN 251 307  
 CC FT DISULFID 38 98  
 CC FT DISULFID 143 207  
 CC FT DISULFID 258 300  
 CC FT CARBOHYD 25 25  
 CC FT CARBOHYD 80 80  
 CC SEQUENCE 403 AA; 42668 MW; 1279796F5D1579357 CRC64;  
 CC  
 CC Query Match 92.0%; Score 149; DB 1; Length 403;  
 CC Best Local Similarity 93.1%; Pred. No. 9.1e-14;  
 CC

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: April 24, 2002, 09:20:39 ; Search time 21.42 Seconds  
(without alignments)  
51.351 Million cell updates/sec

Title: US-09-689-469-5  
Perfect score: 162  
Sequence: 1 AONTATIGEPVLKCKGAPKKPPORLEWK 30

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues  
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Swissprot\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB        | ID                 | Description         |
|------------|-------|-------------|--------|-----------|--------------------|---------------------|
| 1          | 162   | 100.0       | 404    | 1         | RAGE_HUMAN         | Q15109 homo sapien  |
| 2          | 149   | 92.0        | 403    | 1         | RAGE_MOUSE         | O62151 mus musculu  |
| 3          | 145   | 89.5        | 416    | 1         | RAGE_BOVIN         | Q28173 bos taurus   |
| 4          | 139   | 85.8        | 402    | 1         | RAGE_RAT           | O63495 rattus norv  |
| 5          | 64    | 39.5        | 2481   | 1         | UN52_CAEEL         | O06561 caenorhabdi  |
| 6          | 34.6  | 819         | 1      | FYB_MOUSE | O35601 mus musculu |                     |
| 7          | 33    | 32.7        | 588    | 1         | C166_CHICK         | Q42292 gallus gall  |
| 8          | 53    | 32.7        | 602    | 1         | NRG1_CHICK         | O05199 gallus galli |
| 9          | 52    | 32.1        | 298    | 1         | VEJA_HUMAN         | P57080 homo sapien  |
| 10         | 51    | 31.5        | 677    | 1         | NRG1_XENLA         | O93383 xenopus lae  |
| 11         | 51    | 31.5        | 757    | 1         | PIGR_BOVIN         | P81265 bos taurus   |
| 12         | 51    | 31.5        | 1260   | 1         | CAML_MOUSE         | P11627 mus musculu  |
| 13         | 51    | 31.5        | 1356   | 1         | VGR2_HUMAN         | P39568 homo sapien  |
| 14         | 50.5  | 31.2        | 812    | 1         | NAH2_HUMAN         | Q9U0Y0 homo sapien  |
| 15         | 50    | 30.9        | 1257   | 1         | CAML_HUMAN         | O05204 homo sapien  |
| 16         | 50    | 30.9        | 1259   | 1         | CAML_RAT           | P32095 rattus norv  |
| 17         | 50    | 30.9        | 1487   | 1         | ICP4_HSVB          | P28925 equine herp  |
| 18         | 50    | 30.9        | 1487   | 1         | ICP4_HSVB          | P17473 equine herp  |
| 19         | 49.5  | 30.6        | 478    | 1         | NRPA_ECOLI         | P32050 escherichia  |
| 20         | 49.5  | 30.6        | 922    | 1         | NRPA_RAT           | Q9QWJ9 rattus norv  |
| 21         | 49    | 30.2        | 223    | 1         | MUTH_HAEN          | P44688 haemophilus  |
| 22         | 49    | 30.2        | 430    | 1         | TPSN_CHICK         | O73895 gallus galli |
| 23         | 49    | 30.2        | 850    | 1         | NRG2_HUMAN         | O14511 homo sapien  |
| 24         | 49    | 30.2        | 1302   | 1         | NRG2_MOUSE         | P20241 drosophila   |
| 25         | 48.5  | 29.9        | 827    | 1         | TRRG_CHICK         | O91044 gallus galli |
| 26         | 48.5  | 29.9        | 937    | 1         | ROR1_HUMAN         | O01973 homo sapien  |
| 27         | 48.5  | 29.9        | 937    | 1         | ROR1_MOUSE         | O92139 mus musculu  |
| 28         | 48.5  | 29.9        | 3038   | 1         | TRIO_HUMAN         | O75662 homo sapien  |
| 29         | 48    | 29.6        | 375    | 1         | SRE_CHICK          | O90718 gallus galli |
| 30         | 48    | 29.6        | 441    | 1         | DHOK_MYCTU         | O10601 mycobacteri  |
| 31         | 48    | 29.6        | 448    | 1         | SRE_XENLA          | P23790 xenopus lae  |
| 32         | 48    | 29.6        | 508    | 1         | SRE_HUMAN          | P11831 homo sapien  |
| 33         | 48    | 29.6        | 756    | 1         | NRG2_MOUSE         | P56974 mus musculu  |

|    |      |      |      |   |            |
|----|------|------|------|---|------------|
| 34 | 48   | 29.6 | 811  | 1 | PS22_DROME |
| 35 | 48   | 29.6 | 868  | 1 | NRG2_RAT   |
| 36 | 48   | 29.6 | 873  | 1 | NRG2_DROME |
| 37 | 47.5 | 29.3 | 837  | 1 | NRG2_MOUSE |
| 38 | 47.5 | 29.3 | 923  | 1 | NRG1_MOUSE |
| 39 | 47.5 | 29.3 | 943  | 1 | NRG2_HUMAN |
| 40 | 47.5 | 29.3 | 944  | 1 | NRG2_MOUSE |
| 41 | 47.5 | 29.3 | 953  | 1 | LYAG_MOUSE |
| 42 | 47.5 | 29.3 | 1147 | 1 | KMS_RABIT  |
| 43 | 47   | 29.0 | 400  | 1 | HHP2_SCHPO |
| 44 | 47   | 29.0 | 985  | 1 | REV1_YEAST |
| 45 | 46.5 | 28.7 | 326  | 1 | UL10_HCMVA |

## ALIGNMENTS

| RESULT | ID   | STANDARD                        | PRT | 404 AA |
|--------|--|---------------------------------|-----|--------|
| 1      | RAGE_HUMAN   | 015109: 015279; 09Y3R3; 09H2X7; |     |        |
| AC     | 01-NOV-1997 (Rel. 35, Created)   |                                 |     |        |
| DT     | 01-NOV-1997 (Rel. 35, Last sequence update)                              |                                 |     |        |
| DT     | 20-AUG-2001 (Rel. 40, Last annotation update)                            |                                 |     |        |
| DE     | ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR           |                                 |     |        |
| DE     | (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).                      |                                 |     |        |
| GN     | AGER OR RAGE.  |                                 |     |        |
| OS     | Homo sapiens (Human).  |                                 |     |        |
| OC     | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;                  |                                 |     |        |
| OC     | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.                |                                 |     |        |
| OX     | NCBI_TaxID=9606;   |                                 |     |        |
| RN     | [1]  |                                 |     |        |
| RP     | SEQUENCE FROM N.A. (ISOFORM 1).  |                                 |     |        |
| RC     | TISSUE=Lung;   |                                 |     |        |
| RX     | MEDLINE=92340547; PubMed=1378843;  |                                 |     |        |
| RA     | Neepner M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,         |                                 |     |        |
| RA     | Elliston K., Stern D., Shaw A.;  |                                 |     |        |
| RT     | "Cloning and expression of a cell surface receptor for advanced          |                                 |     |        |
| RT     | glycosylation end products of proteins."                                 |                                 |     |        |
| RL     | J. Biol. Chem. 267:14998-15004(1992).                                    |                                 |     |        |
| RN     | [2]  |                                 |     |        |
| RP     | SEQUENCE FROM N.A. (ISOFORM 1).  |                                 |     |        |
| RX     | MEDLINE=95137587; PubMed=7835890;  |                                 |     |        |
| RA     | Sugaya K., Fukagawa T., Matsumoto K., Mita K., Takahashi E., Ando A.,    |                                 |     |        |
| RA     | Inoko H., Ikemura T.;  |                                 |     |        |
| RT     | "Three genes in the human MHC class III region near the junction with    |                                 |     |        |
| RT     | the class II: gene for receptor of advanced glycosylation end            |                                 |     |        |
| RT     | products, PBX2 homeobox gene and a notch homolog, human counterpart      |                                 |     |        |
| RT     | of mouse mammary tumor gene int-3."                                      |                                 |     |        |
| RL     | Genomics 23:408-419(1994).   |                                 |     |        |
| RN     | [3]  |                                 |     |        |
| RP     | SEQUENCE FROM N.A. (ISOFORM 1).  |                                 |     |        |
| RA     | Rowen L., Dankers C., Baskin D., Faust J., Loretz C., Ahearn M.E.,       |                                 |     |        |
| RA     | Banta A., Spies T., Hood L.;   |                                 |     |        |
| RT     | Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.                  |                                 |     |        |
| RN     | [4]  |                                 |     |        |
| RP     | SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-100.                     |                                 |     |        |
| RA     | Abedin M.J., Yonekura H., Migita H., Karsawa J., Yamamoto Y.,            |                                 |     |        |
| RA     | Yamamoto H.;   |                                 |     |        |
| RT     | "Molecular heterogeneity of the receptor for advanced glycosylation      |                                 |     |        |
| RT     | endproducts."  |                                 |     |        |
| RL     | Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.                  |                                 |     |        |
| RN     | [5]  |                                 |     |        |
| RP     | SEQUENCE FROM N.A. (ISOFORM 2)   |                                 |     |        |
| RA     | Malherbe P., Richards J., Gaillard H., Thompson A., Diener C.,           |                                 |     |        |
| RA     | Schuler A., Huber G.;  |                                 |     |        |
| RT     | "CDNA cloning of a novel secreted isoform of the human Receptor for      |                                 |     |        |
| RT     | advanced glycosylation end products (RAGE) and characterization of cells |                                 |     |        |
| RT     | co-expressing cell-surface scavenger receptors and Swedish mutant        |                                 |     |        |
| RT     | amyloid precursor protein."  |                                 |     |        |
| RL     | Submitted (May-1999) to the EMBL/GenBank/DBJ databases.                  |                                 |     |        |
| RN     | [6]  |                                 |     |        |
| RP     | SEQUENCE OF 1-12 FROM N.A.   |                                 |     |        |

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:20:11 : Search time 62.94 Seconds  
(without alignments)  
69.720 Million cell updates/sec

Title: US-09-689-469-5  
Perfect score: 162  
Sequence: 1 AONTARIGEPVLKCKGAPKPPQRLFWK 30

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues  
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SPTEMBL\_17:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mhc:\*  
8: sp\_mammal:\*  
9: sp\_organelle:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description               |
|------------|-------|-------------|-----------|----|---------------------------|
| 1          | 162   | 100.0       | 342       | 4  | 09Y3R3 homo sapien        |
| 2          | 149   | 92.0        | 402       | 11 | 035444 mus musculu        |
| 3          | 108   | 66.7        | 32        | 6  | 09TR01 09trgl bos taurus  |
| 4          | 64    | 39.5        | 2295      | 5  | 09XRD2 018263 caenorhabdi |
| 5          | 64    | 39.5        | 2482      | 5  | 018263 caenorhabdi        |
| 6          | 64    | 39.5        | 3375      | 5  | 09XRT5 09xrt5 caenorhabdi |
| 7          | 63    | 38.9        | 1482      | 5  | 09V4Y0 09v4y0 drosophila  |
| 8          | 61    | 37.7        | 2016      | 5  | 09V4J9 09v4j9 drosophila  |
| 9          | 61    | 37.7        | 2016      | 5  | 09V4J9 09v4j9 drosophila  |
| 10         | 58    | 35.8        | 1215      | 5  | 09V787 09v787 drosophila  |
| 11         | 56.5  | 34.9        | 1791      | 5  | 09N5C2 09n5c2 caenorhabdi |
| 12         | 55.5  | 34.3        | 1496      | 4  | 092626 homo sapien        |
| 13         | 55    | 34.0        | 848       | 5  | 025198 hydra atten        |
| 14         | 54    | 33.3        | 1344      | 11 | 09Z214 09z214 mus musculu |
| 15         | 53.5  | 33.0        | 483       | 4  | 09UF14 09uf14 homo sapien |
| 16         | 53.5  | 33.0        | 1094      | 4  | 09BYB8 09byb8 homo sapien |
| 17         | 53    | 32.7        | 762       | 5  | 09U2E2 09u2e2 caenorhabdi |
| 18         | 53    | 32.7        | 886       | 5  | 09VM64 09vm64 drosophila  |
| 19         | 53    | 32.7        | 1612      | 11 | 089026 mus musculu        |

|    |      |      |      |    |                            |
|----|------|------|------|----|----------------------------|
| 20 | 53   | 32.7 | 1651 | 4  | 09Y6N7 09y6n7 homo sapien  |
| 21 | 53   | 32.7 | 1651 | 11 | 055005 055005 ratus norv   |
| 22 | 52.5 | 32.4 | 7962 | 4  | 010465 010465 homo sapien  |
| 23 | 52   | 32.1 | 99   | 10 | 09FR57 09fr57 lycopersico  |
| 24 | 52   | 32.1 | 181  | 11 | 09CWD9 09cwd9 mus musculu  |
| 25 | 52   | 32.1 | 298  | 11 | 09J159 09j159 mus musculu  |
| 26 | 52   | 32.1 | 1793 | 5  | 09NKJ4 09nkj4 leishmania   |
| 27 | 51   | 31.5 | 305  | 7  | 098261 098261 homo sapien  |
| 28 | 51   | 31.5 | 455  | 4  | 09UR0 09ur0 homo sapien    |
| 29 | 51   | 31.5 | 1442 | 12 | 042066 042066 equine heip  |
| 30 | 50.5 | 31.2 | 212  | 10 | 09FGP8 09fgp8 arabidopsis  |
| 31 | 50.5 | 31.2 | 793  | 11 | 070246 070246 mus musculu  |
| 32 | 50.5 | 31.2 | 1114 | 4  | 09BWL1 09bwl1 homo sapien  |
| 33 | 50   | 30.9 | 284  | 2  | 09I452 09i452 pseudomonas  |
| 34 | 50   | 30.9 | 372  | 7  | 031406 031406 gallus galli |
| 35 | 50   | 30.9 | 377  | 5  | 09VHR0 09vhr0 drosophila   |
| 36 | 50   | 30.9 | 386  | 10 | 004645 004645 arabidopsis  |
| 37 | 50   | 30.9 | 392  | 2  | 09K6C8 09k6c8 bacillus ha  |
| 38 | 50   | 30.9 | 538  | 11 | 09OX07 09ox07 mus musculu  |
| 39 | 50   | 30.9 | 1154 | 3  | 09PM63 09pm63 neurospora   |
| 40 | 50   | 30.9 | 1234 | 11 | 09R044 09r044 ratus norv   |
| 41 | 50   | 30.9 | 1252 | 11 | 09QXX7 09qxx7 ratus norv   |
| 42 | 50   | 30.9 | 1252 | 11 | 09J1X2 09j1x2 ratus norv   |
| 43 | 50   | 30.9 | 1259 | 11 | 09QY38 09qy38 mus musculu  |
| 44 | 49.5 | 30.6 | 921  | 11 | 09QX38 09qx38 ratus norv   |
| 45 | 49.5 | 30.6 | 968  | 5  | 09VCM6 09vcm6 drosophila   |

## ALIGNMENTS

RESULT 1  
ID 09Y3R3 PRELIMINARY; PRT; 342 AA.  
AC 09Y3R3;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE RECEPTOR FOR ADVANCED GLYCATION END PRODUCTS PRECURSOR.  
GN RAGESEC.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid:9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Matherbe P., Richards J., Gaillard H., Thompson A., Diener C.,  
RA Schuler A., Huber G.;  
RT "CDNA cloning of a novel secreted isoform of the human Receptor for  
RT Advanced Glycation End products (RAGE) and characterization of cells  
RT co-expressing cell-surface scavenger receptors and Swedish mutant  
RT amyloid precursor protein.";  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
CC 1-SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
CC DOMAIN.  
DR EMBL: AJ133822; CAB43108.1; -  
DR InterPro: IPR003598; Ig\_c2.  
DR InterPro: IPR003600; Ig\_like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR Pfam: PF00047; Ig; 2.  
DR SMART: SM00408; Igc2; 1.  
DR SMART: SM00410; Ig\_Like; 1.  
KW Signal; Receptor.  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 342 RECEPTOR FOR ADVANCED GLYCATION END  
FT PRODUCTS.  
SQ SEQUENCE 342 AA; 36193 MW; 35DDF66A13E39B38 CRC64;  
Query Match 100.0%; Score 162; DB 4; Length 342;  
Best Local Similarity 100.0%; Pred. No. 5.1e-16;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGEPVLKCKGAPKKPPORLEWK 30  
 DB 23 AONTARIGEPVLKCKGAPKKPPORLEWK 52

RESULT 2  
 ID 035444 PRELIMINARY; PRT; 402 AA.  
 AC 035444;  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE RAGE.  
 GN RAGE.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Loren L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,  
 RA Loretz C., Schmidt S., Tipton S., Traicoff R., Zackrone K., Hood L.;  
 RL Submitted (JCT-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 DR EMBL; AF030001; AAB82007.1; -  
 DR InterPro: IPR003598; Ig\_G2.  
 DR InterPro: IPR003600; Ig\_Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig; 3.  
 DR SMART: SM00408; IgC2; 1.  
 DR SMART: SM00410; Ig\_Like; 1.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN.1.  
 DR SEQUENCE 402 AA; 42653 MW; DBFC050A6C8CB902 CRC64;

Query Match 92.0%; Score 149; DB 11; Length 402;  
 Best Local Similarity 93.1%; Pred. No. 5.1e-14;  
 Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ONTARIGEPVLKCKGAPKKPPORLEWK 30  
 DB 24 ONTARIGEPVLKCKGAPKKPPORLEWK 52

RESULT 3  
 ID 09TR01 PRELIMINARY; PRT; 32 AA.  
 AC 09TR01;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
 DE 35 KDA ADVANCED GLYCOSYLATION END PRODUCT BINDING PROTEIN (FRAGMENT).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecorida; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE=92340546; PubMed=1321822;  
 RA Schmidt A.M., Viana M., Gerlach M., Brett J., Ryan J., Kao J.,  
 RA Esposito C., Hegarty H., Hurley W., Claus M.;  
 RT Isolation and characterization of two binding proteins for advanced  
 RT glycosylation end products from bovine lung which are present on the  
 RT endothelial cell surface.;  
 RL J. Biol. Chem. 267:14987-14997(1992).  
 SL J. Biol. Chem. 267:14987-14997(1992).  
 SQ SEQUENCE 32 AA; 3507 MW; AEA43147CE5B3D91 CRC64;

Query Match 66.7%; Score 108; DB 6; Length 32;  
 Best Local Similarity 75.9%; Pred. No. 4.7e-09;  
 Matches 22; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 ONTARIGEPVLKCKGAPKKPPORLEWK 30  
 DB 2 ONTARIGEPVLKCKGAPKKPPORLEWK 30

RESULT 4  
 ID 09XTD2 PRELIMINARY; PRT; 2295 AA.  
 AC 09XTD2;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE UNC-52 PROTEIN.  
 GN UNC-52 OR ZC101.2.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Percy C., Baynes C.;  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- ALTERNATIVE PRODUCTS: FOUR FORMS: ISOFORM ZC101.2A (O18263),  
 CC ISOFORM ZC101.2B (O18261), ISOFORM ZC101.2C (SHOWN HERE) AND  
 CC ISOFORM ZC101.2E (O9XTI5); MAY BE PRODUCED BY ALTERNATIVE  
 CC SPLICING.  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 CC -1- SIMILARITY: TO LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR CLASS A  
 CC (LDLR) DOMAIN.  
 DR EMBL; Z93395; CAB07707.1; -  
 DR EMBL; Z93375; CAB07568.1; JOINED.  
 DR EMBL; Z93375; CAB07568.1; -  
 DR EMBL; Z93395; CAB07568.1; JOINED.  
 DR HSSP; P01130; ILDR.  
 DR WormPep; ZC101.2C; CE15034.  
 DR InterPro: IPR000561; EGF\_Like.  
 DR InterPro: IPR003598; Ig\_G2.  
 DR InterPro: IPR003600; Ig\_Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR000034; Laminin\_B.  
 DR InterPro: IPR002049; Laminin\_EGF.  
 DR InterPro: IPR002172; LDL\_recept\_A.  
 DR InterPro: IPR001993; Mitoch\_carrier.  
 DR InterPro: IPR000519; P\_trefoll.  
 DR Pfam; PF00047; Ig; 14.  
 DR Pfam; PF00052; Laminin\_B; 2.  
 DR Pfam; PF00053; Laminin\_EGF; 5.  
 DR Pfam; PF00057; Idl\_recept\_a; 3.  
 DR PRINTS; PR00011; EGF\_LAMININ.  
 DR PRINTS; PR00261; LDLRECEPTOR.  
 DR PRODOM; PD003031; Laminin\_B; 2.  
 DR SMART; SM00180; EGF\_Lam; 5.  
 DR SMART; SM00408; IgC2; 9.  
 DR SMART; SM00410; Ig\_Like; 5.  
 DR SMART; SM00281; Lamb; 2.  
 DR SMART; SM00192; LDua; 3.  
 DR SMART; SM00018; P; 1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_4.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 7.  
 DR PROSITE; PS01209; LDLRA\_1; 3.  
 DR PROSITE; PS00068; LDLRA\_2; 3.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; UNKNOWN\_1.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; UNKNOWN\_1.  
 KW Alternative splicing: EGF-like domain; Glycoprotein;  
 KW Hypothetical protein: Laminin EGF-like domain; Repeat.  
 SQ SEQUENCE 2295 AA; 251087 MW; F6BC6067ABF86C48 CRC64;

Query Match 39.5%; Score 64; DB 5; Length 2295;  
 Best Local Similarity 50.0%; Pred. No. 1.2;



Matches 12; Conservative 4; Mismatches 6; Indels 2; Gaps 1;  
QY 8 IGEPLVKCK--GAPKKPQRLFM 29  
Db 1803 VGEPLQKCEAFGAPGDPPEVEM 1826

```
RESULT 5
ID 018263 PRELIMINARY; PRT: 2482 AA.
AC 018263;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE UNC-52 PROTEIN
GN UNC-52 OR ZC101.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Percy C., Baynes C.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- ALTERNATIVE PRODUCTS: FOUR FORMS: ISOFORM ZC101.2A (SHOWN HERE),
CC ISOFORM ZC101.2B (O18261), ISOFORM ZC101.2C (O9XTD2) AND ISOFORM
CC ZC101.2E (O9XTI5); MAY BE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
CC -1- SIMILARITY: TO LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR CLASS A
CC (LDLRA) DOMAIN.
DR EMBL: Z93395; CAB07706.1; JOINED.
DR EMBL: Z93375; CAB07569.1; JOINED.
DR EMBL: Z93395; CAB07569.1; JOINED.
DR HSSP: P01130; ILDR.
DR Wormpep: ZC101.2A; CE15028.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003600; Ig_c2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR000034; Laminin_B.
DR InterPro: IPR002049; Laminin_EGF.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR002172; LDL_recept_A.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR000519; P_trefoll.
DR Pfam: PF00047; Ig_16.
DR Pfam: PF00052; Laminin_B_2.
DR Pfam: PF00053; Laminin_EGF_5.
DR Pfam: PF00057; Idl_recept_a; 3.
DR ProDom: PD003031; Laminin_B_2.
DR SMART: SM00180; EGF_Lam; 5.
DR SMART: SM00408; Igc2; 11.
DR SMART: SM00410; Ig_Like; 5.
DR SMART: SM00281; Lamb; 2.
DR SMART: SM00192; LDLA; 3.
DR SMART: SM00018; P_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_4.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01248; LAMININ_TYPE_EGF; 7.
DR PROSITE: PS01209; LDLRA_1; 3.
DR PROSITE: PS50068; LDLRA_2; 3.
DR PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN_1.
DR PROSITE: PS01248; LAMININ_TYPE_EGF; 7.
DR PROSITE: PS01209; LDLRA_1; 3.
DR PROSITE: PS50068; LDLRA_2; 3.
DR PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN_1.
KW Hypothetical protein; EGF-like domain; Glycoprotein;
KW Hypothetical protein; Laminin EGF-like domain; Repeat.
SQ SEQUENCE 2482 AA; 270943 MW; B24096F7DB694D70 CRC64;
```

Query Match 39.5%; Score 64; DB 5; Length 2482;  
Best Local Similarity 50.0%; Pred. No. 1.4;  
Matches 12; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

QY 8 IGEPLVKCK--GAPKKPQRLFM 29  
Db 1990 VGEPLQKCEAFGAPGDPPEVEM 2013

```
RESULT 6
ID 09XTI5 PRELIMINARY; PRT: 3375 AA.
AC 09XTI5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE UNC-52 PROTEIN
GN UNC-52 OR ZC101.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Percy C., Baynes C.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- ALTERNATIVE PRODUCTS: FOUR FORMS: ISOFORM ZC101.2C (O9XTI5),
CC ISOFORM ZC101.2B (O18261), ISOFORM ZC101.2C (O9XTD2) AND ISOFORM
CC ZC101.2E (SHOWN HERE); MAY BE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
CC -1- SIMILARITY: TO LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR CLASS A
CC (LDLRA) DOMAIN.
DR EMBL: Z93395; CAB07708.1; JOINED.
DR EMBL: Z93375; CAB07708.1; JOINED.
DR EMBL: Z93375; CAB07569.1; JOINED.
DR EMBL: Z93395; CAB07569.1; JOINED.
DR HSSP: P01130; ILDR.
DR Wormpep: ZC101.2E; CE18424.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003600; Ig_c2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR000034; Laminin_B.
DR InterPro: IPR002049; Laminin_EGF.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR002172; LDL_recept_A.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR000519; P_trefoll.
DR Pfam: PF00047; Ig_17.
DR Pfam: PF00052; Laminin_B_2.
DR Pfam: PF00053; Laminin_EGF_5.
DR Pfam: PF00057; Idl_recept_a; 3.
DR ProDom: PD003031; Laminin_B_2.
DR SMART: SM00180; EGF_Lam; 5.
DR SMART: SM00001; EGF_Like; 3.
DR SMART: SM00408; Igc2; 12.
DR SMART: SM00410; Ig_Like; 5.
DR SMART: SM00281; Lamb; 2.
DR SMART: SM00282; Lamb; 3.
DR SMART: SM00192; LDLA; 3.
DR SMART: SM00018; P_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_7.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01248; LAMININ_TYPE_EGF; 7.
DR PROSITE: PS01209; LDLRA_1; 3.
DR PROSITE: PS50068; LDLRA_2; 3.
DR PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN_1.
KW Hypothetical protein; EGF-like domain; Glycoprotein;
KW Hypothetical protein; Laminin EGF-like domain; Repeat.
SQ SEQUENCE 3375 AA; 369049 MW; IAA418B84E5D67AA CRC64;
```

Query Match 39.5%; Score 64; DB 5; Length 3375;

Best Local Similarity 50.0%; Pred. No. 1.9;  
Matches 12; Conservative 4; Mismatches 6; Indels 2; Gaps 1;  
QY 8 IGEPLVLCCK--GAPKKPPQRLM 29  
DB 1990 VGEPLVLCCKAFCGAPDPEPEVM 2013

RESULT 7  
Q9V4Y0 PRELIMINARY; PRT: 1482 AA.  
AC Q9V4Y0; Q9V4Y1; Q9V4Y2; Q9V4Y3; Q9V4Y4; Q9V4Y5; Q9V4Y6;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE SNS PROTEIN.  
GN SNS OR CG2385 OR CG8278 OR CG12495 OR CG13752 OR CG13753 OR CG13754 OR CG13755 OR CG18464.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_Taxid=7227;

RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20317033; PubMed=10859168;  
RA Bour B.A., Chakravarti M., West J.M., Abmayr S.M.;  
RT "Drosophila SNS, a member of the immunoglobulin superfamily that is  
RT essential for myoblast fusion."  
RL Genes Dev. 14:1498-1511(2000).  
RN [2]  
RP SEQUENCE OF 1-224; 334-477; 491-1061 AND 1274-1482 FROM N.A.  
RX STRAIN-BERKELEY;  
RA MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Aghayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,  
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
RA Burtis J.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harits N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,  
RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Mlshina N.V., Moberg C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Murry D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
RA Palczolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reihert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svitskas R., Tector C., Turner K., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster."  
RL Science 287:2185-2195(2000).  
DB EMBL; AF254867; AAF77184.1;

DR EMBL; AE003835; AAF59037.1; ALT\_SEQ.  
DR EMBL; AE003835; AAF59038.1; ALT\_SEQ.  
DR EMBL; AE003835; AAF59039.1; ALT\_SEQ.  
DR EMBL; AE003835; AAF59040.1; ALT\_SEQ.  
DR EMBL; AE003835; AAF59041.1; ALT\_SEQ.  
DR EMBL; AE003835; AAF59042.1; ALT\_SEQ.  
DR EMBL; AE003835; AAF59043.1; ALT\_SEQ.  
DR FLYBase; FBgn0024189; sns.  
DR InterPro; IPR003961; FN.III.  
DR InterPro; IPR003598; Ig.C2.  
DR InterPro; IPR003600; Ig.Like.  
DR SMART; SM0060; FN3; 1.  
DR SMART; SM00408; IgC2; 4.  
DR SMART; SM00410; Ig\_Like; 4.  
FT FT  
FT CONFLICT 622 622  
FT MISSING (IN REF. 2).  
FT ACOSLKRFFFTHTSTLPLPCPINILCPPTGTTPMDQ  
PT (IN REF. 2).  
FT C -> F (IN REF. 2).  
FT A -> T (IN REF. 2).  
FT MISSING (IN REF. 2).  
SQ SEQUENCE 1482 AA; 162163 MM; 100C730FA1FA5357 CRC64;

Query Match 38.9%; Score 63; DB 5; Length 1482;  
Best Local Similarity 41.7%; Pred. No. 1.1;  
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;  
QY 6 ARGEPLVLCCKGAPKKPPQRLM 29  
DB 393 ARVGDIVLTCTTAPSNPAEIKW 416

RESULT 8  
Q9V4J9 PRELIMINARY; PRT: 2016 AA.  
AC Q9V4J9;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE CG17800 PROTEIN.  
GN DSCAM OR CG17800.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_Taxid=7227;

RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN-BERKELEY;  
RA MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Aghayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,  
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
RA Burtis J.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harits N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,  
RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarly B., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195(2000).  
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
DOMAIN.  
CC EMBL: AE003841; AAF59271.1; -  
DR HSSP: PA0189; IBOU.  
DR FlyBase: FBgn0033159; Dscam.  
DR InterPro: IPR000267; Asparaginse-glutamase.  
DR InterPro: IPR003961; FN\_III.  
DR InterPro: IPR003598; Ig\_c2.  
DR InterPro: IPR003600; Ig\_1like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR Pfam: PF00041; fn3; 6.  
DR Pfam: PF00047; Ig; 10.  
DR SMART: SM00060; FN3; 6.  
DR SMART: SM00408; Ig\_c2; 7.  
DR SMART: SM00410; Ig\_1like; 2.  
DR PROSITE: PS00144; ASN\_GLM\_ASE\_1; UNKNOWN\_1.  
SQ SEQUENCE 2016 AA; 222109 MW; 6A48DE3B7BD0ABD CRC64;

Query Match 37.7%; Score 61; DB 5; Length 2016;  
Best Local Similarity 54.5%; Pred. No. 3.1;  
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
QY 2 QNTARIGEPLVLCCKGAPKRP 23  
Db 819 RNOYARGEPAVLQCEAKGKRP 840

RESULT 9  
Q9NBA1 PRELIMINARY; PRT; 2016 AA.  
ID Q9NBA1;  
AC 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE DSCAM PRECURSOR.  
GN DSCAM OR CG17800.  
OS *Drosophila melanogaster* (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; *Drosophila*.  
OX NCBI\_TaxId=7227;  
RN 11  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20348742; PubMed=10892653;  
RA Schmucker D., Clemens J.C., Shu H., Morby C.A., Xiao J., Mada M.,  
RA Dixon J.E., Zibursky S.L.;  
RT "Drosophila Dscam is an Axon Guidance Receptor Exhibiting  
RT Extraordinary Molecular Diversity.";  
RL Cell 101:671-684(2000).  
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
DOMAIN.  
CC EMBL: AF260530; AAF71926.1; -  
DR FlyBase: FBgn0033159; Dscam.  
DR InterPro: IPR000267; Asparaginse-glutamase.  
DR InterPro: IPR003961; FN\_III.  
DR InterPro: IPR003598; Ig\_c2.

DR InterPro: IPR003600; Ig\_1like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR Pfam: PF00041; fn3; 6.  
DR Pfam: PF00047; Ig; 10.  
DR SMART: SM00060; FN3; 6.  
DR SMART: SM00408; Ig\_c2; 7.  
DR SMART: SM00410; Ig\_1like; 3.  
DR PROSITE: PS00144; ASN\_GLM\_ASE\_1; UNKNOWN\_1.  
KM SIGNAL.  
FT SIGNAL.  
SQ SEQUENCE 2016 AA; 222124 MW; 95CF95488F2AD36C CRC64;  
POTENTIAL.  
QY 2 QNTARIGEPLVLCCKGAPKRP 23  
Db 819 RNOYARGEPAVLQCEAKGKRP 840  
RESULT 10  
ID Q9V787 PRELIMINARY; PRT; 1215 AA.  
AC Q9V787; Q9U3Y6.  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE HIBRIS PROTEIN.  
GN HBS OR CG7449.  
OS *Drosophila melanogaster* (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; *Drosophila*.  
OX NCBI\_TaxId=7227;  
RN 11  
RP SEQUENCE FROM N.A.  
RA Atterio R., Baylies M.;  
RT "Characterization of genes involved in *Drosophila* myogenesis.";  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
RN 12  
RP SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY.  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Aghayani A., An H.-G., Andrews-Pfankoch C., Baldwin D.,  
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarly B., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spter E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000)  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 CC EMBL: AF210316; AAF19446.1; ALT\_INIT.  
 DR EMBL: AEO03812; AAF58172.2; -.  
 DR FLYBASE: FBgn0029082; hbs.  
 DR InterPro: IPR003961; FN11.  
 DR InterPro: IPR003598; Ig\_C2.  
 DR InterPro: IPR003600; Ig\_Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00041; fn3; 1.  
 DR Pfam: PF00047; Ig; 9.  
 DR SMART: SM00060; FN3; 1.  
 DR SMART: SM00408; IgC2; 3.  
 DR SMART: SM00410; Ig\_Like; 6.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN.1.  
 SQ SEQUENCE 1215 AA; 132053 MW; 62CD064968141C9F CRC64;

Query Match 35.8%; Score 58; DB 5; Length 1215;  
 Best Local Similarity 37.5%; Pred. No. 5.1;  
 Matches 9; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 6 ARIGEPVLKCKGAPKPPORLEW 29  
 Db 337 AKYGDSYQLSCVTRAPSPQARISH 360

RESULT 11  
 ID 09NSC2 PRELIMINARY; PRT; 1791 AA.

AC 09NSC2; 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE W06H8.3 PROTEIN.  
 GN W06H8.3.  
 OS *Caenorhabditis elegans*.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Pelodierinae; *Caenorhabditis*.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA None;  
 RT "Name sequence of the nematode *C. elegans*: a platform for  
 RT investigating biology. The *C. elegans* Sequencing Consortium.";  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Wilson R.;  
 RT "The sequence of *C. elegans* cosmid W06H8.";  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Waterston R.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 CC EMBL: AC006695; AAF39981.1; -.  
 DR InterPro: IPR003598; Ig\_C2.

DR InterPro: IPR003600; Ig\_Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig; 3.  
 DR SMART: SM00408; IgC2; 2.  
 DR SMART: SM00410; Ig\_Like; 3.  
 SQ SEQUENCE 1791 AA; 199071 MW; 59A9761BCB8B20DA CRC64;

Query Match 34.9%; Score 56.5; DB 5; Length 1791;  
 Best Local Similarity 48.1%; Pred. No. 13;  
 Matches 13; Conservative 3; Mismatches 10; Indels 1; Gaps 1;  
 QY 3 NITARIGEPVLKCKGAPKPPORLEW 29  
 Db 1708 NCEGRIGEPVQLKCLGMPQPE-IEW 1733

RESULT 12  
 ID 092626 PRELIMINARY; PRT; 1496 AA.  
 AC 092626;  
 DT 01-FEB-1997 (Tremblrel. 02, Created)  
 DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE MYELOBLAST KIAA0230 (FRAGMENT).  
 DE KIAA0230.  
 GN Homo sapiens (Human).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BONE MARROW;  
 RX MEDLINE=97191544; PubMed=9039502;  
 RA Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayashi Y., Ohara O.,  
 RA Tanaka A., Kotani H., Miyajima N., Nomura N.;  
 RT "Prediction of the coding sequences of unidentified human genes. VI.  
 RT The coding sequences of 80 new genes (KIA0201-KIA0280) deduced by  
 RT analysis of cDNA clones from cell line KG-1 and brain.";  
 RL DNA Res. 3:321-329(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-MELANOMA;  
 RX MEDLINE=95048383; PubMed=7959781;  
 RA Weiler S.R., Taylor S.M., Deans R.J., Kan-Mitchell J., Mitchell M.S.,  
 RA Trent J.M.;  
 RT "Assignment of a human melanoma associated gene MG50 (D2S448) to  
 RT chromosome 2p25.3 by fluorescence in situ hybridization.";  
 RL Genomics 22:243-244(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-MELANOMA;  
 RA Mitchell M.S., Kan-Mitchell J., Minev B., Edman C., Deans R.J.;  
 RT "Identification of a novel melanoma gene (MG50) - likely the gene for  
 RT IL-1 receptor antagonist - which encodes epitopes recognized by human  
 RT cytolytic T lymphocytes.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 CC EMBL: D86983; BAA13219.1; -.  
 DR EMBL: AE200348; AAF06354.1; -.  
 DR HSSP: P05164; IXP.  
 DR InterPro: IPR002007; Anln\_peroxidase.  
 DR InterPro: IPR003598; Ig\_C2.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000483; LRR\_Cterm.  
 DR InterPro: IPR000372; LRR\_Nterm.  
 DR InterPro: IPR003591; LRR\_tyr.  
 DR InterPro: IPR001536; Peroxidase\_3.  
 DR InterPro: IPR002016; Peroxidase.  
 DR InterPro: IPR001007; VMFC.  
 DR Pfam: PF00047; Ig; 4.

DR Pfam: PF00560; LRR; 5.  
DR Pfam: PF01463; LRCT; 1.  
DR Pfam: PF00141; peroxidase; 1.  
DR Pfam: PF00093; VWC; 1.  
DR PRINTS: PR00457; ANPEROXIDASE.  
DR SMART: SM00408; Igc2; 4.  
DR SMART: SM00082; LRCT; 1.  
DR SMART: SM00013; LRNT; 1.  
DR SMART: SM00369; LRR\_TYP; 4.  
DR PROSITE: PS01208; VWC; 1.  
FT NON\_TER 1  
SQ SEQUENCE 1496 AA; 167209 MW; E9B9A7069BFLBFF CRC64;

Query Match 34.3%; Score 55.5; DB 4; Length 1496;  
Best Local Similarity 39.3%; Pred. No. 15;  
Matches 11; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

OY 2 ONITARIGEPLVLCCKGAPKPPORLEW 29  
DB 366 QNTEVLVGESEVTLCC-SATGHPPLRISW 392

RESULT 13  
ID 025198 PRELIMINARY; PRT; 848 AA.  
AC 025198:  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
DE RECEPTOR TYROSINE KINASE 90.  
GN HTK90.  
OS Hydra attenuata (Hydra) (Hydra vulgaris)  
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroids; Anthomedusae;  
OC Hydridae; Hydra.  
OX NCBI\_TaxID=6087;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Miller M.A., Steele R.E.;  
RL Submitted (May-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.  
DR EMBL: U59448; AAB03389.1; -.  
DR HSSP: P06213; IIRK.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR003598; Ig\_C2.  
DR InterPro: IPR003600; Ig\_Like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR01245; Tyr\_kin.  
DR Pfam: PF00047; Ig\_5.  
DR Pfam: PF00069; pkinase; 1.  
DR PRINTS: PR00109; TYRKINASE.  
DR SMART: SM00408; Igc2; 2.  
DR SMART: SM00410; Ig\_Like; 3.  
DR SMART: SM00219; Tyrc; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
KW ATP-binding; Transferase; Tyrosine-protein kinase.  
SQ SEQUENCE 848 AA; 95551 MW; D0A52ED6A8760C07 CRC64;

Query Match 34.0%; Score 55; DB 5; Length 848;  
Best Local Similarity 59.1%; Pred. No. 9.8;  
Matches 13; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

OY 2 ONITARIGEPLVLCCKGAPK 21  
DB 422 KNITATIGEPANVHCCKGKFPK 443

RESULT 14

O94214  
ID 094214 PRELIMINARY; PRT; 1344 AA.  
AC 094214:  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
DE RIG-1 PROTEIN.  
GN RIG1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yuan S.-S.F., Cox L.A., Dasika G.K., Lee E.Y.-H.P.;  
RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.  
DR EMBL: AF060570; AAD11628.1; -.  
DR HSSP: P56276; ITLK.  
DR MGD: MGI:1343102; Rb1g1.  
DR InterPro: IPR003961; FN\_III.  
DR InterPro: IPR003598; Ig\_C2.  
DR InterPro: IPR003006; Ig\_MHC.  
DR Pfam: PF00041; fn3; 3.  
DR Pfam: PF00047; Ig\_5.  
DR SMART: SM00060; FN3; 3.  
DR SMART: SM00408; Igc2; 5.  
SQ SEQUENCE 1344 AA; 143439 MW; 8B0060341C49CFEA CRC64;

Query Match 33.3%; Score 54; DB 11; Length 1344;  
Best Local Similarity 32.1%; Pred. No. 22;  
Matches 9; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 3 NITARIGEPLVLCCKGAPKPPORLEW 30  
DB 152 NVYVAVGEPAVMCEVPPKGPHEPLVTWK 179

RESULT 15  
ID 090F14  
AC 090F14 PRELIMINARY; PRT; 483 AA.  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)  
DE HYPOTHETICAL 51.9 KDA PROTEIN (FRAGMENT).  
GN DKFZP586O1624.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Duesterhoelt A., Lauber J., Mewes H.W., Gassenhuber J., Wiemann S.;  
RL Submitted (Sep-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.  
DR EMBL: AL117666; CAB56036.1; -.  
DR InterPro: IPR003598; Ig\_C2.  
DR InterPro: IPR003006; Ig\_MHC.  
DR Pfam: PF00047; Ig\_2.  
DR SMART: SM00408; Igc2; 2.  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 483 AA; 51907 MW; B3DFEC945C0DF8FC CRC64;

Query Match 33.0%; Score 53.5; DB 4; Length 483;  
Best Local Similarity 45.5%; Pred. No. 9.2;  
Matches 10; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

Wed Apr 24 09:48:11 2002

us-09-689-469-5.rsp

Page 8

```
QY      8 IGEPLVLCKGAPKKPPQRLW 29
      :||:|:| | ||:|
Db     96 VGETVALOCK-ATGNPPPRITW 116
```

Search completed: April 24, 2002, 09:20:13  
Job time: 242 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:21:51 ; Search time 66.52 Seconds  
(without alignments)  
11.135 Million cell updates/sec

Title: US-09-689-469-6  
Perfect score: 10  
Sequence: 1 AONITARIGE 10

Scoring table:

OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 522463 seqs, 74073290 residues

Word size : 0

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database :

A\_Geneseq\_1101.\*  
1: /SID88/gcgdata/geneseq/geneseqp/AA1980.DAT:\*  
2: /SID88/gcgdata/geneseq/geneseqp/AA1981.DAT:\*  
3: /SID88/gcgdata/geneseq/geneseqp/AA1982.DAT:\*  
4: /SID88/gcgdata/geneseq/geneseqp/AA1983.DAT:\*  
5: /SID88/gcgdata/geneseq/geneseqp/AA1984.DAT:\*  
6: /SID88/gcgdata/geneseq/geneseqp/AA1985.DAT:\*  
7: /SID88/gcgdata/geneseq/geneseqp/AA1986.DAT:\*  
8: /SID88/gcgdata/geneseq/geneseqp/AA1987.DAT:\*  
9: /SID88/gcgdata/geneseq/geneseqp/AA1988.DAT:\*  
10: /SID88/gcgdata/geneseq/geneseqp/AA1989.DAT:\*  
11: /SID88/gcgdata/geneseq/geneseqp/AA1990.DAT:\*  
12: /SID88/gcgdata/geneseq/geneseqp/AA1991.DAT:\*  
13: /SID88/gcgdata/geneseq/geneseqp/AA1992.DAT:\*  
14: /SID88/gcgdata/geneseq/geneseqp/AA1993.DAT:\*  
15: /SID88/gcgdata/geneseq/geneseqp/AA1994.DAT:\*  
16: /SID88/gcgdata/geneseq/geneseqp/AA1995.DAT:\*  
17: /SID88/gcgdata/geneseq/geneseqp/AA1996.DAT:\*  
18: /SID88/gcgdata/geneseq/geneseqp/AA1997.DAT:\*  
19: /SID88/gcgdata/geneseq/geneseqp/AA1998.DAT:\*  
20: /SID88/gcgdata/geneseq/geneseqp/AA2000.DAT:\*  
21: /SID88/gcgdata/geneseq/geneseqp/AA2001.DAT:\*  
22: /SID88/gcgdata/geneseq/geneseqp/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description         |
|------------|-------|-------------|--------|----------|---------------------|
| 1          | 10    | 100.0       | 10     | AAV09353 | Human RAGE V-domain |
| 2          | 10    | 100.0       | 10     | AAV52135 | Human Receptor to   |
| 3          | 10    | 100.0       | 15     | AAW44208 | Human soluble RAGE  |
| 4          | 10    | 100.0       | 15     | AAW33762 | Human RAGE polyep   |
| 5          | 10    | 100.0       | 16     | AAW44214 | Human soluble RAGE  |
| 6          | 10    | 100.0       | 16     | AAW33768 | Human RAGE polyep   |
| 7          | 10    | 100.0       | 30     | AAV09349 | Human RAGE V-domain |
| 8          | 10    | 100.0       | 30     | AAV52134 | Human Receptor to   |
| 9          | 10    | 100.0       | 318    | AAW44200 | Human mature recep  |
| 10         | 10    | 100.0       | 318    | AAW33754 | Human RAGE polyep   |
| 11         | 10    | 100.0       | 332    | AAV52130 | Human Receptor to   |

|    |    |       |     |    |          |                      |
|----|----|-------|-----|----|----------|----------------------|
| 12 | 10 | 100.0 | 340 | 18 | AAW44199 | Human soluble rece   |
| 13 | 10 | 100.0 | 340 | 18 | AAW33753 | Human RAGE polyep    |
| 14 | 10 | 100.0 | 404 | 22 | AAW81925 | Extracellular cit    |
| 15 | 9  | 90.0  | 30  | 20 | AAV09350 | Mouse RAGE V-domain  |
| 16 | 9  | 90.0  | 30  | 20 | AAV09351 | Rat RAGE V-domain    |
| 17 | 8  | 80.0  | 30  | 20 | AAV09352 | Bovine RAGE V-domain |
| 18 | 6  | 60.0  | 30  | 18 | AAW23337 | N-terminal sequec    |
| 19 | 6  | 60.0  | 369 | 21 | AAW52004 | Arabidopsis thalia   |
| 20 | 6  | 60.0  | 400 | 21 | AAW52003 | Arabidopsis thalia   |
| 21 | 6  | 60.0  | 452 | 21 | AAW52002 | Arabidopsis thalia   |
| 22 | 6  | 60.0  | 456 | 21 | AAW20758 | Arabidopsis thalia   |
| 23 | 6  | 60.0  | 456 | 21 | AAW50449 | Arabidopsis thalia   |
| 24 | 6  | 60.0  | 481 | 21 | AAW20757 | Arabidopsis thalia   |
| 25 | 6  | 60.0  | 481 | 21 | AAW50448 | Arabidopsis thalia   |
| 26 | 6  | 60.0  | 548 | 21 | AAW20755 | Arabidopsis thalia   |
| 27 | 6  | 60.0  | 548 | 21 | AAW50447 | Arabidopsis thalia   |
| 28 | 6  | 60.0  | 741 | 17 | AAW89327 | Membrane anchor pr   |
| 29 | 6  | 60.0  | 788 | 22 | AAW88505 | Haemophilus influe   |
| 30 | 5  | 50.0  | 5   | 21 | AAV90767 | Human V-domain N-t   |
| 31 | 5  | 50.0  | 30  | 22 | AAW05141 | Peptide #3823 enco   |
| 32 | 5  | 50.0  | 44  | 21 | AAW08055 | Arabidopsis thalia   |
| 33 | 5  | 50.0  | 45  | 21 | AAW33101 | Zea mays protein f   |
| 34 | 5  | 50.0  | 50  | 21 | AAW22634 | Peptide #6843 enco   |
| 35 | 5  | 50.0  | 54  | 22 | AAW20409 | Peptide #8931 enco   |
| 36 | 5  | 50.0  | 54  | 22 | AAW34894 | Human secreted pro   |
| 37 | 5  | 50.0  | 61  | 21 | AAW08913 | Human secreted pro   |
| 38 | 5  | 50.0  | 69  | 21 | AAW32098 | Human secreted pro   |
| 39 | 5  | 50.0  | 69  | 21 | AAW44665 | Human secreted pro   |
| 40 | 5  | 50.0  | 69  | 21 | AAW08054 | Arabidopsis thalia   |
| 41 | 5  | 50.0  | 69  | 21 | AAW00645 | Human secreted pro   |
| 42 | 5  | 50.0  | 70  | 21 | AAW22559 | Zea mays protein f   |
| 43 | 5  | 50.0  | 70  | 21 | AAW33100 | Zea mays protein f   |
| 44 | 5  | 50.0  | 70  | 21 | AAW64760 | Human 5' EST relat   |
| 45 | 5  | 50.0  | 72  | 19 | AAW5093  | Human secreted pro   |

#### ALIGNMENTS

|          |  |
|----------|--|
| RESULT 1 |  |
| AAV09353 | standard; peptide: 10 AA.  |
| ID       | AAV09353;  |
| XX       | 09-JUL-1999 (first entry)  |
| XX       | Human RAGE V-domain peptide SEQ ID NO:5.                                 |
| XX       | RAGE: V-domain; receptor for advanced glycation endproduct;              |
| XX       | ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome; |
| XX       | senility; renal failure; hyperlipidaemic atherosclerosis; dementia;      |
| XX       | neutonal cytotoxicity; head trauma; amyotrophic lateral sclerosis;       |
| XX       | multiple sclerosis; amyloidosis; autoimmune disease; inflammation;       |
| XX       | tumour; cancer; male impotence; wound healing; periodontal disease;      |
| XX       | neuropathy; retinopathy; nephropathy; neuronal degeneration.             |
| XX       | Homo sapiens.  |
| XX       | OS   |
| XX       | WO9918987-A1.  |
| XX       | 22-APR-1999.   |
| XX       | 09-OCT-1998; 98WO-US21346.   |
| XX       | 09-OCT-1997; 97US-0948131.   |
| XX       | (UYCO) UNIV COLUMBIA NEW YORK.   |
| XX       | Lamster I, Schmidt AM, Stern D, Yan SD;                                  |
| XX       | WPI, 1999-277439/23.   |

PT New peptides based on an advanced glycation end product receptor are  
 PT useful for treating Alzheimer's disease and Down's syndrome  
 XX  
 PS Claim 55: Page 85; 101pp; English.

XX The present invention describes novel isolated peptides (1) having an  
 CC amino acid sequence corresponding to an amino acid sequence of a  
 CC V-domain of a receptor for an advanced glycation end product (RAGE).  
 CC Also described are methods for: (1) inhibiting an amyloid-beta peptide  
 CC (ABP) interaction with a receptor for RAGE when the receptor is on the  
 CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)  
 CC extracellular assembly of an ABP into a fibril; (4) inhibiting  
 CC aggregation of ABP on the surface of a cell; (5) inhibiting  
 CC of a microglial cell into senile plaques; (7) inhibiting activation of a  
 CC microglial cell by an ABP; (8) treating a subject with a condition  
 CC associated with an interaction of an ABP with a receptor for RAGE on a  
 CC cell; (9) evaluating the ability of an agent to inhibit binding of an  
 CC ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)  
 CC inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting  
 CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction  
 CC with a receptor for RAGE when the receptor is on the surface of a cell;  
 CC and (13) treating a subject with a condition associated with an  
 CC interaction of an RAGE with a receptor for RAGE on a cell. The methods  
 CC can be used for treating conditions associated with an interaction of an  
 CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's  
 CC disease, senility, renal failure, hyperlipidemic atherosclerosis,  
 CC neuronal cytotoxicity, Down's syndrome, dementia associated with head  
 CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,  
 CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,  
 CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy  
 CC or neuronal degeneration.  
 XX

SO Sequence 10 AA;

Query Match 100.0%; Score 10; DB 20; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.00011;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITARIGE 10  
 | | | | | | | | | |  
 Db 1 agnitarige 10

# RESULT 2

AA52135  
 ID AAY52135 standard; peptide; 10 AA.

XX  
 AC AAY52135;

DT 28-JAN-2000 (first entry)

DE Human Receptor to AGE (RAGE) amino acid sequence fragment #4.

KW Soluble receptor for advanced glycation endproducts; RAGE; tumour;  
 invasion; metastasis; amphoterin; neuron; inhibit; therapy.

OS Homo sapiens.

PN WO954485-A1.

PD 28-OCT-1999.

PF 16-APR-1999; 99WO-US08427.

PR 17-APR-1998; 98US-0062365.

PA (UYCO ) UNIV COLUMBIA NEW YORK.

PI Schmidt AM, Stern D;

DR WPI; 2000-013260/01.

XX Inhibiting tumour invasion or spreading by administration of soluble  
 PT receptor for advanced glycation endproducts -  
 XX  
 PS Claim 30: Page 62; 88pp; English.

XX This is the amino acid sequence of a fragment of the human soluble  
 CC Receptor for Advanced Glycation Endproducts (RAGE). RAGE interacts with  
 CC a range of physiologically and pathophysiologically relevant ligands  
 CC when considering tumour invasion. In normal developing neurons RAGE  
 CC colocalizes with amphoterin which is a matrix associated polypeptide.  
 CC The expression of both RAGE and amphoterin decreases after birth, but  
 CC both have increased expression in tumours. RAGE polypeptides  
 CC AAY52132-Y52135 are used in the invention in a method for inhibiting  
 CC tumour invasion and metastasis. The method involves inhibiting tumour  
 CC invasion and metastasis via administration of a therapeutically effective  
 CC amount of the pharmaceutical composition containing a RAGE polypeptide.  
 CC The invention also relates to a method for evaluating the ability of an  
 CC agent to inhibit tumour invasion in a local cellular environment. RAGE  
 CC can be administered to a patient in a pharmaceutically acceptable  
 CC carrier.  
 XX

SO Sequence 10 AA;

Query Match 100.0%; Score 10; DB 21; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.00011;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITARIGE 10  
 | | | | | | | | | |  
 Db 1 agnitarige 10

# RESULT 3

AAW4208  
 ID AAW4208 standard; peptide; 15 AA.

XX  
 AC AAW4208;

DT 14-MAY-1998 (first entry)

DE Human soluble RAGE immunologically active fragment SEQ ID NO:12.

KW Human: soluble receptor; advanced glycosylation end product; RAGE;  
 AGE; antibody; vascular permeability; immunologically active fragment;  
 diabetes mellitus.

OS Homo sapiens.

PN WO9739125-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01834.

PR 16-APR-1996; 96US-0633148.

PA (SCHD ) SCHERING PATENTE AG.

PI Hollander DA, Morser MJ, Nagashima M;

DR WPI; 1997-558580/51.

PD 1997-558580/51.

PF Anti-advanced glycosylation end product polypeptide antibody

PT prevents receptor binding and therefore reduces vascular

PS permeability, useful to treat diabetes mellitus

CC Claim 2: Page 46; 90pp; English.

CC The present sequence represents an immunologically active fragment  
 CC of a soluble human receptor to an advanced glycosylation end  
 CC product (RAGE) polypeptide. The present invention describes



CC an isolated antibody (Ab), specifically immunoreactive with  
 CC RAGE. Advanced glycosylation end products (AGE) of proteins are  
 CC non-enzymatically glycosylated proteins, which accumulate in vascular  
 CC tissue in ageing, and at an accelerated rate in individuals with  
 CC diabetes. The Ab, which prevents the interaction between an AGE and its  
 CC receptor (RAGE), reduces vascular permeability. The Ab can be used to  
 CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive  
 CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis  
 CC associated amyloidosis or atherosclerosis. The Ab can also be used for  
 CC the isolation and purification of human RAGE polypeptide.

XX Sequence 15 AA;

Query Match 100.0%; Score 10; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.00015;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10  
 |||||  
 Db 1 agnitarige 10

RESULT 4  
 AAW33762

ID AAW33762 standard; peptide; 15 AA.

XX AAW33762;

DT 08-MAY-1998 (first entry)

DE Human RAGE polypeptide fragment 8.

KW Advanced glycosylation end-product receptor; RAGE; screening; AGE;  
 KW vascular permeability; diabetes mellitus; treatment; atherosclerosis;  
 KW Alzheimer's disease.

OS Homo sapiens.

PN W09739121-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01832.

PR 16-APR-1996; 96US-0633147.

XX (SCHD ) SCHERING AG.

PA Morser MJ, Nagashima M;

PI WPI; 1997-526458/48.

DR New soluble advanced glycosylation end-product receptor polypeptide  
 XX - used for reducing vascular permeability, complications of diabetes  
 XX etc., also for purification and to screen for modulators

PS Claim 6; Page 55; 91pp; English.

CC This is a peptide fragment of a human advanced glycosylation end-product  
 CC receptor (RAGE) polypeptide. The RAGE polypeptides and its active  
 CC fragments or their mimetics can inhibit interaction between advanced  
 CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They  
 CC are used to treat diseases associated with AGE/RAGE interaction, such as  
 CC increased vascular permeability, diabetes mellitus (particularly  
 CC complications such as micro- or macro- vasculopathy or occlusive vascular  
 CC disorders such as neuropathy, nephropathy, atherosclerosis or  
 CC retinopathy) or haemodialysis-associated amyloidosis, also activation  
 CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or  
 CC age-related disorders such as oxidative stress. These RAGE polypeptides  
 CC are also used, when immobilised, to purify AGE from a protein mixture and  
 CC to screen for compounds that are agonists and antagonists of AGE/RAGE  
 CC interaction. They can also be used diagnostically to detect abnormal

CC levels of AGE. Antibodies against RAGE polypeptides are useful as  
 CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of  
 CC interaction between AGE and RAGE or other receptors and for purification  
 CC and quantification of RAGE polypeptides. The encoding nucleic acids are  
 CC used to express recombinant RAGE and as probes for isolating related  
 CC genes.

XX Sequence 15 AA;

Query Match 100.0%; Score 10; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.00015;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10  
 |||||  
 Db 1 agnitarige 10

RESULT 5

AAW44214

ID AAW44214 standard; peptide; 16 AA.

XX AAW44214;

DT 14-MAY-1998 (first entry)

DE Human soluble RAGE immunologically active fragment SEQ ID NO:18.

KW Human; soluble receptor; advanced glycosylation end product; RAGE;  
 KW AGE; antibody; vascular permeability; immunologically active fragment;  
 KW diabetes mellitus.

OS Homo sapiens.

PN W09739125-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01834.

PR 16-APR-1996; 96US-0633148.

PA (SCHD ) SCHERING PATENTE AG.

PI Hollander DA, Morser MJ, Nagashima M;

DR WPI; 1997-558580/51.

PT Anti-advanced glycosylation end product polypeptide antibody -  
 PT prevents receptor binding and therefore reduces vascular  
 PT permeability, useful to treat diabetes mellitus

PS Claim 2; Page 49; 90pp; English.

CC The present sequence represents an immunologically active fragment  
 CC of a soluble human receptor to an advanced glycosylation end  
 CC product (RAGE) polypeptide. The present invention describes  
 CC an isolated antibody (Ab), specifically immunoreactive with  
 CC RAGE. Advanced glycosylation end products (AGE) of proteins are  
 CC non-enzymatically glycosylated proteins, which accumulate in vascular  
 CC tissue in ageing, and at an accelerated rate in individuals with  
 CC diabetes. The Ab, which prevents the interaction between an AGE and its  
 CC receptor (RAGE), reduces vascular permeability. The Ab can be used to  
 CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive  
 CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis  
 CC associated amyloidosis or atherosclerosis. The Ab can also be used for  
 CC the isolation and purification of human RAGE polypeptide.

XX Sequence 16 AA;

Query Match 100.0%; Score 10; DB 18; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.00016;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITARIGE 10  
Db 1 agnitarrige 10

## RESULT 6

AAW33768  
ID AAW33768 standard; peptide; 16 AA.

AAW33768;

08-MAY-1998 (first entry)

Human RAGE polypeptide fragment 14.

Advanced glycosylation end-product receptor; RAGE; screening; AGE;  
vascular permeability; diabetes mellitus; treatment; atherosclerosis;  
Alzheimer's disease.

Homo sapiens.

MO9739121-A1.

23-OCT-1997.

11-APR-1997; 97WO-EP01832.

16-APR-1996; 96US-0633147.

(SCHD) SCHERING AG.

Morser MJ, Nagashima M;

WPI; 1997-526458/48.

New soluble advanced glycosylation end-product receptor polypeptide  
- used for reducing vascular permeability; complications of diabetes  
etc., also for purification and to screen for modulators

Disclosure: Page 9, 91pp; English.

This is a peptide fragment of a human advanced glycosylation end-product  
receptor (RAGE) polypeptide. The RAGE polypeptides and its active  
fragments or their mimetics can inhibit interaction between advanced  
glycosylation end-products (AGE) and a receptor (specifically RAGE). They  
are used to treat diseases associated with AGE/RAGE interaction, such as  
increased vascular permeability, diabetes mellitus (particularly  
complications such as micro- or macro- vasculopathy or occlusive vascular  
disease) or haemodialysis-associated amyloidosis, also activation  
of microglial cells by beta-amyloid peptides in Alzheimer's disease or  
age-related disorders such as oxidative stress. These RAGE polypeptides  
are also used, when immobilised, to purify AGE from a protein mixture and  
to screen for compounds that are agonists and antagonists of AGE/RAGE  
interaction. They can also be used diagnostically to detect abnormal  
levels of AGE. Antibodies against RAGE polypeptides are useful as  
immunoassay reagents for measurement of RAGE levels, and as inhibitors of  
interaction between AGE and RAGE or other receptors and for purification  
and quantification of RAGE polypeptides. The encoding nucleic acids are  
used to express recombinant RAGE and as probes for isolating related  
genes.

Sequence 16 AA:

Query Match 100.0%; Score 10; DB 18; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00016;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITARIGE 10

Db 1 agnitarrige 10

## RESULT 7

AAV09349  
ID AAV09349 standard; peptide; 30 AA.

AAV09349;

09-JUL-1999 (first entry)

Human RAGE V-domain peptide SEQ ID NO:1.

RAGE: V-domain; receptor for advanced glycation endproduct;  
ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;  
senility; renal failure; hyperlipidaemic atherosclerosis; dementia;  
neural cytotoxicity; head trauma; amyotrophic lateral sclerosis;  
multiple sclerosis; amyloidosis; autoimmune disease; inflammation;  
tumour; cancer; male impotence; wound healing; periodontal disease;  
neuropathy; retinopathy; nephropathy; neuronal degeneration.

Homo sapiens.

WO9918987-A1.

22-APR-1999.

09-OCT-1998; 98WO-US21346.

09-OCT-1997; 97US-0948131.

(UYCO) UNIV COLUMBIA NEW YORK.

Lamster I, Schmidt AM, Stern D, Yan SD;

WPI; 1999-277439/23.

New peptides based on an advanced glycation end product receptor are  
useful for treating Alzheimer's disease and Down's syndrome

Claim 2; Page 78; 101pp; English.

The present invention describes novel isolated peptides (I) having an  
amino acid sequence corresponding to an amino acid sequence of a  
V-domain of a receptor for an advanced glycation end product (RAGE).  
Also described are methods for: (1) inhibiting an amyloid-beta peptide  
(ABP) interaction with a receptor for RAGE when the receptor is on the  
surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)  
inhibiting formation of an ABP fibril on a cell; (4) inhibiting  
extracellular assembly of an ABP into a fibril; (5) inhibiting  
aggregation of ABP on the surface of a cell; (6) inhibiting infiltration  
of a microglial cell into senile plaques; (7) inhibiting activation of a  
microglial cell by an ABP; (8) treating a subject with a condition  
associated with an interaction of an ABP with a receptor for RAGE on a  
cell; (9) evaluating the ability of an agent to inhibit binding of an  
ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)  
inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting  
periodontal disease in a subject; (12) inhibiting an RAGE's interaction  
with a receptor for RAGE when the receptor is on the surface of a cell;  
and (13) treating a subject with a condition associated with an  
interaction of an RAGE with a receptor for RAGE on a cell. The methods  
can be used for treating conditions associated with an interaction of an  
ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's  
disease, senility, renal failure, hyperlipidaemic atherosclerosis,  
neural cytotoxicity, Down's syndrome, dementia associated with head  
trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,  
an autoimmune disease, inflammation, a tumour, cancer, male impotence,  
wound healing, periodontal disease, neuropathy, retinopathy, nephropathy  
or neuronal degeneration.

Sequence 30 AA:

Query Match 100.0%; Score 10; DB 20; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 0.00027;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10  
 |||||  
 Db 1 aqntarige 10

## RESULT 8

AAV52134  
 ID AAV52134 standard; protein; 30 AA.

AC AAV52134;

DT 28-JAN-2000 (first entry)

DE Human Receptor to AGE (RAGE) amino acid sequence fragment #3.

KM Soluble receptor for advanced glycation endproducts; RAGE; tumour;  
 invasion; metastasis; amphoterin; neuron; inhibit; therapy.

OS Homo sapiens.

PN W0954485-A1.

PD 28-OCT-1999.

PF 16-APR-1999; 99WO-US08427.

PR 17-APR-1998; 98US-0062365.

PA (UYCO ) UNIV COLUMBIA NEW YORK.

PI Schmidt AM, Stern D;

DR WPI; 2000-013260/01.

PT Inhibiting tumour invasion or spreading by administration of soluble  
 receptor for advanced glycation endproducts -

PS Claim 29; Page 62; 88pp; English.

CC This is the amino acid sequence of a fragment of the human soluble  
 CC Receptor for Advanced Glycation Endproducts (RAGE). RAGE interacts with  
 CC a range of physiologically and pathophysiologically relevant ligands  
 CC when considering tumour invasion. In normal developing neurons RAGE  
 CC colocalizes with amphoterin which is a matrix associated polypeptide.  
 CC The expression of both RAGE and amphoterin decreases after birth, but  
 CC both have increased expression in tumours. RAGE polypeptides  
 CC AAV52132-Y52135 are used in the invention in a method for inhibiting  
 CC tumour invasion and metastasis. The method involves inhibiting tumour  
 CC invasion and metastasis via administration of a therapeutically effective  
 CC amount of the pharmaceutical composition containing a RAGE polypeptide.  
 CC The invention also relates to a method for evaluating the ability of an  
 CC agent to inhibit tumour invasion in a local cellular environment. RAGE  
 CC can be administered to a patient in a pharmaceutically acceptable  
 CC carrier.

SQ Sequence 30 AA;

Query Match 100.0%; Score 10; DB 21; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.00027;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10  
 |||||  
 Db 1 aqntarige 10

## RESULT 9

AAW44200  
 ID AAW44200 standard; Protein; 318 AA.

AC AAW44200;

DT 14-MAY-1998 (first entry)

DE Human mature receptor to an advanced glycosylation end product.

KM Human; soluble receptor; advanced glycosylation end product; RAGE;  
 AGE; antibody; vascular permeability; diabetes mellitus.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Misc-difference 66 /note="encoded by CCR"

FT W09739125-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01834.

PR 16-APR-1996; 96US-0633148.

PA (SCHD ) SCHERING PATENTE AG.

PI Hollander DA, Morser MJ, Nagashima M;

DR WPI; 1997-558580/51.

DT N-PSDB; AAV12395.

PT Anti-advanced glycosylation end product polypeptide antibody -  
 PT prevents receptor binding and therefore reduces vascular  
 PT permeability, useful to treat diabetes mellitus

PS Claim 2; Page 42-43; 90pp; English.

CC The present sequence represents a mature human receptor to an advanced  
 CC glycosylation end product (RAGE) polypeptide. The present invention  
 CC describes an isolated antibody (Ab), specifically immunoreactive with  
 CC RAGE. Advanced glycosylation end products (AGE) of proteins are  
 CC non-enzymatically glycosylated proteins, which accumulate in vascular  
 CC tissue in ageing, and at an accelerated rate in individuals with  
 CC diabetes. The Ab, which prevents the interaction between an AGE and its  
 CC receptor (RAGE), reduces vascular permeability. The Ab can be used to  
 CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive  
 CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis  
 CC associated amyloidosis or atherosclerosis. The Ab can also be used for  
 CC the isolation and purification of human RAGE polypeptide.

SQ Sequence 318 AA;

Query Match 100.0%; Score 10; DB 18; Length 318;

Best Local Similarity 100.0%; Pred. No. 0.0019;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10  
 |||||  
 Db 1 aqntarige 10

## RESULT 10

AAW33754  
 ID AAW33754 standard; Protein; 318 AA.

AC AAW33754;

DT 08-MAY-1998 (first entry)

DE Human RAGE polypeptide (318 amino acid residues).

|   |   |
|---|---|
| XX  | Homo sapiens.   |
| OS  |   |
| XX  |   |
| PN  | M09954485-A1.   |
| PD  | 28-OCT-1999.  |
| XX  |   |
| Pf  | 16-APR-1999; 99MO-US08427.  |
| PR  | 17-APR-1998; 98US-0062365.  |
| XX  |   |
| PA  | (UYCO ) UNIV COLUMBIA NEW YORK.   |
| XX  |   |
| PI  | Schmidt AM, Stern D;  |
| XX  |   |
| DR  | WPT; 2000-013260/01.  |
| XX  |   |
| PT  | Inhibiting tumour invasion or spreading by administration of soluble receptor for advanced glycation endproducts -  |
| PS  | Disclosure; Page 10-11; 88pp; English.  |
| XX  |   |
| CC  | This is the amino acid sequence of the human soluble Receptor for Advanced Glycation Endproducts (RAGE). RAGE interacts with a range of physiologically and pathophysiologically relevant ligands when considering tumour invasion. In normal developing neurons RAGE localizes with amphoterin which is a matrix associated polypeptide. The expression of both RAGE and amphoterin decreases after birth, but both have increased expression in tumours. RAGE polypeptides AA952132-952135 are used in the invention in a method for inhibiting tumour invasion and metastasis. The method involves inhibiting tumour invasion and metastasis via administration of a therapeutically effective amount of the pharmaceutical composition containing a RAGE polypeptide. The invention also relates to a method for evaluating the ability of an agent to inhibit tumour invasion in a local cellular environment. RAGE can be administered to a patient in a pharmaceutically acceptable carrier. |
| CC  |   |
| CC  |   |
| XX  |   |
| Sequence  | 332 AA:   |
| Query Match   | 100.0%; Score 10; DB 21; Length 332;  |
| Best Local Similarity   | 100.0%; Pred. No. 0.002;  |
| Matches 10; Conservative  | 0; Mismatches 0; Indels 0; Gaps 0.  |
| Oy  | 1 ACONTARIGE 10<br>   |
| Dd  | 1 agnitarige 10   |
| RESULT 12   |   |
| AAM44199  | ID AAM44199 standard; Protein; 340 AA.  |
| AA44199;  | DT 14-MAY-1998 (first entry)  |
| Human soluble receptor to an advanced glycosylation end product.  |   |
| Human; soluble receptor; advanced glycosylation end product; RAGE; AGE; antibody; vascular permeability; diabetes mellitus. |   |
| Homo sapiens.   |   |
| WO9739125-A1.   |   |
| 23-OCT-1997.  |   |
| 11-APR-1997;  | 97WO-EPO1834.   |
| 16-APR-1996;  | 96US-0633148.   |

PA (SCHD ) SCHERING PATENTE AG.  
 XX  
 PI Hollander DA, Morser MJ, Nagashima M;  
 XX WPI, 1997-556580/51.  
 DR N-PSDB; AAV12394.  
 XX  
 PT Anti-advanced glycosylation end-product polypeptide antibody -  
 PT prevents receptor binding and therefore reduces vascular  
 PT permeability, useful to treat diabetes mellitus  
 XX  
 PS Claim 2; Page 40-41; 90pp; English.  
 XX  
 CC The present sequence represents a soluble human receptor to an advanced  
 CC glycosylation end-product (RAGE) polypeptide. The present invention  
 CC describes an isolated antibody (Ab), specifically immunoreactive with  
 CC RAGE. Advanced glycosylation end-products (AGE) of proteins are  
 CC non-enzymatically glycosylated proteins, which accumulate in vascular  
 CC tissue in ageing, and at an accelerated rate in individuals with  
 CC diabetes. The Ab, which prevents the interaction between an AGE and its  
 CC receptor (RAGE), reduces vascular permeability. The Ab can be used to  
 CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive  
 CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis  
 CC associated amyloidosis or atherosclerosis. The Ab can also be used for  
 CC the isolation and purification of human RAGE polypeptide.  
 CC  
 SQ Sequence 340 AA;

Query Match 100.0%; Score 10; DB 18; Length 340;  
 Best Local Similarity 100.0%; Pred. No. 0.002;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGE 10  
 |||||||||  
 Db 23 agnitarige 32

RESULT 13  
 AAW33753  
 ID AAW33753 standard; Protein; 340 AA.  
 XX  
 AC AAW33753;  
 XX  
 DT 08-MAY-1998 (first entry)  
 XX  
 DE Human RAGE polypeptide (340 amino acid residues).  
 XX  
 KW Advanced glycosylation end-product receptor; RAGE; screening; AGE;  
 KW vascular permeability; diabetes mellitus; treatment; atherosclerosis;  
 KW Alzheimer's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9739121-A1.  
 XX  
 PD 23-OCT-1997.  
 XX  
 PF 11-APR-1997; 97WO-EP01832.  
 XX  
 PR 16-APR-1996; 96US-0633147.  
 XX  
 PA (SCHD ) SCHERING AG.  
 XX  
 PI Morser MJ, Nagashima M;  
 XX WPI, 1997-526458/48.  
 DR N-PSDB; AAV06517.  
 XX  
 PT New soluble advanced glycosylation end-product receptor polypeptide  
 PT - used for reducing vascular permeability, complications of diabetes  
 PT etc., also for purification and to screen for modulators  
 XX

PS Claim 3; Fig 1A; 91pp; English.  
 XX  
 CC This is a human advanced glycosylation end-product receptor (RAGE)  
 CC polypeptide (340 amino acid residues). The RAGE polypeptides and its  
 CC active fragments or their mimetics, inhibit interaction between advanced  
 CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They  
 CC are used to treat diseases associated with AGE/RAGE interaction, such as  
 CC increased vascular permeability, diabetes mellitus (particularly  
 CC complications such as micro- or macro-vasculopathy or occlusive vascular  
 CC disorders such as neuropathy, nephropathy, retinopathy or  
 CC atherosclerosis) or haemodialysis-associated amyloidosis, also activation  
 CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or  
 CC age-related disorders such as oxidative stress. These RAGE polypeptides  
 CC are also used, when immobilised, to purify AGE from a protein mixture and  
 CC to screen for compounds that are agonists and antagonists of AGE/RAGE  
 CC interaction. They can also be used diagnostically to detect abnormal  
 CC levels of AGE. Antibodies against RAGE polypeptides are useful as  
 CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of  
 CC interaction between AGE and RAGE or other receptors and for purification  
 CC and quantification of RAGE polypeptides. The encoding nucleic acids are  
 CC used to express recombinant RAGE and as probes for isolating related  
 CC genes.  
 CC  
 SQ Sequence 340 AA;

Query Match 100.0%; Score 10; DB 18; Length 340;  
 Best Local Similarity 100.0%; Pred. No. 0.002;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGE 10  
 |||||||||  
 Db 23 agnitarige 32

RESULT 14  
 AAB81925  
 ID AAB81925 standard; protein; 404 AA.  
 XX  
 AC AAB81925;  
 XX  
 DT 15-JUN-2001 (first entry)  
 XX  
 DE Extracorporeal circulation material receptor protein.  
 XX  
 DE Extracorporeal circulation; carbonyl stress product; receptor;  
 KW diabetes; vascular lesion; excretory dysfunction.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200118060-A1.  
 XX  
 PD 15-MAR-2001.  
 XX  
 PF 08-SEP-2000; 2000WO-JP06172.  
 XX  
 PR 08-SEP-1999; 99JP-0254463.  
 XX  
 PA (TORA ) TORAY IND INC.  
 XX  
 PI Shimizu S, Kubota M, Akiyama H, Usui M;  
 XX WPI, 2001-290314/30.  
 XX  
 PT Material for extracorporeal circulation, applicable in selective  
 PT elimination of diabetic complication factors such as carbonyl stress  
 PT products caused by abnormally promoted carbonyl stress from excretory  
 PT dysfunction in vascular lesions -  
 XX  
 PS Claim 1; Page 31-32; 36pp; Japanese.  
 XX  
 CC The present invention describes a material for extracorporeal circulation  
 CC which is made from a water-insoluble carrier immobilized with a protein

CC having the sequence shown here. The materials of the invention, including  
 CC adsorbents, are for extracorporeal circulation, which are applicable in  
 CC the selective elimination of diabetic complication factors from a body  
 CC fluid, and are therefore useful in treating vascular lesions like  
 CC arteriosclerosis due to carbonyl stress products caused by abnormally  
 CC promoted carbonyl stress from excretory dysfunction.

SO Sequence 404 AA;

Query Match 100.0%; Score 10; DB 22; Length 404;  
 Best Local Similarity 100.0%; Pred. No. 0.0023;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10  
 Db 23 agntarige 32

RESULT 15

AA09350  
 ID AA09350 standard; peptide; 30 AA.

AC AA09350;

DT 09-JUL-1999 (first entry)

DE Mouse RAGE V-domain peptide SEQ ID NO:2.

KW RAGE: V-domain; receptor for advanced glycation endproduct;  
 KW ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;  
 KW senility; renal failure; hyperlipidaemic atherosclerosis; dementia;  
 KW neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;  
 KW multiple sclerosis; amyloidosis; autoimmune disease; inflammation;  
 KW tumour; cancer; male impotence; wound healing; periodontal disease;  
 KW neuropathy; retinopathy; nephropathy; neuronal degeneration.

OS Mus sp.

PN W09918987-A1.

PD 22-APR-1999.

PF 09-OCT-1998; 98WO-US21346.

PR 09-OCT-1997; 97US-0948131.

PA (UYCO ) UNIV COLUMBIA NEW YORK.

PI Lamster I, Schmidt AM, Stern D, Yan SD;

DR WPI; 1999-277439/23.

PT New peptides based on an advanced glycation end product receptor are  
 useful for treating Alzheimer's disease and Down's syndrome

PS Claim 3; Page 78; 101pp; English.

CC The present invention describes novel isolated peptides (1) having an  
 CC amino acid sequence corresponding to an amino acid sequence of a  
 CC V-domain of a receptor for an advanced glycation end product (RAGE).  
 CC Also described are methods for: (1) inhibiting an amyloid-beta peptide  
 CC (ABP) interaction with a receptor for RAGE when the receptor is on the  
 CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)  
 CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting  
 CC extracellular assembly of an ABP into a fibril; (5) inhibiting  
 CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration  
 CC of a microglial cell into senile plaques; (7) inhibiting activation of a  
 CC microglial cell by an ABP; (8) treating a subject with a condition  
 CC associated with an interaction of an ABP with a receptor for RAGE on a  
 CC cell; (9) evaluating the ability of an agent to inhibit binding of an  
 CC ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)  
 CC inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting

CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction  
 CC with a receptor for RAGE when the receptor is on the surface of a cell;  
 CC and (13) treating a subject with a condition associated with an  
 CC interaction of an RAGE with a receptor for RAGE on a cell. The methods  
 CC can be used for treating conditions associated with an interaction of an  
 CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's  
 CC disease, senility, renal failure, hyperlipidaemic atherosclerosis,  
 CC neuronal cytotoxicity, Down's syndrome, dementia associated with head  
 CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,  
 CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,  
 CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy  
 CC or neuronal degeneration.

SO Sequence 30 AA;

Query Match 90.0%; Score 9; DB 20; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 0.0031;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ONITARIGE 10  
 Db 2 qntarige 10

Search completed: April 24, 2002, 09:21:51  
 Job time: 250 sec



THIS PAGE BLANK (USPTO)



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein -- protein search, using sw model

Run on: April 24, 2002, 09:22:30 ; Search time 32.21 Seconds  
(without alignments)  
6.986 Million cell updates/sec

Title: US-09-689-469-6  
Perfect score: 10  
Sequence: 1 AONITARICE 10

Scoring table:  
OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 212252 seqs, 22503292 residues

Word size : 0

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Issued\_Patents\_Aa.\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PT05.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID                 | Description       |
|------------|-------|-------------|--------|--------------------|-------------------|
| 1          | 10    | 100.0       | 15     | US-08-633-148-12   | Sequence 12, Appl |
| 2          | 10    | 100.0       | 16     | US-08-633-148-18   | Sequence 18, Appl |
| 3          | 10    | 100.0       | 318    | US-08-633-148-4    | Sequence 4, Appl  |
| 4          | 10    | 100.0       | 340    | US-08-633-148-2    | Sequence 2, Appl  |
| 5          | 6     | 60.0        | 741    | US-08-277-231A-4   | Sequence 4, Appl  |
| 6          | 6     | 60.0        | 741    | US-08-473-750-7    | Sequence 7, Appl  |
| 7          | 6     | 60.0        | 741    | US-08-477-326-7    | Sequence 7, Appl  |
| 8          | 5     | 50.0        | 63     | US-08-637-759B-191 | Sequence 191, App |
| 9          | 5     | 50.0        | 63     | US-08-871-355A-191 | Sequence 191, App |
| 10         | 5     | 50.0        | 72     | US-09-188-930-153  | Sequence 153, App |
| 11         | 5     | 50.0        | 72     | US-09-188-930-304  | Sequence 304, App |
| 12         | 5     | 50.0        | 146    | US-08-543-238-11   | Sequence 11, Appl |
| 13         | 5     | 50.0        | 146    | US-08-420-526-11   | Sequence 11, Appl |
| 14         | 5     | 50.0        | 198    | US-08-278-091-16   | Sequence 16, Appl |
| 15         | 5     | 50.0        | 198    | US-08-483-859-16   | Sequence 16, Appl |
| 16         | 5     | 50.0        | 198    | US-08-472-173-16   | Sequence 16, Appl |
| 17         | 5     | 50.0        | 198    | US-08-487-167-16   | Sequence 16, Appl |
| 18         | 5     | 50.0        | 198    | US-08-483-816-16   | Sequence 16, Appl |
| 19         | 5     | 50.0        | 198    | US-08-296-149-16   | Sequence 16, Appl |
| 20         | 5     | 50.0        | 198    | US-08-801-499-16   | Sequence 16, Appl |
| 21         | 5     | 50.0        | 198    | US-08-615-271-16   | Sequence 16, Appl |
| 22         | 5     | 50.0        | 198    | US-09-074-660-16   | Sequence 16, Appl |
| 23         | 5     | 50.0        | 198    | US-09-074-659-16   | Sequence 16, Appl |
| 24         | 5     | 50.0        | 198    | US-09-106-468-16   | Sequence 16, Appl |
| 25         | 5     | 50.0        | 198    | US-09-106-466A-16  | Sequence 16, Appl |
| 26         | 5     | 50.0        | 198    | US-09-106-467-16   | Sequence 16, Appl |
| 27         | 5     | 50.0        | 236    | PCT-US91-08177-17  | Sequence 17, Appl |

|    |   |      |     |   |                   |                   |
|----|---|------|-----|---|-------------------|-------------------|
| 28 | 5 | 50.0 | 241 | 5 | PCT-US91-08177-7  | Sequence 7, Appl  |
| 29 | 5 | 50.0 | 305 | 4 | US-09-248-588-11  | Sequence 11, Appl |
| 30 | 5 | 50.0 | 305 | 4 | US-09-248-588-13  | Sequence 13, Appl |
| 31 | 5 | 50.0 | 352 | 3 | US-08-967-272-2   | Sequence 2, Appl  |
| 32 | 5 | 50.0 | 373 | 1 | US-07-723-002C-2  | Sequence 2, Appl  |
| 33 | 5 | 50.0 | 373 | 1 | US-07-723-002C-4  | Sequence 4, Appl  |
| 34 | 5 | 50.0 | 379 | 1 | US-07-723-002C-6  | Sequence 6, Appl  |
| 35 | 5 | 50.0 | 379 | 2 | US-08-887-365-36  | Sequence 36, Appl |
| 36 | 5 | 50.0 | 397 | 1 | US-07-956-697B-5  | Sequence 5, Appl  |
| 37 | 5 | 50.0 | 397 | 1 | US-08-263-098-5   | Sequence 5, Appl  |
| 38 | 5 | 50.0 | 420 | 5 | PCT-US96-10602-10 | Sequence 10, Appl |
| 39 | 5 | 50.0 | 439 | 3 | US-08-993-359-24  | Sequence 24, Appl |
| 40 | 5 | 50.0 | 439 | 3 | US-09-221-654-2   | Sequence 2, Appl  |
| 41 | 5 | 50.0 | 439 | 3 | US-08-989-358A-2  | Sequence 2, Appl  |
| 42 | 5 | 50.0 | 453 | 4 | US-09-013-881-5   | Sequence 5, Appl  |
| 43 | 5 | 50.0 | 461 | 2 | US-08-630-822A-68 | Sequence 68, Appl |
| 44 | 5 | 50.0 | 461 | 2 | US-09-005-069-68  | Sequence 68, Appl |
| 45 | 5 | 50.0 | 507 | 1 | US-08-097-829-6   | Sequence 6, Appl  |

## ALIGNMENTS

```
RESULT 1
US-08-633-148-12
Sequence 12, Application US/08633148
Patent No. 5864018
GENERAL INFORMATION:
APPLICANT: MORSEY, MICHAEL J.
APPLICANT: NAGASHIMA, MARIKO
APPLICANT: HOLLANDER, DORIS A.
TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESS: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,148
FILING DATE: 16-APR-1996
CLASSIFICATION: A35
ATTORNEY/AGENT INFORMATION:
NAME: MORPHY ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 014618-005600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-633-148-12
Query Match 100.0% Score 10; DB 2; Length 15;
Best Local Similarity 100.0% Pred. No. 2.7e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 AONITARICE 10
|||||||||
```

Db 1 AONITARIGE 10

## RESULT 2

US-08-633-148-18  
Sequence 18, Application US/08633148  
Patent No. 5864018

## GENERAL INFORMATION:

APPLICANT: MORSER, MICHAEL J.  
APPLICANT: NAGASHIMA, MARIKO  
APPLICANT: HOLLANDER, DORIS A.

TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION  
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR  
NUMBER OF SEQUENCES: 23

## CORRESPONDENCE ADDRESSES:

ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP  
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: U.S.A.

ZIP: 94111

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/633,148  
FILING DATE: 16-APR-1996

## CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

NAME: MURPHY ESO., MATTHEW B.

REGISTRATION NUMBER: 39,787

REFERENCE/DOCKET NUMBER: 014618-0056000US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 18:

## SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-633-148-18

## Query Match

Best Local Similarity 100.0%; Score 10; DB 2; Length 16;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITARIGE 10

Db 1 AONITARIGE 10

## RESULT 3

US-08-633-148-4  
Sequence 4, Application US/08633148  
Patent No. 5864018

## GENERAL INFORMATION:

APPLICANT: MORSER, MICHAEL J.  
APPLICANT: NAGASHIMA, MARIKO  
APPLICANT: HOLLANDER, DORIS A.

TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION  
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR  
NUMBER OF SEQUENCES: 23

## CORRESPONDENCE ADDRESSES:

ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP  
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: U.S.A.

ZIP: 94111

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/633,148

FILING DATE: 16-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURPHY ESO., MATTHEW B.

REGISTRATION NUMBER: 39,787

REFERENCE/DOCKET NUMBER: 014618-0056000US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 318 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-633-148-4

## Query Match

Best Local Similarity 100.0%; Score 10; DB 2; Length 318;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITARIGE 10

Db 1 AONITARIGE 10

## RESULT 4

US-08-633-148-2  
Sequence 2, Application US/08633148  
Patent No. 5864018

## GENERAL INFORMATION:

APPLICANT: MORSER, MICHAEL J.  
APPLICANT: NAGASHIMA, MARIKO  
APPLICANT: HOLLANDER, DORIS A.

TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION  
TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR  
NUMBER OF SEQUENCES: 23

## CORRESPONDENCE ADDRESSES:

ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP  
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: U.S.A.

ZIP: 94111

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/633,148

FILING DATE: 16-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURPHY ESO., MATTHEW B.

REGISTRATION NUMBER: 39,787

REFERENCE/DOCKET NUMBER: 014618-0056000US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 340 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-633-148-2

Query Match 100.0%; Score 10; DB 2; Length 340;  
Best Local Similarity 100.0%; Pred. No. 0.0004;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONTARIGE 10  
|||||  
DB 23 AONTARIGE 32

RESULT 5  
US-08-277-231A-4  
Sequence 4, Application US/08277231A  
Patent No. 5643725  
GENERAL INFORMATION:  
APPLICANT: Green, Bruce A.  
APPLICANT: Brinton, Charles C.  
TITLE OF INVENTION: Sequence and Analysis of LKP P11n  
Patent No. 5643725  
TITLE OF INVENTION: Structural Genes and the LKP P11 Operon of No. 5643725typable  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/277.231A  
FILING DATE: 19-JUL-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Carroll, Alice O.  
REGISTRATION NUMBER: 32,542  
REFERENCE/DOCKET NUMBER: ACC94-02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 741 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-277-231A-4

Query Match 60.0%; Score 6; DB 1; Length 741;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TARIGE 10  
|||||  
DB 157 TARIGE 162

RESULT 6  
US-08-473-750-7  
Sequence 7, Application US/08473750  
Patent No. 5834187

Patent No. 5834187 5786143  
GENERAL INFORMATION:  
APPLICANT: Green, Bruce A.  
APPLICANT: Brinton, Jr., Charles C.  
TITLE OF INVENTION: Sequence and Analysis of LKP P11n  
Patent No. 5834187  
Patent No. 5834187 5786143  
TITLE OF INVENTION: Structural Gene and the LKP P11 Operon of No. 5834187 5786  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/473.750  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/277,321  
FILING DATE: 19-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Carroll, Alice O.  
REGISTRATION NUMBER: 33,542  
REFERENCE/DOCKET NUMBER: ACC94-02B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 741 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-473-750-7

Query Match 60.0%; Score 6; DB 2; Length 741;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TARIGE 10  
|||||  
DB 157 TARIGE 162

RESULT 7  
US-08-477-326-7  
Sequence 7, Application US/08477326  
Patent No. 5968769  
GENERAL INFORMATION:  
APPLICANT: Green, Bruce A.  
APPLICANT: Brinton, Jr., Charles C.  
TITLE OF INVENTION: Sequence and Analysis of LKP P11n  
Patent No. 5968769  
TITLE OF INVENTION: Structural Gene and the LKP P11 Operon of No. 5968769typab  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02173

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,326  
FILING DATE: 07-JUN-1995  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/277,231  
FILING DATE: July 19, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Carroll, Alice O.  
REGISTRATION NUMBER: 33,542  
REFERENCE/DOCKET NUMBER: ACC94-02A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 741 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-477-326-7

Query Match 60.0%; Score 6; DB 2; Length 741;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TARIGE 10  
|||||  
Db 157 TARIGE 162

RESULT 8  
US-08-637-759B-191  
Sequence 191, Application US/08637759B  
Patent No. 5876931  
GENERAL INFORMATION:  
APPLICANT: David William Holden  
TITLE OF INVENTION: Identification of Genes  
NUMBER OF SEQUENCES: 501  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/637,759B  
FILING DATE: 03-MAY-1996  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB95/02875  
FILING DATE: 11-DEC-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: RPS 101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 873-8794  
TELEFAX: (404) 873-8795

INFORMATION FOR SEQ ID NO: 191:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 63 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-08-637-759B-191

Query Match 50.0%; Score 5; DB 2; Length 63;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 QNITA 6  
|||||  
Db 28 QNITA 32

RESULT 9  
US-08-871-355A-191  
Sequence 191, Application US/08871355A  
Patent No. 6015669  
GENERAL INFORMATION:  
APPLICANT: David William Holden  
TITLE OF INVENTION: Identification of Genes  
NUMBER OF SEQUENCES: 501  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/871,355A  
FILING DATE: 09-JUN-1997  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB95/02875  
FILING DATE: 11-DEC-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: RPS 101 CON  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 873-8794  
TELEFAX: (404) 873-8795  
INFORMATION FOR SEQ ID NO: 191:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 63 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-08-871-355A-191

Query Match 50.0%; Score 5; DB 3; Length 63;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2 QNITA 6  
|||||

Db 28 ONITA 32

RESULT 10

US-09-188-930-153  
; Sequence 153, Application US/09188930A  
; Patent No. 6150502

; GENERAL INFORMATION:

; APPLICANT: Watson, James D.

; APPLICANT: Strachan, Lorna

; APPLICANT: Sleeman, Matthew

; APPLICANT: Murison, James Greg

; TITLE OF INVENTION: Compositions Isolated From Skin Cells

; FILE REFERENCE: 11000.1011c1

; CURRENT APPLICATION NUMBER: US/09/188,930A

; NUMBER OF SEQ ID NOS: 348

; SOFTWARE: FASTSEQ for Windows Version 3.0

; SEQ ID NO: 153

; LENGTH: 72

; TYPE: PRT

; ORGANISM: mouse

US-09-188-930-153

Query Match 50.0%; Score 5; DB 4; Length 72;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 ARIGE 10

; ; ; ; ;

Db 47 ARIGE 51

RESULT 11

US-09-188-930-304  
; Sequence 304, Application US/09188930A  
; Patent No. 6150502

; GENERAL INFORMATION:

; APPLICANT: Watson, James D.

; APPLICANT: Strachan, Lorna

; APPLICANT: Sleeman, Matthew

; APPLICANT: Murison, James Greg

; TITLE OF INVENTION: Compositions Isolated From Skin Cells

; FILE REFERENCE: 11000.1011c1

; CURRENT APPLICATION NUMBER: US/09/188,930A

; NUMBER OF SEQ ID NOS: 348

; SOFTWARE: FASTSEQ for Windows Version 3.0

; SEQ ID NO: 304

; LENGTH: 72

; TYPE: PRT

; ORGANISM: Mouse

US-09-188-930-304

Query Match 50.0%; Score 5; DB 4; Length 72;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 ARIGE 10

; ; ; ; ;

Db 47 ARIGE 51

RESULT 12

US-08-543-238-11  
; Sequence 11, Application US/08543238  
; Patent No. 5607919

; GENERAL INFORMATION:

; APPLICANT: Bojsen, Kirsten

; APPLICANT: Kragh, Karsten M.

; APPLICANT: Mikkelsen, Jørn D.

; APPLICANT: Nielsen, Klaus K.

; TITLE OF INVENTION: Anti-Microbial Proteins

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sandoz Agro, Inc.

; STREET: 975 California Avenue

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/543,238

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Marcus-Wyner, Lynn

; REGISTRATION NUMBER: 34,869

; REFERENCE/DOCKET NUMBER: 137-1078/MA

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/354-3588

; TELEFAX: 415/857-1125

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 146 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-543-238-11

Query Match 50.0%; Score 5; DB 1; Length 146;

Best Local Similarity 100.0%; Pred. No. 56;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ITARI 8

; ; ; ; ;

Db 99 ITARI 103

RESULT 13

US-08-420-526-11  
; Sequence 11, Application US/08420526  
; Patent No. 5608151

; GENERAL INFORMATION:

; APPLICANT: Bojsen, Kirsten

; APPLICANT: Kragh, Karsten M.

; APPLICANT: Mikkelsen, Jørn D.

; APPLICANT: Nielsen, Klaus K.

; TITLE OF INVENTION: Anti-Microbial Proteins

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sandoz Agro, Inc.

; STREET: 975 California Avenue

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/420,526

FILING DATE:  
 CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Marcus-Wyner, Lynn  
 REGISTRATION NUMBER: 34,869  
 REFERENCE/DOCKET NUMBER: 137-1078/MA  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/354-3588  
 TELEFAX: 415/857-1125  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 146 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-420-526-11

Query Match 50.0%; Score 5; DB 1; Length 146;  
 Best Local Similarity 100.0%; Pred. No. 56;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ITARI 8  
 |||||  
 DB 99 ITARI 103

RESULT 14  
 US-08-278-091-16  
 Sequence 16, Application US/08278091  
 Patent No. 5506139  
 GENERAL INFORMATION:  
 APPLICANT: LOOSMORE, Sheena M  
 APPLICANT: YANG, Yan-Ping  
 APPLICANT: CHONG, Pele  
 APPLICANT: OOMEN, Raymond P.  
 APPLICANT: KLEIN, Michel H.  
 TITLE OF INVENTION: Analog of Haemophilus Hln47 Protein with  
 TITLE OF INVENTION: Reduced Protease Activity  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sim & McBurney  
 STREET: Suite 701, 330 University Avenue  
 CITY: Toronto  
 STATE: Ontario  
 COUNTRY: Canada  
 ZIP: M5G 1R7  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentln Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/278,091  
 FILING DATE: 21-JUL-1994  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Stewart, Michael I  
 REGISTRATION NUMBER: 24,973  
 REFERENCE/DOCKET NUMBER: 1038-371  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (416) 595-1155  
 TELEFAX: (416) 595-1163  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 198 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-278-091-16

Query Match 50.0%; Score 5; DB 1; Length 198;

Best Local Similarity 100.0%; Pred. No. 73;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TARIG 9  
 |||||  
 DB 43 TARIG 47

RESULT 15  
 US-08-483-859-16  
 Sequence 16, Application US/08483859  
 Patent No. 5656436  
 GENERAL INFORMATION:  
 APPLICANT: LOOSMORE, Sheena M.  
 APPLICANT: YANG, Yan-Ping  
 APPLICANT: CHONG, Pele  
 APPLICANT: OOMEN, Raymond P.  
 APPLICANT: KLEIN, Michel H.  
 TITLE OF INVENTION: Analog of Haemophilus Hln47 Protein with  
 TITLE OF INVENTION: Reduced Protease Activity  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sim & McBurney  
 STREET: Suite 701, 330 University Avenue  
 CITY: Toronto  
 STATE: Ontario  
 COUNTRY: Canada  
 ZIP: M5G 1R7  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentln Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/483,859  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/296,149  
 FILING DATE: 26-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/278,091  
 FILING DATE: 21-JUL-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Stewart, Michael I  
 REGISTRATION NUMBER: 24,973  
 REFERENCE/DOCKET NUMBER: 1038-495 MIS:vg  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (416) 595-1155  
 TELEFAX: (416) 595-1163  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 198 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-483-859-16

Query Match 50.0%; Score 5; DB 1; Length 198;  
 Best Local Similarity 100.0%; Pred. No. 73;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TARIG 9  
 |||||  
 DB 43 TARIG 47

Search completed: April 24, 2002, 09:22:30  
 Job time: 249 sec



**THIS PAGE BLANK (USPTO)**



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:23:17 ; Search time 38.65 Seconds  
(without alignments)  
19.709 Million cell updates/sec

Title: US-09-689-469-6  
Perfect score: 10  
Sequence: 1 AONTARIGE 10

Scoring table:  
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID  | Description        |
|------------|-------|-------------|--------|--------|--------------------|
| 1          | 100.0 | 402         | 1      | I61596 | advanced glycosyla |
| 2          | 90.0  | 402         | 1      | T09062 | probable advanced  |
| 3          | 80.0  | 416         | 1      | A42879 | advanced glycosyla |
| 4          | 70.0  | 223         | 2      | H64065 | mutator muth - Hae |
| 5          | 60.0  | 234         | 1      | Q0BE43 | membrane antigen g |
| 6          | 60.0  | 238         | 2      | H64181 | ABC-type transport |
| 7          | 60.0  | 298         | 2      | T51746 | RNA helicase RH17  |
| 8          | 60.0  | 389         | 2      | S33667 | probable integrase |
| 9          | 60.0  | 429         | 2      | T23984 | hypothetical prote |
| 10         | 60.0  | 468         | 2      | H69133 | argininosuccinate  |
| 11         | 60.0  | 471         | 2      | S30585 | hypothetical prote |
| 12         | 60.0  | 548         | 2      | T05671 | hypothetical prote |
| 13         | 60.0  | 609         | 2      | G84832 | ATP-dependent RNA  |
| 14         | 60.0  | 635         | 2      | E71733 | threonine-cRNA 11  |
| 15         | 60.0  | 788         | 2      | I64045 | recombination prot |
| 16         | 60.0  | 837         | 1      | S54429 | outer membrane ush |
| 17         | 50.0  | 100         | 2      | S68627 | p24 protein - born |
| 18         | 50.0  | 118         | 2      | D75580 | hypothetical prote |
| 19         | 50.0  | 124         | 2      | S56506 | hypothetical 13.7K |
| 20         | 50.0  | 125         | 2      | A53882 | Darwin homolog whe |
| 21         | 50.0  | 125         | 2      | A43474 | Darwin homolog whe |
| 22         | 50.0  | 125         | 2      | A83256 | conserved hypotet  |
| 23         | 50.0  | 137         | 2      | T05526 | acyl carrier prote |
| 24         | 50.0  | 146         | 2      | T06169 | pathogenesis-relat |
| 25         | 50.0  | 146         | 2      | T06485 | barrin homolog whe |
| 26         | 50.0  | 147         | 2      | S41381 | hypothetical prote |
| 27         | 50.0  | 148         | 2      | T06486 | Darwin homolog whe |
| 28         | 50.0  | 157         | 2      | D84243 | hypothetical prote |
| 29         | 50.0  | 157         | 2      | S49793 | hypothetical prote |

|    |   |      |     |   |        |                    |
|----|---|------|-----|---|--------|--------------------|
| 30 | 5 | 50.0 | 163 | 2 | S67038 | ribosomal protein  |
| 31 | 5 | 50.0 | 164 | 2 | H64329 | hypothetical prote |
| 32 | 5 | 50.0 | 164 | 2 | S38089 | hypothetical prote |
| 33 | 5 | 50.0 | 166 | 2 | A82946 | ribosomal protein  |
| 34 | 5 | 50.0 | 175 | 2 | JN0681 | gamma2-crystallin  |
| 35 | 5 | 50.0 | 180 | 2 | S75124 | thioredoxin-like p |
| 36 | 5 | 50.0 | 183 | 2 | T10192 | senescence-associ  |
| 37 | 5 | 50.0 | 185 | 2 | S20593 | alcohol dehydrogen |
| 38 | 5 | 50.0 | 186 | 2 | T50361 | hypothetical prote |
| 39 | 5 | 50.0 | 190 | 2 | T09136 | ADP-ribosylation F |
| 40 | 5 | 50.0 | 196 | 2 | E86553 | 3-methyladenine DN |
| 41 | 5 | 50.0 | 196 | 2 | C72071 | DNA-3-methyladenin |
| 42 | 5 | 50.0 | 197 | 2 | A83092 | probable phospho   |
| 43 | 5 | 50.0 | 201 | 2 | G70874 | probable transcrip |
| 44 | 5 | 50.0 | 204 | 2 | S30165 | repressor protein  |
| 45 | 5 | 50.0 | 220 | 2 | T51827 | MADS-box protein ( |

#### ALIGNMENTS

RESULT 1  
I61596  
advanced glycosylation end-products receptor precursor - human  
N:Alternate names: advanced glycosylation end product-binding protein, 35K; glycoprot  
C:Species: Homo sapiens (man)  
C:Date: 24-May-1996 #sequence, revision 07-Feb-1997 #text, change 16-Jul-1999  
C:Accession: I61596; B42879; S27968  
R:Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, G.  
Genomics 23, 408-419, 1994  
A>Title: Three genes in the human MHC class III region near the junction with the class II part of mouse mammary tumor gene int-3.  
A:Reference number: A55562; M01D:95137587  
A:Accession: I61596  
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
A:Molecule type: DNA  
A:Residues: 1-404 <RES>  
A:Cross-references: GB:D28769; NID:9561657; PIDN:BA05958.1; PID:9561659  
R:Neepfer, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; J. Biol. Chem. 267, 14998-15004, 1992  
A>Title: Cloning and expression of a cell surface receptor for advanced glycosylation  
A:Reference number: A42879; M01D:92340547  
A:Accession: B42879  
A:Molecule type: mRNA  
A:Residues: 'G', 2-99, 'R', 101-404 <NE>  
A:Cross-references: EMBL:M91211; NID:g190845; PIDN:AAA03574.1; PID:g190846  
A:Experimental source: Lung  
A:Note: sequence extracted from NCBI backbone (NCBIP:109438)  
C:Comment: Advanced glycosylation end products are heterogeneous nonenzymatically gly cellular function, thus contributing to tissue lesions in diabetes.  
C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.  
C:Genetics:  
A:Gene: GDB:AGER  
A:Cross-references: GDB:306354; OMIM:600214  
A:Map position: 6p21.3-6p21.3  
A:Intons: 18/1; 53/3; 119/1; 140/3; 170/1; 231/1; 274/3; 322/1; 331/1; 373/2  
C:Function:  
A:Description: neuronal receptor for amphoterin, a DNA-binding protein involved in ne C:Superfamily: advanced glycosylation end products receptor; immunoglobulin homology C:Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-404/Product: advanced glycosylation end products receptor #status predicted <MAT F:23-344/Domain: extracellular #status predicted <EXT>  
F:31-101/Domain: immunoglobulin homology <IM1>  
F:137-210/Domain: immunoglobulin homology <IM2>  
F:252-303/Domain: immunoglobulin homology <IM3>  
F:345-362/Domain: transmembrane #status predicted <TM>  
F:363-404/Domain: intracellular #status predicted <INT>  
F:25,81/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:38-99, 144-208, 259-301/Disulfide bonds: #status predicted

Query Match 100.0%; Score 10; DB 1; Length 404;  
 Best Local Similarity 100.0%; Pred. No. 0.0005;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10  
 |||||||||  
 DB 23 AONTARIGE 32

RESULT 2  
 T09062  
 probable advanced glycosylation end-products receptor precursor - mouse  
 N:Alternate names: RAGE  
 C:Species: Mus musculus (house mouse)  
 C>Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jan-2000  
 C:Accession: T09062  
 R:Rowen, U.; Maniatis, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Loretz, C.; So  
 submitted to the EMBL Data Library, October 1997  
 A:Description: Sequence of the mouse major histocompatibility locus class III region.  
 A:Reference number: 216543  
 A:Accession: T09062  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-402 <ROM>  
 A:Cross-references: EMBL:AF030001; NID:92564945; PID:92564950  
 C:Genetics:  
 A:Gene: RAGE  
 A:Map position: 17  
 A:Introns: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1; 272/3; 320/1; 329/1; 371/2  
 C:Superfamily: advanced glycosylation end products receptor: immunoglobulin homology  
 C:Keywords: receptor; transmembrane protein  
 F:31-100/Domain: immunoglobulin homology <IMM>

Query Match 90.0%; Score 9; DB 2; Length 402;  
 Best Local Similarity 100.0%; Pred. No. 0.0065;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 QNTARIGE 10  
 |||||||||  
 DB 24 QNTARIGE 32

RESULT 3  
 A42879  
 advanced glycosylation end-products receptor precursor - bovine  
 N:Alternate names: advanced glycosylation end product-binding protein, 35k; glycoprotein  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 04-Mar-1993 #sequence\_revision 07-Feb-1997 #text\_change 16-Jul-1999  
 C:Accession: A42879; A42878; S27949  
 R:Nepper, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; St  
 J. Biol. Chem. 267, 14998-15004, 1992  
 A:Title: Cloning and expression of a cell surface receptor for advanced glycosylation en  
 A:Reference number: A42879; M0ID:92340547  
 A:Accession: A42879  
 A:Molecule type: mRNA  
 A:Residues: 1-416 <NDE>  
 A:Cross-references: GB:M91212; NID:q163650; PIDN:AAA03575.1; PID:q163651  
 A:Experimental source: lung  
 A:Note: sequence extracted from NCBI backbone (NCBI:109436)  
 A:Note: parts of this sequence, including the amino end of the mature protein, were dete  
 R:Schmidt, A.M.; Vienna, M.; Gerlach, M.; Brett, J.; Ryan, J.; Kao, J.; Esposito, C.; He  
 J. Biol. Chem. 267, 14987-14997, 1992  
 A:Title: Isolation and characterization of two binding proteins for advanced glycosylati  
 A:Reference number: A42878; M0ID:92340546  
 A:Accession: A42878  
 A:Molecule type: protein  
 A:Residues: 23-24,'X',26-37,'X',39-49,'XX',52-54 <SCH>  
 A:Experimental source: endothelial cells  
 A:Note: sequence extracted from NCBI backbone (NCBI:109434)  
 C:Comment: Advanced glycosylation end products are heterogeneous nonenzymatically glycos  
 cellular function, thus contributing to tissue lesions in diabetes.  
 C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide on

ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.  
 C:Function:  
 A:Description: neuronal receptor for amphoterin, a DNA-binding protein involved in ne  
 C:Superfamily: advanced glycosylation end products receptor: immunoglobulin homology  
 C:Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-416/Product: advanced glycosylation end-products receptor RAGE #status predicted  
 F:23-354/Domain: extracellular #status predicted <EXT>  
 F:31-100/Domain: immunoglobulin homology <IM1>  
 F:136-209/Domain: immunoglobulin homology <IM2>  
 F:262-313/Domain: immunoglobulin homology <IM3>  
 F:355-372/Domain: transmembrane #status predicted <TM>  
 F:373-416/Domain: intracellular #status predicted <INT>  
 F:25/80/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:38-98,143-207,269-311/Disulfide bonds: #status predicted

Query Match 80.0%; Score 8; DB 1; Length 416;  
 Best Local Similarity 100.0%; Pred. No. 0.086;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 QNTARIG 9  
 |||||||||  
 DB 24 QNTARIG 31

RESULT 4  
 H64065  
 mutator muth - Haemophilus influenzae (strain Rd KW20)  
 N:Alternate names: DNA mismatch protein  
 C:Species: Haemophilus influenzae  
 C>Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 26-Aug-1999  
 C:Accession: H64065  
 R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage  
 ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodok, A.; Kelley, J.M.; Weidman  
 , D.M.; Brandon, R.C.; Fine, L.D.; Frittmann, J.L.; Fuhmann, J.L.; Georgiagen, N.S.M.  
 Science 269, 496-512, 1995  
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente  
 A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
 A:Reference number: A64000; M0ID:95350630  
 A:Accession: H64065  
 A>Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-223 <TIGR>  
 A:Cross-references: GB:U32723; GB:LA2023; NID:q1573363; PIDN:AA022062.1; PID:q1573374  
 C:Genetics:  
 A:Gene: muth  
 C:Superfamily: mutator muth

Query Match 70.0%; Score 7; DB 2; Length 223;  
 Best Local Similarity 100.0%; Pred. No. 0.65;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ITARIGE 10  
 |||||||||  
 DB 165 ITARIGE 171

RESULT 5  
 Q08B43  
 membrane antigen gp85 - human herpesvirus 4 (strain B95-8)  
 C:Species: human herpesvirus 4, Epstein-Barr virus  
 C>Date: 25-Feb-1985 #sequence\_revision 25-Feb-1985 #text\_change 16-Jul-1999  
 C:Accession: F43044; A03787; S33040  
 R:Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.  
 Mol. Biol. Med. 1, 21-45, 1983  
 A:Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr vi  
 A:Reference number: A93065; M0ID:85035713  
 A:Accession: F43044  
 A:Molecule type: DNA  
 A:Residues: 1-234 <BAN>  
 A:Cross-references: EMBL:V01555; NID:q59074; PIDN:CAA24835.1; PID:q1334899

R:Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H  
 Nature 310, 207-211, 1984  
 A:Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.  
 A:Reference number: A03794; MUID:84270667  
 A:Contents: annotation; protein coding region  
 C:Superfamily: Epstein-Barr virus membrane antigen gp85

Query Match 60.0%; Score 6; DB 1; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 8.9;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONITA 6  
 |||||  
 Db 108 AONITA 113

## RESULT 6

H64181  
 ABC-type transport system probable membrane spanning protein - Haemophilus influenzae (S

C:Species: Haemophilus influenzae

C>Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 21-Aug-1998

C:Accession: H64181

R:Flaischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A  
 ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Feldman, J  
 ; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
 Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,  
 A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630

A:Accession: H64181

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-238 <TIGR>

A:Cross-references: GB:I42023; TIGR:H11079

C:Superfamily: histidine permease protein M

Query Match 60.0%; Score 6; DB 2; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 9;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONITA 6  
 |||||  
 Db 195 AONITA 200

## RESULT 7

T51746  
 RNA helicase RH17 [imported] - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 17-Nov-2000

C:Accession: T51746

R:Aubourg, S.; Kreis, M.; Lecharny, A.

Nucleic Acids Res. 27, 628-636, 1999

A:Title: The DEAD box RNA helicase family in Arabidopsis thaliana.

A:Reference number: Z22965; MUID:9862990

A:Accession: T51746

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-298 <AUB>

A:Cross-references: EMBL:AJ010468; PIDN:CAA09207.1

C:Experimental source: cultivar Columbia

C:Genetics:

A:Gene: RH17

A:Map position: 2

Query Match 60.0%; Score 6; DB 2; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TARIGE 10

Db 129 TARIGE 134  
 |||||

RESULT 8  
 S33667  
 probable integrase - Pseudomonas aeruginosa phage CTX

C:Species: Pseudomonas aeruginosa phage CTX

C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 20-Jun-2000

C:Accession: S33667

R:Hayashi, T.; Matsumoto, H.; Ohnishi, M.; Terawaki, Y.

Mol. Microbiol. 7, 657-667, 1993

A:Title: Molecular analysis of a cytotoxin-converting phage, phi-CTX, of Pseudomonas

A:Reference number: S33665; MUID:93225809

A:Accession: S33667

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-389 <HAY>

A:Cross-references: EMBL:D13409; NID:q217776; PIDN:BA02675.1; PID:q217779

C:Superfamily: hypothetical protein b1579

Query Match 60.0%; Score 6; DB 2; Length 389;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TARIGE 10  
 |||||  
 Db 191 TARIGE 196

## RESULT 9

T23984  
 hypothetical protein R06F6.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T23984

R:Chui, C.

submitted to the EMBL Data Library, November 1994

A:Reference number: Z19826

A:Accession: T23984

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-429 <WIL>

A:Cross-references: EMBL:Z46794; PIDN:CAA86783.1; GSPDB:GND0020; CESP:R06F6.4

A:Experimental source: clone R06F6

C:Genetics:

A:Gene: CESP:R06F6.4

A:Map position: 2

A:introns: 68/3; 189/2; 228/3; 347/2

Query Match 60.0%; Score 6; DB 2; Length 429;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AONITA 6  
 |||||  
 Db 345 AONITA 350

## RESULT 10

H69133

argininosuccinate lyase - Methanobacterium thermoautotrophicum (strain Delta H)

C:Species: Methanobacterium thermoautotrophicum

C>Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 16-Jul-1999

C:Accession: H69133

R:Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T

; Qiu, D.; Spadafora, R.; Vitale, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani,

K.; S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Neelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu

A:Reference number: A69000; MUID:98037514

A:Accession: H69133  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-468 <MTH>  
 A:Cross-references: GB:AE000812; GB:AE000666; NID:g2621298; PIDN:AAB84775.1; PID:g262131  
 A:Experimental source: strain Delta H  
 C:Genetics:  
 A:Gene: MTH269  
 A:Start codon: TTG  
 C:Superfamily: argininosuccinate lyase

Query Match 60.0%; Score 6; DB 2; Length 468;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 5 TARIGE 10  
 Db 91 TARIGE 96

RESULT 11  
 S30585  
 hypothetical protein 5 - Methanobacterium thermoformicum  
 C:Species: Methanobacterium thermoformicum  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 10-Dec-1999  
 C:Accession: S30585  
 R.Noelling, J.; van Eden, F.J.M.; de Vos, W.M.  
 submitted to the EMBL Data Library, November 1992  
 A:Description: Distribution and characterization of plasmid-related sequence in the chrc  
 A:Reference number: S30583  
 A:Accession: S30585  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-471 <NOE>  
 A:Cross-references: EMBL:X69114; NID:g44581; PIDN:CAA48867.1; PID:g44582  
 C:Superfamily: Methanobacterium thermoformicum hypothetical protein 5

Query Match 60.0%; Score 6; DB 2; Length 471;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 3 NITARI 8  
 Db 311 NITARI 316

RESULT 12  
 T05671  
 hypothetical protein F22113.200 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 02-Sep-2000  
 C:Accession: T05671  
 R.Beyan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.  
 submitted to the Protein Sequence Database, February 1999  
 A:Reference number: Z15420  
 A:Accession: T05671  
 A:Molecule type: DNA  
 A:Residues: 1-548 <BEV>  
 A:Cross-references: EMBL:AL035539  
 A:Experimental source: cultivar Columbia; BAC clone F22113  
 C:Genetics:  
 A:Map position: 4  
 A:Introns: 90/1; 129/1; 302/3; 420/3  
 A:Note: F22113.200  
 C:Superfamily: Arabidopsis thaliana hypothetical protein T7H20.60

Query Match 60.0%; Score 6; DB 2; Length 548;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 NITARI 8  
 Db 440 NITARI 445

RESULT 13  
 G84832  
 ATP-dependent RNA helicase [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
 C:Accession: G84832  
 R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.L.; Town, C.D.; Fujii, C.Y.  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,  
 eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter  
 Nature 402, 761-768, 1999  
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A:Reference number: A84420; M0ID:20083487  
 A:Accession: G84832  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-609 <STO>  
 A:Cross-references: GB:AE002093; NID:g4895231; PIDN:AAD32817.1; GSPDB:GN00139  
 C:Genetics:  
 A:Gene: AT9g40700  
 A:Map position: 2

Query Match 60.0%; Score 6; DB 2; Length 609;  
 Best Local Similarity 100.0%; Pred. No. 20;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 5 TARIGE 10  
 Db 440 TARIGE 445

RESULT 14  
 E71733  
 threonine--tRNA ligase (EC 6.1.1.3) - Rickettsia prowazekii  
 N:Alternate names: threonyl-tRNA synthetase  
 C:Species: Rickettsia prowazekii  
 C:Date: 21-Nov-1998 #sequence\_revision 21-Nov-1998 #text\_change 03-Nov-2000  
 C:Accession: E71733  
 R.Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Slicheritz-Ponten, T.; Alsmark  
 Nature 396, 133-140, 1998  
 A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.  
 A:Reference number: A71630; M0ID:99039499  
 A:Accession: E71733  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-635 <AND>  
 A:Cross-references: GB:AJ235270; GB:AJ235269; NID:g3860572; PIDN:CAA14684.1; PID:g386  
 A:Experimental source: strain Madrid E  
 C:Genetics:  
 A:Gene: thrs; RP221  
 C:Function:  
 A:Description: activates L-threonine and transfers it to the specific tRNA  
 A:Pathway: protein biosynthesis  
 A:Note: belongs to class-II synthetases  
 C:Superfamily: threonine-tRNA ligase  
 C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 60.0%; Score 6; DB 2; Length 635;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 AONITA 6  
 Db 15 AONITA 20

RESULT 15

I64045  
recombination protein rec2 - Haemophilus influenzae (strain Rd KW20)  
C:Species: Haemophilus influenzae  
C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 08-Oct-1999  
C:Accession: I64045  
R:Flatschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.  
; Gocayne, J.D.; Scott, J.; Shiley, R.; Liu, L.I.; Glodok, A.; Kelley, J.M.; Weidman, J.  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.  
Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,  
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630  
A:Accession: I64045  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-788 <TIGR>  
A:Cross-references: GB:U32691; GB:I42023; NID:g1573004; PIDN:AAC21739.1; PID:g1573009; T  
C:Genetics:  
A:Gene: rec2

Query Match 60.0%; Score 6; DB 2; Length 788;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AONITA 6  
|||||  
DB 76 AONITA 81

Search completed: April 24, 2002, 09:23:17  
Job time: 246 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:24:54 ; Search time 21.46 Seconds

(without alignments)  
17.085 Million cell updates/sec

Title: US-09-689-469-6

Perfect score: 10

Sequence: 1 AQNITARIGE 10

Scoring table: OLIGO

Searched: 100059 seqs, 36664827 residues

Word size: 0

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 10    | 100.0       | 404    | 1  | RAGE_HUMAN  |
| 2          | 9     | 90.0        | 402    | 1  | RAGE_RAT    |
| 3          | 9     | 90.0        | 403    | 1  | RAGE_MOUSE  |
| 4          | 8     | 80.0        | 416    | 1  | RAGE_BOVIN  |
| 5          | 7     | 70.0        | 223    | 1  | MURH_HAIEIN |
| 6          | 6     | 60.0        | 210    | 1  | YA79_HAIEIN |
| 7          | 6     | 60.0        | 234    | 1  | PGP8_EBV    |
| 8          | 6     | 60.0        | 278    | 1  | PROC_VIBAL  |
| 9          | 6     | 60.0        | 401    | 1  | ENO_THDAC   |
| 10         | 6     | 60.0        | 429    | 1  | YRM4_CAEEL  |
| 11         | 6     | 60.0        | 468    | 1  | ARYX_METTH  |
| 12         | 6     | 60.0        | 635    | 1  | STY_RICPR   |
| 13         | 6     | 60.0        | 788    | 1  | REC2_HAIEIN |
| 14         | 6     | 60.0        | 837    | 1  | HFC2_HAIEIN |
| 15         | 6     | 60.0        | 837    | 1  | HFC2_HAIEIN |
| 16         | 6     | 60.0        | 837    | 1  | HFC2_HAIEIN |
| 17         | 6     | 60.0        | 850    | 1  | DEXT_STRMD  |
| 18         | 5     | 50.0        | 125    | 1  | BARW_HORVU  |
| 19         | 5     | 50.0        | 148    | 1  | MYG_GALJA   |
| 20         | 5     | 50.0        | 157    | 1  | YI17_YEAST  |
| 21         | 5     | 50.0        | 164    | 1  | Y239_METUA  |
| 22         | 5     | 50.0        | 164    | 1  | YK00_YEAST  |
| 23         | 5     | 50.0        | 166    | 1  | RL10_UREPA  |
| 24         | 5     | 50.0        | 169    | 1  | GBP_XENLA   |
| 25         | 5     | 50.0        | 175    | 1  | CRG2_XENLA  |
| 26         | 5     | 50.0        | 180    | 1  | TXLA_SYNY3  |
| 27         | 5     | 50.0        | 183    | 1  | DINI_RAPSA  |
| 28         | 5     | 50.0        | 185    | 1  | ADH_ANAPL   |
| 29         | 5     | 50.0        | 204    | 1  | LEXA_PSEAE  |
| 30         | 5     | 50.0        | 224    | 1  | PURQ_MCTCO  |
| 31         | 5     | 50.0        | 226    | 1  | PURQ_MCTCO  |
| 32         | 5     | 50.0        | 227    | 1  | YPVA_METTF  |
| 33         | 5     | 50.0        | 241    | 1  | MXIU_SHIFT  |

## ALIGNMENTS

| RESULT ID | 1  | STANDARD: | PRT: | 404 AA. |
|-----------|--|-----------|------|---------|
| AC        | 015109; Q15279; Q9Y3R3; Q9H2X7;  |           |      |         |
| DT        | 01-NOV-1997 (Rel. 35, Created)   |           |      |         |
| DT        | 01-NOV-1997 (Rel. 35, Last sequence update)  |           |      |         |
| DT        | 20-AUG-2001 (Rel. 40, Last annotation update)  |           |      |         |
| DE        | ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS). |           |      |         |
| GN        | AGER OR RAGE.  |           |      |         |
| OS        | Homo sapiens (Human).  |           |      |         |
| OC        | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |           |      |         |
| OC        | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  |           |      |         |
| OX        | NCBI_TaxID=9606;   |           |      |         |
| RN        | [1]  |           |      |         |
| RP        | SEQUENCE FROM N.A. (ISOFORM 1).  |           |      |         |
| RC        | TISSUE=Lung;   |           |      |         |
| RX        | MEDLINE=92340547; PubMed=1378843;  |           |      |         |
| RA        | Nepper M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,  |           |      |         |
| RA        | Elliston K., Stern D., Shaw A.;  |           |      |         |
| RT        | "Cloning and expression of a cell surface receptor for advanced  |           |      |         |
| RT        | glycosylation end products of proteins.";  |           |      |         |
| RL        | J. Biol. Chem. 267:14998-15004(1992).  |           |      |         |
| RN        | [2]  |           |      |         |
| RP        | SEQUENCE FROM N.A. (ISOFORM 1).  |           |      |         |
| RX        | MEDLINE=95137587; PubMed=7835890;  |           |      |         |
| RA        | Sugaya K., Fukagawa T., Matsumoto K., Mita K., Takahashi E., Ando A.,  |           |      |         |
| RA        | Inoko H., Ikemura T.;  |           |      |         |
| RT        | "Three genes in the human MHC class III region near the junction with  |           |      |         |
| RT        | the class II: gene for receptor of advanced glycosylation end  |           |      |         |
| RT        | products, PBX2 homeobox gene and a notch homolog, human counterpart  |           |      |         |
| RT        | of mouse mammary tumor gene int-3.";   |           |      |         |
| RL        | Genomics 23:408-419(1994).   |           |      |         |
| RN        | [3]  |           |      |         |
| RP        | SEQUENCE FROM N.A. (ISOFORM 1).  |           |      |         |
| RA        | Rosen L., Dankers C., Baskin D., Faust J., Loretz C., Ahearn M.E.,   |           |      |         |
| RA        | Banta A., Spies T., Hood L.;   |           |      |         |
| RT        | Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  |           |      |         |
| RN        | [4]  |           |      |         |
| RP        | SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-100.   |           |      |         |
| RA        | Abedin M.J., Yonekura H., Migita H., Karasawa J., Yamamoto Y.,   |           |      |         |
| RA        | Yamamoto H.;   |           |      |         |
| RT        | "Molecular heterogeneity of the receptor for advanced glycation  |           |      |         |
| RT        | endproducts.";   |           |      |         |
| RL        | Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  |           |      |         |
| RN        | [5]  |           |      |         |
| RP        | SEQUENCE FROM N.A. (ISOFORM 2).  |           |      |         |
| RA        | Malherbe P., Richards J., Gaillard H., Thompson A., Diener C.,   |           |      |         |
| RA        | Schuler A., Huber G.;  |           |      |         |
| RT        | "CDNA cloning of a novel secreted isoform of the human Receptor for  |           |      |         |
| RT        | advanced glycation end products (RAGE) and characterization of cells   |           |      |         |
| RT        | co-expressing cell-surface scavenger receptors and Swedish mutant  |           |      |         |
| RT        | amyloid precursor protein.";   |           |      |         |
| RL        | Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  |           |      |         |
| RN        | [6]  |           |      |         |
| RP        | SEQUENCE OF 1-12 FROM N.A.   |           |      |         |

|    |   |      |     |   |            |                    |
|----|---|------|-----|---|------------|--------------------|
| 34 | 5 | 50.0 | 241 | 1 | MXIU_SHISO | O5288 shigella so  |
| 35 | 5 | 50.0 | 241 | 1 | RREP_BRSVA | P33454 bovine resp |
| 36 | 5 | 50.0 | 241 | 1 | RREP_HRSV  | P14156 human resp  |
| 37 | 5 | 50.0 | 241 | 1 | RREP_HRSV1 | P24567 human resp  |
| 38 | 5 | 50.0 | 241 | 1 | RREP_HRSVA | P03421 human resp  |
| 39 | 5 | 50.0 | 241 | 1 | RREP_HRSVL | P12579 human resp  |
| 40 | 5 | 50.0 | 241 | 1 | RREP_ORSVW | O83956 ovine resp  |
| 41 | 5 | 50.0 | 261 | 1 | DRBA_BACSU | P39071 bacillus su |
| 42 | 5 | 50.0 | 262 | 1 | FLGG_AGRU  | O44388 agrobacteri |
| 43 | 5 | 50.0 | 264 | 1 | LPXA_RICRI | P32199 rickettsia  |
| 44 | 5 | 50.0 | 288 | 1 | CRTE_RHOSH | P54976 rhodobacter |
| 45 | 5 | 50.0 | 291 | 1 | AMPM_CHLPN | O92690 chlamydia p |

Hudson B.I., Futers T.S.:  
"Novel polymorphisms in the receptor for advanced glycation end-products (RAGE) gene.", EMBL/GenBank/DBJ databases.  
Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
RL FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED RATE IN DIABETES.  
CC SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1) AND SECRETED (ISOFORM 2).  
CC -1 ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2/RAGESEC;  
CC ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -1 TISSUE SPECIFICITY: ENDOTHELIAL CELLS.  
CC -1 SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS  
CC 2 C2-LIKE AND ONE V-LIKE DOMAINS.

-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See [http://www.isb-sib.ch/announce/  
or-send-an-email-to-license@isb-sib.ch](http://www.isb-sib.ch/announce/or-send-an-email-to-license@isb-sib.ch))

-----  
EMBL; M91211; AAA03574.1; .  
DR EMBL; D28769; BAA05958.1; .  
DR EMBL; U089336; AAB47491.1; .  
DR EMBL; AB036432; BAA89369.1; .  
DR EMBL; AJ133822; CAB43108.1; .  
DR EMBL; AF208289; AAG35728.1; .  
MIM; 600214; .  
DR InterPro: IPRO033006; Ig\_MHC.  
DR InterPro: IPRO033598; Ig\_C2.  
DR InterPro: IPRO036000; Ig\_Like.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00408; IgC2; 1.  
DR SMART; SM00410; IG\_Like; 1.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Immunoglobulin domain; Glycoprotein; Transmembrane; Signal;  
RW Alternative splicing; Polymorphism.  
FT SIGNAL 1 22  
FT CHAIN 23 404  
FT DOMAIN 23 342  
FT TRANSMEM 343 363  
FT DOMAIN 364 404  
FT DOMAIN 31 106  
FT DOMAIN 137 214  
FT DOMAIN 252 308  
FT DISULFD 38 99  
FT DISULFD 144 208  
FT DISULFD 259 301  
FT CARBOHYD 25 25  
FT CARBOHYD 81 81  
FT DOMAIN 380 384  
FT VASPLIC 54 67  
FT VASPLIC 275 404  
FT VASPLIC 275 404  
FT VARIANT 100 100  
FT CONFLICT 1 1  
SQ SEQUENCE 404 AA; 42802 MW; 00584c436c30ccce CRC64;

/FTID=VAR\_011338.  
M -> G (IN REF. 1).  
0584c436c30ccce CRC64;

GACRTESVGGR (IN ISOFORM 2).

POTENTIAL.  
ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR.  
EXTRACELLULAR (POTENTIAL).  
POTENTIAL.  
CYTOPLASMIC (POTENTIAL).  
IG-LIKE V-TYPE DOMAIN.  
IG-LIKE C2-TYPE DOMAIN 1.  
IG-LIKE C2-TYPE DOMAIN 2.  
POTENTIAL.  
POTENTIAL.  
N-LINKED (GLCNAC. . ) (POTENTIAL).  
N-LINKED (GLCNAC. . ) (POTENTIAL).  
POLY-GLU.  
MISSING (IN ISOFORM 2).  
GVLPDPSPVLILPEITCPQDCGYTCYATHSSHPQESRA  
VISIIEEGEGEPAGSGGSLGTALAILGLGTAAL  
LVGIIVMRQRKGEERAPENOEEELRALINSEEEAG  
EESTGGP -> VSDLERAGSTRGGANCRICRGIRAGNS  
PGPDGPFGDSRAHMHCHIVAATPRGEGEGRKPGRC  
GACRTESVGGR (IN ISOFORM 2).

|                          |        |                    |       |             |
|--------------------------|--------|--------------------|-------|-------------|
| Query Match              | 100.0% | Score 10;          | DB 1; | Length 404; |
| Best Local Similarity    | 100.0% | Pred. No. 0.00029; |       |             |
| Matches 10; Conservative | 0;     | Mismatches         | 0;    | Indels 0;   |
| 0y                       | 1      | AONTARIGE          | 10    | .           |

| DB     | 23   | ACONTARIGE | 32                      |
|--------|--|------------|-------------------------|
| RESULT | 2  |            |                         |
| ID     | RAGE_RAT   | STANDARD:  | PRT: 402 AA.            |
| AC     | 063495:  |            |                         |
| DT     | 01-NOV-1997 (Rel. 35, Created)   |            |                         |
| DT     | 01-NOV-1997 (Rel. 35, Last sequence update)  |            |                         |
| DT     | 15-JUL-1998 (Rel. 36, Last annotation update)  |            |                         |
| DE     | ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).   |            |                         |
| DE     | AGER OR RAGE.  |            |                         |
| OC     | Rattus norvegicus (Rat).   |            |                         |
| OC     | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  |            |                         |
| OC     | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  |            |                         |
| OX     | NCBI_TaxID=10116;  |            |                         |
| RN     | [1]  |            |                         |
| RP     | SEQUENCE FROM N.A.   |            |                         |
| RC     | STRAIN=SPRAGUE-DAWLEY; TISSUE=Lung;  |            |                         |
| RA     | MEDLINE=97368045; PubMed=9224812;  |            |                         |
| RA     | Renard C., Chappey O., Wautier M.P., Nagashima M., Lundh E.,   |            |                         |
| RA     | Morser J., Zhao L., Schmidt A.M., Scherrmann J.M., Wautier J.L.;   |            |                         |
| RT     | "Recommendant advanced glycation end product receptor pharmacokinetics   |            |                         |
| RT     | in normal and diabetic rats.";   |            |                         |
| RL     | Mol. Pharmacol. 52:54-62(1997).  |            |                         |
| CC     | -1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END  |            |                         |
| CC     | PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS   |            |                         |
| CC     | WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED   |            |                         |
| CC     | RATE IN DIABETES.  |            |                         |
| CC     | -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.   |            |                         |
| CC     | -1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.   |            |                         |
| CC     | -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS  |            |                         |
| CC     | 2 C2-LIKE AND ONE V-LIKE DOMAINS.  |            |                         |
| CC     | -----  |            |                         |
| CC     | This SWISS-PROT entry is copyright. It is produced through a collaboration   |            |                         |
| CC     | between the Swiss Institute of Bioinformatics and the EMBL outstation --   |            |                         |
| CC     | the European Bioinformatics Institute. There are no restrictions on its  |            |                         |
| CC     | use by non-profit institutions as long as its content is in no way   |            |                         |
| CC     | modified and this statement is not removed. Usage by and for commercial  |            |                         |
| CC     | entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch">http://www.isb-sib.ch/announce/</a> |            |                         |
| CC     | or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).  |            |                         |
| CC     | -----  |            |                         |
| DR     | EMBL: L33413; AAA42027.1; -  |            |                         |
| DR     | InterPro: IPR0033006; IG_MHC.  |            |                         |
| DR     | InterPro: IPR003598; IG_C2.  |            |                         |
| DR     | InterPro: IPR003600; IG_Like.  |            |                         |
| DR     | Pfam: PF00047; Ig_3.   |            |                         |
| DR     | SMART: SM00408; IGC2; 1.   |            |                         |
| DR     | SMART: SM00410; IG_Like; 1.  |            |                         |
| DR     | PROSITE: PS00290; IG_MHC; 1.   |            |                         |
| KM     | Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.  |            |                         |
| FT     | SIGNAL   | 1          | 22                      |
| FT     | CHAIN  | 23         | 402                     |
| FT     |  |            |                         |
| FT     | DOMAIN   | 23         | 341                     |
| FT     | DOMAIN   | 342        | 362                     |
| FT     | DOMAIN   | 363        | 402                     |
| FT     | DOMAIN   | 31         | 105                     |
| FT     | DOMAIN   | 136        | 212                     |
| FT     | DOMAIN   | 250        | 306                     |
| FT     | DISULFID   | 38         | 98                      |
| FT     | DISULFID   | 143        | 206                     |
| FT     | DISULFID   | 257        | 299                     |
| FT     | CARBOHD  | 25         | 25                      |
| FT     | CARBOHD  | 80         | 80                      |
| FT     | CARBOHD  | 402 AA;    | 42663 MW;               |
| SO     | SEQUENCE   |            | 594481BC3A51E94E CXC64; |

```

Query Match      90.0%; Score 9; DB 1; Length 402;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```





|        |  |                 |                            |                            |
|--------|--|-----------------|----------------------------|----------------------------|
| FT     | DOMAIN   | 391             | 396                        | POLY-GU.                   |
| SO     | SEQUENCE   | 416 AA;         | 44182 MW;                  | B703815573E767AE CXC64:    |
|        | Query Match  |                 | 80.0%;                     | Score 8; DB 1; Length 416; |
|        | Best Local Similarity  | 100.0%;         | Pred. No. 0.047;           |                            |
|        | Matches  | 8; Conservative | 0; Mismatches              | 0; Indels                  |
| OY     | 2 ONTARIG 9  |                 |                            | Gaps 0;                    |
|        |  |                 |                            |                            |
| Dd     | 24 ONTARIG 31  |                 |                            |                            |
|        | -----  |                 |                            |                            |
| RESULT | 5  |                 |                            |                            |
| ID     | MUTH_HAEN  | STANDARD;       | PRT;                       | 223 AA.                    |
| AC     | P4688;   |                 |                            |                            |
| DT     | 01-NOV-1995 (Rel. 32, Created)   |                 |                            |                            |
| DT     | 01-NOV-1995 (Rel. 32, Last sequence update)                                |                 |                            |                            |
| DT     | 20-AUG-2001 (Rel. 40, Last annotation update)                              |                 |                            |                            |
| DE     | DNA MISMATCH REPAIR PROTEIN MUTH.  |                 |                            |                            |
| GN     | MUTH OR H10403.  |                 |                            |                            |
| OS     | Haemophilus influenzae.  |                 |                            |                            |
| OC     | Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;              |                 |                            |                            |
| OX     | NCBI_TaxID=727;  |                 |                            |                            |
| RN     | (1)  |                 |                            |                            |
| RP     | SEQUENCE FROM N.A.   |                 |                            |                            |
| RC     | STRAIN-RD / KM20 / ATCC 51907;   |                 |                            |                            |
| RX     | MEDLINE=95350630; PubMed=7542800;  |                 |                            |                            |
| RA     | Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,       |                 |                            |                            |
| RA     | Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,       |                 |                            |                            |
| RA     | McKenny K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,             |                 |                            |                            |
| RA     | Scott J.D., Shiley R., Liu L.-I., Glodek A., Kelley J.M.,                  |                 |                            |                            |
| RA     | Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,          |                 |                            |                            |
| RA     | Utterback T.R., Hanna M.C., Nguyen D.T., Saudke D.M., Brandon R.C.,        |                 |                            |                            |
| RA     | Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,                |                 |                            |                            |
| RA     | Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,            |                 |                            |                            |
| RA     | Venter J.C.;   |                 |                            |                            |
| RT     | "Whole-genome random sequencing and assembly of Haemophilus                |                 |                            |                            |
| RL     | Influenzae Rd.";   |                 |                            |                            |
| RL     | Science 269:496-512(1995).   |                 |                            |                            |
| CC     | -I- FUNCTION: SEQUENCE-SPECIFIC ENDONUCLEASE THAT CLEAVES UNMETHYLATED     |                 |                            |                            |
| CC     | GAFC SEQUENCES. IT IS INVOLVED IN DNA MISMATCH REPAIR (BY                  |                 |                            |                            |
| CC     | SIMILARITY).   |                 |                            |                            |
| CC     | -----  |                 |                            |                            |
| CC     | This SWISS-PROT entry is copyright. It is produced through a collaboration |                 |                            |                            |
| CC     | between the Swiss Institute of Bioinformatics and the EMBL outstation --   |                 |                            |                            |
| CC     | the European Bioinformatics Institute. There are no restrictions on lists  |                 |                            |                            |
| CC     | use by non-profit institutions as long as its content is in no way com-    |                 |                            |                            |
| CC     | modified and this statement is not removed. Usage by and for commercial    |                 |                            |                            |
| CC     | entities requires a license agreement (See http://www.isb-sib.ch/announce/ |                 |                            |                            |
| CC     | or send an email to license@isb-sib.ch).                                   |                 |                            |                            |
| CC     | -----  |                 |                            |                            |
| DR     | EMBL; U32723; AAC22062.1; -.   |                 |                            |                            |
| DR     | HSSP; P06722; ZAZO.  |                 |                            |                            |
| DR     | TIGR; H10403; -.   |                 |                            |                            |
| KW     | DNA repair; Hydrolyase; Endonuclease; Complete proteome.                   |                 |                            |                            |
| SQ     | SEQUENCE 223 AA; 24906 MW; 339AAEF9DA0E622A CXC64;                         |                 |                            |                            |
|        | -----  |                 |                            |                            |
|        | Query Match  | 70.0%;          | Score 7; DB 1; Length 223; |                            |
|        | Best Local Similarity  | 100.0%;         | Pred. No. 0.35;            |                            |
|        | Matches  | 7; Conservative | 0; Mismatches              | 0; Indels                  |
| OY     | 4 ITARIGE 10   |                 |                            | Gaps 0;                    |
|        |  |                 |                            |                            |
| Dd     | 165 ITARIGE 171  |                 |                            |                            |
|        | -----  |                 |                            |                            |
| RESULT | 6  |                 |                            |                            |
| ID     | YA79_HAEN  | STANDARD;       | PRT;                       | 210 AA.                    |
|        | YA79_HAEN  |                 |                            |                            |

```

AC      PA5023: 01-OCT-1996 (Rel. 34, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      20-AUG-2001 (Rel. 40, Last annotation update)
DE      HYPOTHEETICAL AMINO-ACID ABC TRANSPORTER PERMEASE PROTEIN H10179.
GN      H10179.
OS      Haemophilus influenzae.
OC      Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC      Haemophilus.
OX      NCBI_taxid=727;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=RD / KW20 / ATCC 51907.
RX      MEDLINE=95350630; PubMed=7542800.
RA      Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA      Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA      McManey K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA      Scott J.D., Shirley R., Liu L.-I., Gilead A., Kelley J.M.,
RA      Weidman J.F., Phillips C.A., Spizys T., Hedblom E., Cotton M.D.,
RA      Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA      Fline L.D., Fleischman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA      Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA      Venter J.C.;
RT      "Whole-genome random sequencing and assembly of Haemophilus
RT      influenzae Rd."
RL      Science 269:496-512(1995).
RN      [2]
RP      REVISIONS.
RA      White O., Clayton R.A., Kerlavage A.R., Fleischmann R.D.;
RL      Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.
CC      -1- FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT
CC      SYSTEM FOR AN AMINO-ACID. PROBABLY RESPONSIBLE FOR THE
CC      TRANSLLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
CC      (POTENTIAL).
CC      -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
CC      PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE HISMO
CC      SUBFAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U32788; AAC22735.1; -.
DR      TIGR; H11079; -.
DR      InterPro; IPR000515; BPD_transp.
DR      Pfam; PF00528; BPD_transp; 1.
DR      PROSITE; PS00402; BPD_TRANSF_INN_MEMBR; 1.
KW      Hypothetical protein; Transport; Amino-acid transport; Transmembrane;
KW      Inner membrane; Complete proteome.
FT      TRANSMEM 10 30 POTENTIAL.
FT      TRANSMEM 57 77 POTENTIAL.
FT      TRANSMEM 79 99 POTENTIAL.
FT      TRANSMEM 177 197 POTENTIAL.
FT      SEQUENCE 210 AA; 23393 MW; 6622C7C59DDC4FDCD CNC64;
  
```

AC P03224;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-DEC-1993 (Rel. 24, Last annotation update)  
 DE PROBABLE MEMBRANE ANTIGEN GP85.  
 GN BDF3.  
 OS Epstein-Barr virus (strain B95-8) (Human herpesvirus 4).  
 CC Viruses: dsDNA viruses, no RNA stage; Herpesviridae;  
 CC Gammaherpesvirinae; Lymphocryptovirus.  
 CC NCBI\_TaxID=10377;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84270667; PubMed=6087149;  
 RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,  
 RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seglin C.,  
 RA Tuffnell P.S., Barrell B.G.,  
 RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome."  
 RL Nature 310:207-211(1984).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: V01555; CA24835.1; -  
 DR PIR: A03787; Q0BE43.  
 DR PIR: S33040; S33040.  
 KW Membrane; Glycoprotein; Late protein.  
 SO SEQUENCE 234 AA; 23791 MW; 48D6CED09331119E CRC64;

Query Match 60.0%; Score 6; DB 1; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 4.5;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITA 6  
 DB 108 AONITA 113

RESULT 8  
 PROC\_VIBAL STANDARD: PRT: 278 AA.  
 ID PROC\_VIBAL P52053;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).  
 GN PROC.  
 OS Vibrio alginolyticus.  
 CC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrrio.  
 CC NCBI\_TaxID=663;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=138-2;  
 RC MEDLINE=97137009; PubMed=8982386;  
 RC Nakamura T., Katoh Y., Shimizu Y., Matsuba Y., Unemoto T.;  
 RA "Cloning and sequencing of novel genes from *Vibrio alginolyticus* that  
 RT support the growth of K+ uptake-deficient mutant of *Escherichia*  
 RT coli."  
 RL Biochim. Biophys. Acta 1277:201-208(1996).  
 CC -I- CATALYTIC ACTIVITY: L-PYRROLINE + NAD(P)(+) = L-PYRROLINE-5-  
 CC CARBOXYLATE + NAD(P)H.  
 CC -I- PATHWAY: TERMINAL (THIRD) STEP IN PROLINE BIOSYNTHESIS.  
 CC -I- SIMILARITY: BELONGS TO THE PYRROLINE-5-CARBOXYLATE REDUCTASE  
 CC FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: D50472; BAA09063.1; -  
 DR InterPro: IPR000304; P5CR.  
 DR Pfam: PF01089; P5CR: 1.  
 DR PROSITE: PS00521; P5CR: 1.  
 KW Oxidoreductase; Proline biosynthesis; NADP.  
 SO SEQUENCE 278 AA; 29815 MW; 50359E5EF97C068B CRC64;

Query Match 60.0%; Score 6; DB 1; Length 278;  
 Best Local Similarity 100.0%; Pred. No. 5.3;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITA 6  
 DB 35 AONITA 40

RESULT 9  
 ENO\_THEAC STANDARD: PRT: 401 AA.  
 ID ENO\_THEAC Q9HJL1;  
 DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-  
 DE GLYCERATE HYDRO-LYASE).  
 GN ENO OR TA0882.  
 OS Thermoplasma acidophilum.  
 CC Archaea; Euryarchaeota; Thermoplasmatales; Thermoplasmaceae;  
 CC Thermoplasma.  
 CC NCBI\_TaxID=2303;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DSM 1728;  
 RC MEDLINE=20479972; PubMed=11029001;  
 RA Ruepp A., Granel W., Santos-Martinez M.-L., Koretke K.K., Volker C.,  
 RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;  
 RT "The genome sequence of the thermophilic scavenger *Thermoplasma*  
 RT *acidophilum*."  
 RL Nature 407:508-513(2000).  
 CC -I- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE +  
 CC H(2)O.  
 CC -I- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING  
 CC THE DIMER (BY SIMILARITY).  
 CC -I- PATHWAY: GLYCOLYSIS.  
 CC -I- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -I- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).  
 CC -I- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AL445065; CAC12011.1; -  
 DR InterPro: IPR000941; Enolase.  
 DR Pfam: PF00113; enolase: 1.  
 DR ProDom: PD000902; Enolase: 1.  
 DR PROSITE: PS00164; ENOLASE; FALSE NEG.  
 KW Lyase; Glycolysis; Magnesium; Complete proteome.  
 FT ACT\_SITE 146  
 FT METAL 233  
 FT METAL 274  
 FT METAL 301  
 SO SEQUENCE 401 AA; 43401 MW; 56D2C37CCA58AF02 CRC64;

Query Match  
Best Local Similarity 100.0%; Score 6; DB 1; Length 401;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TARIG 9  
DB 288 TARIG 293

RESULT 10  
YR4 CAEEL  
ID YR4 CAEEL STANDARD; PRT; 429 AA.  
AC 009415; 009414;  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE HYPOTHETICAL 48.5 KDA PROTEIN R06F6.4 IN CHROMOSOME II.  
GN R06F6.4.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;  
OC Rhabditidae; Poloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RA Chui C.;  
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP REVISIONS.  
RC STRAIN-BRISTOL N2;  
RA Jones S.J.M.;  
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (PORENTIAL).  
CC -1- SIMILARITY: CONTAINS 1 MYND-TYPE ZINC FINGER.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: Z46794; CAA86783.1; -  
DR WormBep: R06F6.4; CE16303.  
DR InterPro: IPR002893; Znf-MYND.  
DR Pfam: PF01753; Zf-MYND; 1.  
KW Hypothetical protein; Zinc-finger; DNA-binding; Nuclear protein.  
FT ZN\_FING 26 64 MYND-TYPE.  
SQ SEQUENCE 429 AA; 48546 MW; 51F223A6D0B56BA9 CRC64;

Query Match  
Best Local Similarity 100.0%; Score 6; DB 1; Length 429;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITA 6  
DB 345 AONITA 350

RESULT 11  
ARLY\_METH  
ID ARLY\_METH STANDARD; PRT; 468 AA.  
AC 026369;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE ARGININOSUCCINATE LYASE (EC 4.3.2.1) (ARGINOSUCCINASE) (ASAL).  
GN ARGH OR MTH69.  
OS Methanobacterium thermoautotrophicum.

OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;  
OC Methanobacter.  
OX NCBI\_TaxID=145262;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-DELTA H;  
RX MEDLINE=98037514; PubMed=9371463;  
RA Smith D.R., Doucette-Stamm L.A., Delonghery C., Lee H.-M., Dubois J.,  
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,  
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,  
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,  
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,  
RA McDougall S., Shiner G., Goyal A., Pietrowski S., Church G.M.,  
RA Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;  
RT "Complete genome sequence of Methanobacterium thermoautotrophicum  
RT deltaH: functional analysis and comparative genomics."  
RL J. Bacteriol. 179:7135-7155(1997).  
CC -1- CATALYTIC ACTIVITY: L-ARGININOSUCCINATE = FUMARATE + L-ARGININE.  
CC -1- PATHWAY: THE LAST STEP IN ARGININE BIOSYNTHESIS.  
CC -1- SIMILARITY: BELONGS TO THE LYASE 1 FAMILY, ARGININOSUCCINATE LYASE  
CC SUBFAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: AE000812; AAB84775.1; -  
DR InterPro: IPR000362; Fumarate\_Lyase.  
DR Pfam: PF00206; Lyase\_1; 1.  
DR PRINTS: PR00145; DCRYSTALLIN.  
DR PRINTS: PR00149; FUMARATELYASE.  
DR PROSITE: PS00163; FUMARATE\_LYASES; FALSE\_NEG.  
KW Arginine biosynthesis; Lyase; Complete proteome.  
SQ SEQUENCE 468 AA; 52439 MW; 2DD1F7A65F5D57 CRC64;

Query Match  
Best Local Similarity 100.0%; Score 6; DB 1; Length 468;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TARIGE 10  
DB 91 TARIGE 96

RESULT 12  
SYT\_RICPR  
ID SYT\_RICPR STANDARD; PRT; 635 AA.  
AC 005947;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE THREONYL-TRNA SYNTHETASE (EC 6.1.1.3) (THREONINE--TRNA LIGASE)  
DE (THRS).  
GN THRS OR RP221.  
OS Rickettsia prowazekii.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiae; Rickettsia.  
OX NCBI\_TaxID=782;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-MADRID E;  
RX MEDLINE=97419517; PubMed=9274032;  
RA Andersson J.O., Andersson S.G.E.;  
RT "Genomic rearrangements during evolution of the obligate  
RT intracellular parasite Rickettsia prowazekii as inferred from an  
RT analysis of 52015 bp nucleotide sequence.";  
RL Microbiology 143:2783-2795(1997).  
RN [2]

RP SEQUENCE FROM N.A.  
 RC STRAIN-MADRID E;  
 RX MEDLINE=9039499; PubMed=9823893;  
 RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,  
 RA Sichteritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,  
 RA Erilsson A.-S., Winkler H.H., Kurland C.G.;  
 RT "The genome sequence of Rickettsia prowazekii and the origin of  
 RT mitochondria";  
 RL Nature 396:133-140(1998).  
 CC -1- CATALYTIC ACTIVITY: ATP + L-THREONINE + TRNA(THR) = AMP +  
 CC PYROPHOSPHATE + L-THREONYL-TRNA(THR).  
 CC -1- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.  
 CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: Y11780; CAA72469.1; -;  
 DR EMBL: AJ235270; CAA14684.1; -;  
 DR InterPro: IPR002106; AA.Trna\_Ligase\_II.  
 DR InterPro: IPR002314; trna-synt-2b.  
 DR InterPro: IPR002320; trna-synt-1.  
 DR Pfam: PF00587; trna-synt-2b; 1.  
 DR PRINTS: PRO1047; TRNASYNTHTR.  
 DR PROSITE: PS00179; AA-TRNA-LIGASE-II-1; FALSE\_NEG.  
 DR PROSITE: PS00339; AA-TRNA-LIGASE-II-2; 1.  
 DR KMW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;  
 KW Metal-binding; Zinc; Complete proteome.  
 KW DOMAIN 242 533 CATALYTIC.  
 FT METAL 333 333 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL 384 384 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL 510 510 ZINC (CATALYTIC) (BY SIMILARITY).  
 SO SEQUENCE 635 AA; 72676 MW; B000D1514AF728D5 CRC64;

Query Match 60.0%; Score 6; DB 1; Length 635;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITA 6  
 DB 15 AONITA 20  
 |||||  
 |||||

RESULT 13  
 RECD\_HAEIN STANDARD; PRT; 788 AA.  
 ID RECD\_HAEIN  
 AC P4408;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE RECOMBINATION PROTEIN 2.  
 GN RECD OR REC-2 OR HI0061.  
 OS Haemophilus influenzae.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
 CC Haemophilus.  
 OX NCBI\_TaxID=727;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BC200;  
 RX MEDLINE=94341577; PubMed=8063112;  
 RA Clifton S.W., McCarthy D., Roe B.A.;  
 RT "Sequence of the rec-2 locus of Haemophilus influenzae: homologues to  
 RT comE-ORF3 of Bacillus subtilis and msdA of Escherichia coli";  
 RL Gene 146:95-100(1994).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC STRAIN-RD / KM20 / ATCC 51907;  
 RX MEDLINE=95350630; PubMed=7542800;  
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,  
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
 RA Fine L.D., Frichman J.L., Fuhmann J.L., Geoghagen N.S.M.,  
 RA Guelin C.L., McDonald J.A., Small K.V., Fraser C.M., Smith H.O.,  
 RA Venter J.C.;  
 RT "Whole-genome random sequencing and assembly of Haemophilus  
 RT influenzae Rd";  
 RL Science 269:496-512(1995).  
 CC -1- FUNCTION: MIGHT CONTRIBUTE TO TRANSFORMATION AS A MEMBER OF A  
 CC MEMBRANE BOUND PORE COMPLEX AT THE BASE OF THE TRANSFORMASOME. IT  
 CC COULD DIRECTLY INTERACT WITH TRANSFORMING DNA DURING TRANSLOCATION  
 CC INDIRECTLY BY PARTICIPATING IN THE ASSEMBLY OF THE PORE.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE  
 CC (POTENTIAL).  
 CC -1- SIMILARITY: TO B.SUBTILIS COMEC, N.GONORRHOEA COMA, AND E.COLI  
 CC YCAL.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: L20805; AAC13733.1; -;  
 DR EMBL: U32691; AAC21739.1; -;  
 DR TIGR: H10061; -;  
 DR InterPro: IPR001279; Beta\_Lactam\_mel.  
 DR Pfam: PF00753; Lactamase\_B; 1.  
 KW Transport; Transmembrane; Inner membrane; Complete proteome.  
 FT TRANSMEM 3 23 POTENTIAL.  
 FT TRANSMEM 27 47 POTENTIAL.  
 FT TRANSMEM 51 71 POTENTIAL.  
 FT TRANSMEM 226 246 POTENTIAL.  
 FT TRANSMEM 263 283 POTENTIAL.  
 FT TRANSMEM 313 333 POTENTIAL.  
 FT TRANSMEM 367 387 POTENTIAL.  
 FT TRANSMEM 401 421 POTENTIAL.  
 FT TRANSMEM 434 454 POTENTIAL.  
 FT TRANSMEM 456 476 POTENTIAL.  
 FT TRANSMEM 508 528 POTENTIAL.  
 FT TRANSMEM 748 788 POTENTIAL.  
 FT CONFLICT  
 FT VENTAVSGGVAVNEFDORLEIOQARTKFSFWYAVIGLSKE  
 FT -> GRKYRCGASAGKFFSPRINPASPASHKIFPLVCACNMI  
 FT IKIGKIMRAIFTR (IN REF. 1).  
 SO SEQUENCE 788 AA; 89355 MW; F31104595CB4E47A CRC64;

Query Match 60.0%; Score 6; DB 1; Length 788;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONITA 6  
 DB 76 AONITA 81  
 |||||  
 |||||

RESULT 14  
 HECL\_HAEIN STANDARD; PRT; 837 AA.  
 ID HECL\_HAEIN  
 AC P33397;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE OUTER MEMBRANE USHER PROTEIN HIFC PRECURSOR.  
 GN HIFC.

```

OS Haemophilus influenzae.
OC Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-EGAN / SEROTYPE B;
RX MEDLINE=94131580; PubMed=7905461;
RA Watson W.J., Gilsdorf J.R., Tucci M.A., McCrea K.W., Forney L.J.,
RA Mairs C.F.;
RT Identification of a gene essential for piliation in Haemophilus
RT influenzae type b with homology to the pilus assembly platform genes
RT of gram-negative bacteria.
RL Infect. Immun. 62:468-475(1994).
CC -1- FUNCTION: ESSENTIAL FOR PILATION.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-97 IS THE INITIATOR.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U02937; AAB53096.1; -.
DR InterPro: IPR000015; Fimb_usher.
DR Pfam: PF00577; Usher. 1.
DR PROSITE: PS01151; FIMBRIAL_USHER. 1.
KW Outer membrane; Transmembrane; Fimbria; Transport; Signal.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 837 OUTER MEMBRANE USHER PROTEIN HIFC.
FT DISULFID 813 833 POTENTIAL.
SQ SEQUENCE 837 AA; 92733 MW; BA529323AF63BF8B CRC64;

```

## Query Match

Best Local Similarity 60.0%; Score 6; DB 1; Length 837;  
Pred. No. 14;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TARIGE 10  
|||||  
Db 253 TARIGE 258

```

RESULT 15
HFC2_HAEIN STANDARD; PRT: 837 AA.
AC P45957;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE OUTER MEMBRANE USHER PROTEIN HIFC PRECURSOR.
GN HIFC.
OS Haemophilus influenzae.
OC Bacteria: Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AM30 (770235) / SEROTYPE B;
RX MEDLINE=95089703; PubMed=7997179;
RA van Ham M.S., van Alphen L., Mooi F.R., van Putten J.P.;
RT The fimbrial gene cluster of Haemophilus influenzae type b.
RL Mol. Microbiol. 13:673-684(1994).
CC -1- FUNCTION: ESSENTIAL FOR PILATION.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-97 IS THE INITIATOR.
CC -----

```

```

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z33502; CAA83902.1; -.
DR InterPro: IPR000015; Fimb_usher.
DR Pfam: PF00577; Usher. 1.
DR PROSITE: PS01151; FIMBRIAL_USHER. 1.
KW Outer membrane; Transmembrane; Fimbria; Transport; Signal.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 837 OUTER MEMBRANE USHER PROTEIN HIFC.
FT DISULFID 813 833 POTENTIAL.
SQ SEQUENCE 837 AA; 92641 MW; 0992A9F2C71F2774 CRC64;

```

## Query Match

Best Local Similarity 60.0%; Score 6; DB 1; Length 837;  
Pred. No. 14;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TARIGE 10  
|||||  
Db 253 TARIGE 258

Search completed: April 24, 2002, 09:24:55  
Job time: 248 sec



**THIS PAGE BLANK (USPTO)**



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:24:27 ; Search time 63.44 Seconds  
(without alignments)  
23.057 Million cell updates/sec

Title: US-09-689-469-6  
Perfect score: 10  
Sequence: 1 AQNITARICE 10

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 473505 seqs, 146272329 residues

Word size : 0

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPREMBL\_17:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID  | Description        |
|------------|-------|-------------|--------|--------|--------------------|
| 1          | 100.0 | 342         | 4      | Q9Y3R3 | Q9Y3R3 homo sapien |
| 2          | 90.0  | 402         | 11     | Q35444 | Q35444 mus musculu |
| 3          | 60.0  | 32          | 6      | Q9P801 | Q9P801 bos taurus  |
| 4          | 60.0  | 127         | 12     | Q9E8A5 | Q9E8A5 human immun |
| 5          | 60.0  | 298         | 10     | Q9Z504 | Q9Z504 arabidopsis |
| 6          | 60.0  | 389         | 9      | Q38644 | Q38644 bacterioph  |
| 7          | 60.0  | 452         | 10     | Q9LRM5 | Q9LRM5 arabidopsis |
| 8          | 60.0  | 471         | 1      | Q04928 | Q04928 methanobact |
| 9          | 60.0  | 548         | 10     | Q9SVR2 | Q9SVR2 arabidopsis |
| 10         | 60.0  | 609         | 10     | Q9SHB9 | Q9SHB9 arabidopsis |
| 11         | 60.0  | 822         | 2      | Q9L273 | Q9L273 streptomyc  |
| 12         | 60.0  | 837         | 2      | P94813 | P94813 haemophilus |
| 13         | 50.0  | 39          | 2      | Q9RFA3 | Q9RFA3 xenorhabdus |
| 14         | 50.0  | 68          | 2      | Q52235 | Q52235 clostridium |
| 15         | 50.0  | 71          | 4      | Q9NPV6 | Q9NPV6 homo sapien |
| 16         | 50.0  | 72          | 11     | Q9CZU1 | Q9CZU1 mus musculu |
| 17         | 50.0  | 72          | 11     | Q9CR64 | Q9CR64 mus musculu |
| 18         | 50.0  | 74          | 5      | Q9VWH8 | Q9VWH8 dirosophila |
| 19         | 50.0  | 77          | 4      | Q9BZT4 | Q9BZT4 homo sapien |

|    |   |      |     |    |        |                     |
|----|---|------|-----|----|--------|---------------------|
| 20 | 5 | 50.0 | 90  | 12 | Q98XX4 | Q98XX4 human immun  |
| 21 | 5 | 50.0 | 91  | 12 | Q9W063 | Q9W063 human immun  |
| 22 | 5 | 50.0 | 98  | 12 | Q9IXR2 | Q9IXR2 human immun  |
| 23 | 5 | 50.0 | 99  | 12 | Q992E8 | Q992E8 human immun  |
| 24 | 5 | 50.0 | 99  | 12 | Q98X93 | Q98X93 human immun  |
| 25 | 5 | 50.0 | 111 | 4  | Q9Y517 | Q9Y517 homo sapien  |
| 26 | 5 | 50.0 | 114 | 10 | Q9ARE8 | Q9ARE8 lltospermu   |
| 27 | 5 | 50.0 | 118 | 2  | Q9RVP1 | Q9RVP1 deinococcus  |
| 28 | 5 | 50.0 | 120 | 10 | Q9S0G4 | Q9S0G4 tritlicum ae |
| 29 | 5 | 50.0 | 120 | 10 | Q9S0G3 | Q9S0G3 tritlicum ae |
| 30 | 5 | 50.0 | 125 | 2  | Q9HZAI | Q9HZAI pseudomonas  |
| 31 | 5 | 50.0 | 134 | 12 | Q9IHW2 | Q9IHW2 human immun  |
| 32 | 5 | 50.0 | 136 | 12 | Q9E7L8 | Q9E7L8 human cytom  |
| 33 | 5 | 50.0 | 137 | 10 | Q9SW21 | Q9SW21 arabidopsis  |
| 34 | 5 | 50.0 | 139 | 2  | Q931A6 | Q931A6 mycobacteri  |
| 35 | 5 | 50.0 | 142 | 2  | Q9CK57 | Q9CK57 pasteurella  |
| 36 | 5 | 50.0 | 142 | 2  | Q9A2J7 | Q9A2J7 caulobacter  |
| 37 | 5 | 50.0 | 143 | 10 | Q9ZSL4 | Q9ZSL4 chlororium i |
| 38 | 5 | 50.0 | 146 | 10 | P93180 | P93180 hordeum vul  |
| 39 | 5 | 50.0 | 146 | 10 | Q64392 | Q64392 tritlicum ae |
| 40 | 5 | 50.0 | 147 | 2  | Q51542 | Q51542 pseudomonas  |
| 41 | 5 | 50.0 | 147 | 2  | Q9F3H0 | Q9F3H0 streptomyc   |
| 42 | 5 | 50.0 | 148 | 10 | Q64393 | Q64393 tritlicum ae |
| 43 | 5 | 50.0 | 152 | 12 | Q41952 | Q41952 murid herpe  |
| 44 | 5 | 50.0 | 157 | 1  | Q9HR46 | Q9HR46 halobacteri  |
| 45 | 5 | 50.0 | 160 | 2  | Q9JN73 | Q9JN73 streptomyc   |

## ALIGNMENTS

RESULT 1  
ID Q9Y3R3 PRELIMINARY: PRT: 342 AA.  
AC Q9Y3R3;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE RECEPTOR FOR ADVANCED GLYCATION END PRODUCTS PRECURSOR.  
GN RAGESEC.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Malherbe P., Richards J., Galliard H., Thompson A., Diener C.,  
RA Schuler A., Huber G.;  
RT "CDNA cloning of a novel secreted isoform of the human Receptor for  
RT Advanced Glycation End products (RAGE) and characterization of cells  
RT co-expressing cell-surface scavenger receptors and Swedish mutant  
RT amyloid precursor protein.";  
RL Submitted (May-1999) to the EMBL/Genbank/DBJ databases.  
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
CC DOMAIN.  
CC EMBL: AJ133822; CAB43108.1;  
CC InterPro: IPR003598; Ig\_C2.  
CC InterPro: IPR003600; Ig\_Like.  
CC InterPro: IPR003006; Ig\_MHC.  
CC Pfam: PF00047; Ig\_2.  
CC SMART: SM00408; IGC2: 1.  
CC SMART: SM00410; IG\_Like; 1.  
KW Signal; Receptor.  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 342 RECEPTOR FOR ADVANCED GLYCATION END  
FT PRODUCTS.  
SO SEQUENCE 342 AA; 36193 MW; 35DDF6A13E39B38 CRC64;

Query Match 100.0%; Score 10; DB 4; Length 342;  
Best Local Similarity 100.0%; Pred. No. 0.0015;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10  
 |||||  
 DB 23 AONTARIGE 32

## RESULT 2

O35444 PRELIMINARY; PRT; 402 AA.  
 ID O35444  
 AC O35444  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE RAGE.  
 GN RAGE.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NCBI\_Taxid=10090;  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Rowen L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,  
 RA Loretz C., Schmidt S., Tipton S., Traicoff R., Zackrone K., Hood L.;  
 RL Submitted (OC1-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 CC EMBL: AF030001; AAB82007.1; -  
 DR InterPro: IPR003598; Ig\_C2.  
 DR InterPro: IPR003600; Ig\_Like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig\_3.  
 DR SMART: SM00408; IgC2; 1.  
 DR SMART: SM00410; Ig\_Like; 1.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN.1.  
 SO SEQUENCE 402 AA; 42653 MW; DBFDC50A6C8C9902 CRC64;

Query Match 90.0%; Score 9; DB 11; Length 402;  
 Best Local Similarity 100.0%; Pred. No. 0.021;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 QNTARIGE 10  
 |||||  
 DB 24 QNTARIGE 32

RESULT 3  
 O9TR01 PRELIMINARY; PRT; 32 AA.

AC O9TR01  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
 DE 35 KDA ADVANCED GLYCOSYLATION END PRODUCT BINDING PROTEIN (FRAGMENT).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 NCBI\_Taxid=9913;  
 OX NCBI\_Taxid=9913;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE-92340546; PubMed-131822;  
 RA Schmidt A.M., Viana M., Gerlach M., Brett J., Ryan J., Kao J.,  
 RA Espósito C., Hegarty H., Hurley W., Claus M.;  
 RT "Isolation and characterization of two binding proteins for advanced  
 RT glycosylation end products from bovine lung which are present on the  
 RT endothelial cell surface.";  
 RL J. Biol. Chem. 267:14987-14997(1992).  
 SO SEQUENCE 32 AA; 3507 MW; AE4C3147CE5B3D91 CRC64;

Query Match 60.0%; Score 6; DB 6; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 4.7;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ITARIG 9  
 |||||  
 DB 4 ITARIG 9

## RESULT 4

O9EAJ5 PRELIMINARY; PRT; 127 AA.  
 ID O9EAJ5  
 AC O9EAJ5  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE PROTEASE (FRAGMENT).  
 GN POL.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NCBI\_Taxid=11676;  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-99-117635;  
 RA Barlow K.L., Tatt I.D., Cane P.A., Pillay D., Clewley J.P.;  
 RT "Detection of simple and complex recombinant strains of HIV-1 in the  
 RT UK."  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO  
 CC KNOWN AS THE RETROPEPSIN FAMILY.  
 CC EMBL: AJ296662; CAC03693.1; -  
 DR InterPro: IPR001969; Asp\_protase.  
 DR InterPro: IPR001995; Asp\_protetov.  
 DR Pfam: PF00077; rvp; 1.  
 DR PROSITE: PS00141; ASP\_PROTEASE; 1.  
 DR PROSITE: PS50175; ASP\_PROT\_RETROV; 1.  
 KM Aspartyl protease; Hydrolase.  
 FT NON\_TER 1 1  
 FT NON\_TER 127 127  
 SO SEQUENCE 127 AA; 13648 MW; CEAF72745863D5F4 CRC64;

Query Match 60.0%; Score 6; DB 12; Length 127;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ITARIG 9  
 |||||  
 DB 39 ITARIG 44

## RESULT 5

O9ZS04 PRELIMINARY; PRT; 298 AA.  
 ID O9ZS04  
 AC O9ZS04  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE RNA HELICASE (FRAGMENT).  
 GN RH17.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 NCBI\_Taxid=3702;  
 OX NCBI\_Taxid=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-CV. COLUMBIA;  
 RA MEDLINE-99081866; PubMed-9862990;  
 RA Aubourg S., Kreis M., Lecharny A.;  
 RT "The DEAD box RNA helicase family in Arabidopsis thaliana.";  
 RL Nucleic Acids Res. 27:628-636(1999).  
 CC -1- SIMILARITY: TO HELICASE C-TERMINAL DOMAIN.  
 CC EMBL: A010468; CA09207.1; -  
 DR InterPro: IPR001410; DEAD.  
 DR InterPro: IPR001650; Helicase\_C.

DR Pfam; PF00271; helicase-C; 1.  
 DR SMART; SM00490; HelicC; 1.  
 KW ATP-binding; Helicase.  
 FT NON\_TER 1  
 SQ SEQUENCE 298 AA; 33973 MW; 6A38DF06CA2A7F4E CRC64;

Query Match 60.0%; Score 6; DB 10; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TARIGE 10  
 |||||  
 DB 129 TARIGE 134

RESULT 6  
 Q38644 PRELIMINARY; PRT; 389 AA.  
 ID Q38644  
 AC Q38644; 038566;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE PORE-FORMING CYTOTOXIN INTEGRASE.  
 GN INT.  
 OS bacteriophage phi CTX.  
 OC Viruses.  
 OX NCBI\_TaxID=35343;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95124301; PubMed=7823914;  
 RA Wang Z., Xiong G., Lutz F.;  
 RT "Site-specific integration of the phage phi CTX genome into the  
 RT Pseudomonas aeruginosa chromosome: characterization of the functional  
 RT Integrase gene located close to and upstream of atpP";  
 RL Mol. Gen. Genet. 246:72-79(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Hayashi T., Matsumoto H., Ohnishi M., Terawaki Y.;  
 RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Langewiesche F.W., Balzer A., Lutz F.;  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PHICTX-C;  
 RA Nakayama K., Hayashi T.;  
 RT "Whole genome sequence of Pseudomonas aeruginosa cytotoxin-converting  
 RT phage: phiCTX.";  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PHICTX-C;  
 RA MEDLINE=90014160; PubMed=2507866;  
 RA Hayashi T., Kamio Y., Hishinuma F., Usami Y., Titani K., Terawaki Y.;  
 RT "Pseudomonas aeruginosa cytotoxin: the nucleotide sequence of the gene  
 RT and the mechanism of activation of the protoxin";  
 RL Mol. Microbiol. 3:861-868(1989).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PHICTX-C;  
 RA MEDLINE=93225809; PubMed=8469112;  
 RA Hayashi T., Matsumoto H., Ohnishi M., Terawaki Y.;  
 RT "Molecular analysis of a cytotoxin-converting phage, phi CTX, of  
 RT Pseudomonas aeruginosa: structure of the atpP-cotX region and  
 RT integration into the serine tRNA gene.";  
 RL Mol. Microbiol. 7:657-667(1993).  
 DR EMBL; S75107; AAD14164.1; -  
 DR EMBL; D13409; BA02675.1; -  
 DR EMBL; S75107; AAD14165.1; -  
 DR EMBL; Y13918; CAA74224.1; -  
 DR EMBL; AB008550; BAA36272.1; -

DR InterPro; IPR002104; Phage\_integrase.  
 DR Pfam; PF00589; Phage\_integrase; 1.  
 SQ SEQUENCE 389 AA; 44431 MW; DA98223148071EF1 CRC64;

Query Match 60.0%; Score 6; DB 9; Length 389;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TARIGE 10  
 |||||  
 DB 191 TARIGE 196

RESULT 7  
 Q9LRM5 PRELIMINARY; PRT; 452 AA.  
 ID Q9LRM5  
 AC Q9LRM5;  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE PECTATE LYASE.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RA MEDLINE=20277480; PubMed=10819329;  
 RA Nakamura Y.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence  
 RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC  
 RT clones";  
 RL DNA Res. 7:131-135(2000).  
 DR EMBL; AB028621; BAB01365.1; -  
 DR InterPro; IPR002022; Amb.allergen.  
 DR Pfam; PF00544; pec\_lyase; 1  
 DR PRINTS; PR00807; AMBALLEGEN.  
 KW Lyase.  
 SQ SEQUENCE 452 AA; 49985 MW; F31AD9097F923249 CRC64;

Query Match 60.0%; Score 6; DB 10; Length 452;  
 Best Local Similarity 100.0%; Pred. No. 46;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QNTTAR 7  
 |||||  
 DB 87 QNTTAR 92

RESULT 8  
 Q04928 PRELIMINARY; PRT; 471 AA.  
 ID Q04928  
 AC Q04928;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE HYPOTHETICAL 51.6 KDA PROTEIN (ORF5).  
 OS Methanobacterium thermoautotrophicum.  
 OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;  
 OC Methanobacterium.  
 OX NCBI\_TaxID=145262;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93341463; PubMed=8393514;

RA Noelling J., Van Eden F.J.M., De Vos W.M.;  
 RT "Distribution and characterization of plasmid-related sequences in the  
 RL chromosomal DNA of different thermophilic *Methanobacterium* strains.";  
 DR Mol. Gen. Genet. 240:81-91(1993).  
 DR EMBL: X69114; CAA48867.1; -  
 DR InterPro: IPR001434; DUF11.  
 DR Pfam: PF01345; DUF11; 2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 471 AA; 51595 MW; 4AB8DB34FAB57BDE CRC64;

Query Match 60.0%; Score 6; DB 1; Length 471;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 NITARI 8  
 DB 311 NITARI 316

RESULT 9  
 ID 09SVE2 PRELIMINARY; PRT; 548 AA.  
 AC 09SVE2:  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE HYPOHETICAL 60.8 KDA PROTEIN.  
 GN F22113.200 OR ATG438430.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bevan M., Medler H., Kutzner M., Wambutt R., Bancroft I., Mewes H.W.,  
 RA Mayer K.F.X., Schueller C.;  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Medler H., Kutzner M., Wambutt R., Mewes H.W., Lemcke K.,  
 RA Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL035539; CAB37499.1; -  
 DR EMBL: AL161593; CAB80508.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 548 AA; 60847 MW; 7E6A8086E0FA5EC6 CRC64;

Query Match 60.0%; Score 6; DB 10; Length 548;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 NITARI 8  
 DB 440 NITARI 445

RESULT 10  
 ID 09SHB9 PRELIMINARY; PRT; 609 AA.  
 AC 09SHB9:  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE ATP-DEPENDENT RNA HELICASE.  
 GN ATG40700.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RX MEDLINE=20083487; PubMed=10617197;  
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,  
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,  
 RA Buell C.R., Ketchum K.A., Lee J.J., Rensing C.M., Koo H., Moffat K.S.,  
 RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,  
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,  
 RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,  
 RA Salzberg S.L., Fraser C.M., Venter J.C.;  
 RT "Sequence and analysis of chromosome II of Arabidopsis thaliana.";  
 RL Nature 402:761-768(1999).  
 CC -1- SIMILARITY: TO DEAD/DEAD BOX HELICASE FAMILY.  
 CC -1- SIMILARITY: TO HELICASE C-TERMINAL DOMAIN.  
 DR EMBL: AC007660; AAD32817.1; -  
 DR InterPro: IPR001410; DEAD.  
 DR InterPro: IPR001650; Helicase\_C.  
 DR Pfam: PF002270; DEAD; 1.  
 DR Pfam: PF002271; helicase\_C; 1.  
 DR SMART: SM00487; DEXDC; 1.  
 DR SMART: SM00490; HELIC; 1.  
 KW ATP-binding; Helicase.  
 SQ SEQUENCE 609 AA; 68213 MW; 0AB50FD42FE50DA0 CRC64;

Query Match 60.0%; Score 6; DB 10; Length 609;  
 Best Local Similarity 100.0%; Pred. No. 59;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TARIGE 10  
 DB 440 TARIGE 445

RESULT 11  
 ID 09L273 PRELIMINARY; PRT; 822 AA.  
 AC 09L273:  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE HYPOHETICAL 91.7 KDA PROTEIN.  
 GN SCL2.26C.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Seeger K.J., Harris D.;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Cerdano A.M., Parkhill J., Barrell B.G., Rajandream M.A.;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RX MEDLINE=97000351; PubMed=8843436;  
 RA Redenbach M., Kleser H.M., Denaplatte D., Eichner A., Cullum J.,  
 RA Kinashi H., Hopwood D.A.;  
 RT "A set of ordered cosmids and a detailed genetic and physical map for

RT the 8 Mb Streptomyces coelicolor A3(2) chromosome."  
 RL Mol. Microbiol. 21:77-96(1996).  
 DR EMBL; AL137778; CAB70938.1; -.  
 KW Hypothetical protein.  
 SO SEQUENCE 822 AA; 91739 MW; F210BCA05DA3C3E7 CRC64;

Query Match 60.0%; Score 6; DB 2; Length 822;  
 Best Local Similarity 100.0%; Pred. No. 76;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ITARIG 9  
 DB 58 ITARIG 63

RESULT 12  
 ID P94813 PRELIMINARY; PRT; 837 AA.  
 AC P94813;  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE USHER PROTEIN.  
 GN HAF.  
 OS Haemophilus influenzae.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
 OC Haemophilus.  
 OX NCBI\_Taxid=727;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=F3031;  
 RX MEDLINE=97086624; PubMed=8932313;  
 RA Read T.D.; Dowdell M.; Satola S.W.; Farley M.M.;  
 RT "Duplication of pilus gene complexes of Haemophilus influenzae  
 RT biogroup aegyptius.";  
 RL J. Bacteriol. 178:6564-6570(1996).  
 DR EMBL; U54780; AAB70873.1; -.  
 DR InterPro: IPR000015; Fimb\_usher.  
 DR Pfam: PF00577; Usher.1.  
 DR PROSITE: PS01151; FIMBRIAL\_USHER.1.  
 SO SEQUENCE 837 AA; 92683 MW; 6F01ED1D2FFC4176 CRC64;

Query Match 60.0%; Score 6; DB 2; Length 837;  
 Best Local Similarity 100.0%; Pred. No. 77;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TARIGE 10  
 DB 253 TARIGE 258

RESULT 13  
 ID Q9RFA3 PRELIMINARY; PRT; 39 AA.  
 AC Q9RFA3;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE MIAE (FRAGMENT).  
 GN MIAE.  
 OS Xenorhabdus nematophilus.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Xenorhabdus.  
 OX NCBI\_Taxid=628;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC19061;  
 RA Vivas E.I.; Goodrich-Blair H.;  
 RT "Tpos is necessary for Xenorhabdus nematophilus to colonize its  
 RT nematode host, Steinernema carpocapsae."  
 RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF198628; AAF20817.1; -.  
 FT NON\_TER 1  
 SO SEQUENCE 39 AA; 4465 MW; 910FCBEC87E9E4C CRC64;

Query Match 50.0%; Score 5; DB 2; Length 39;  
 Best Local Similarity 100.0%; Pred. No. 70;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 NITAR 7  
 DB 7 NITAR 11

RESULT 14  
 ID Q52235 PRELIMINARY; PRT; 68 AA.  
 AC Q52235;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE PLASMID PNB2 (FROM CLOSTRIDIUM THERMOSACCHAROLYTICUM) REPN (FROM  
 DE CLOSTRIDIUM THERMOSACCHAROLYTICUM).  
 OS Clostridium thermosaccharolyticum (Thermoanaerobacterium  
 OS thermosaccharolyticum).  
 GN Plasmid PNB2.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Thermoanaerobacter group; Thermoanaerobacterium.  
 OX NCBI\_Taxid=1517;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Belogurova N.G.; Delver E.P.; Kalyuzhnyi S.V.; Varfolomeyev S.D.;  
 RA Belogurov A.A.;  
 RL Nucleic Acids Res. 0:0-0(0).  
 DR EMBL; L38403; AAD12629.1; -.  
 KW Plasmid.  
 SO SEQUENCE 68 AA; 8115 MW; 36F4B9FDF9ED44FF CRC64;

Query Match 50.0%; Score 5; DB 2; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 11e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ITARI 8  
 DB 35 ITARI 39

RESULT 15  
 ID Q9NPY6 PRELIMINARY; PRT; 71 AA.  
 AC Q9NPY6;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE D6631M13.1 (SIMILAR TO MOUSE SEL1L (SEL-1 (SUPPRESSOR OF LIN-12,  
 DE C.ELEGANS)-LIKE.) (FRAGMENT).  
 GN D6631M13.1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Laird G.;  
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL117333; CAC01943.1; -.  
 FT NON\_TER 71  
 SO SEQUENCE 71 AA; 7756 MW; 3EF2C63469879DF4 CRC64;

Query Match 50.0%; Score 5; DB 4; Length 71;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;

|         |    |              |    |            |    |        |    |      |    |
|---------|----|--------------|----|------------|----|--------|----|------|----|
| Matches | 5; | Conservative | 0; | Mismatches | 0; | Indels | 0; | Gaps | 0; |
| QY      | 2  | QNTA         | 6  |            |    |        |    |      |    |
|         |    |              |    |            |    |        |    |      |    |
| Db      | 49 | QNTA         | 53 |            |    |        |    |      |    |

Search completed: April 24, 2002, 09:24:28  
Job time: 252 sec

---

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:17:37 ; Search time 66.28 Seconds  
(without alignments)  
11.176 Million cell updates/sec

Title: US-09-689-469-6  
Perfect score: 48  
Sequence: 1 AONTARIGE 10

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues  
Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A.Geneseq\_1101.\*  
1: /SID8/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID8/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID8/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID8/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID8/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SID8/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SID8/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SID8/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SID8/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SID8/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SID8/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SID8/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SID8/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SID8/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SID8/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SID8/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SID8/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SID8/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SID8/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID8/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID8/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID8/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 48    | 100.0       | 10     | 20    | AAV09353    |
| 2          | 48    | 100.0       | 10     | 21    | AAV52135    |
| 3          | 48    | 100.0       | 15     | 18    | AAW44208    |
| 4          | 48    | 100.0       | 15     | 18    | AAW33762    |
| 5          | 48    | 100.0       | 16     | 18    | AAW44214    |
| 6          | 48    | 100.0       | 16     | 18    | AAW33768    |
| 7          | 48    | 100.0       | 30     | 20    | AAV09349    |
| 8          | 48    | 100.0       | 30     | 21    | AAV52134    |
| 9          | 48    | 100.0       | 318    | 18    | AAW44200    |
| 10         | 48    | 100.0       | 318    | 18    | AAW33754    |
| 11         | 48    | 100.0       | 332    | 21    | AAV52130    |

|    |    |       |      |    |          |
|----|----|-------|------|----|----------|
| 12 | 48 | 100.0 | 340  | 18 | AAW44199 |
| 13 | 48 | 100.0 | 340  | 18 | AAW33753 |
| 14 | 48 | 100.0 | 404  | 22 | AAW81925 |
| 15 | 44 | 91.7  | 30   | 20 | AAV09350 |
| 16 | 44 | 91.7  | 30   | 20 | AAV09351 |
| 17 | 40 | 83.3  | 30   | 20 | AAV09352 |
| 18 | 33 | 68.8  | 30   | 18 | AAW23337 |
| 19 | 33 | 68.8  | 420  | 21 | AAV32428 |
| 20 | 32 | 66.7  | 269  | 16 | AAW66289 |
| 21 | 32 | 66.7  | 269  | 16 | AAW66293 |
| 22 | 32 | 66.7  | 269  | 18 | AAW40807 |
| 23 | 32 | 66.7  | 269  | 18 | AAW40808 |
| 24 | 32 | 66.7  | 269  | 20 | AAW25522 |
| 25 | 32 | 66.7  | 772  | 19 | AAW57632 |
| 26 | 32 | 66.7  | 1160 | 21 | AAV52036 |
| 27 | 32 | 66.7  | 1160 | 21 | AAV51665 |
| 28 | 32 | 66.7  | 1160 | 22 | AAV34615 |
| 29 | 31 | 64.6  | 594  | 20 | AAV45222 |
| 30 | 31 | 64.6  | 594  | 20 | AAV39992 |
| 31 | 31 | 64.6  | 594  | 20 | AAV95537 |
| 32 | 31 | 64.6  | 594  | 21 | AAV96761 |
| 33 | 31 | 64.6  | 594  | 21 | AAW03181 |
| 34 | 31 | 64.6  | 769  | 17 | AAW8428  |
| 35 | 31 | 64.6  | 945  | 20 | AAW69368 |
| 36 | 31 | 64.6  | 945  | 21 | AAV10145 |
| 37 | 31 | 64.6  | 3722 | 12 | AAW34806 |
| 38 | 30 | 62.5  | 79   | 22 | AAV75595 |
| 39 | 30 | 62.5  | 260  | 21 | AAV75595 |
| 40 | 30 | 62.5  | 272  | 22 | AAW79602 |
| 41 | 30 | 62.5  | 315  | 17 | AAW89323 |
| 42 | 30 | 62.5  | 315  | 17 | AAW89322 |
| 43 | 30 | 62.5  | 317  | 22 | AAW79601 |
| 44 | 30 | 62.5  | 328  | 20 | AAV74117 |
| 45 | 30 | 62.5  | 420  | 21 | AAW39434 |

## ALIGNMENTS

|  |   |
|--|---|
| RESULT 1   |   |
| AAV09353   | standard; peptide; 10 AA.               |
| AAV09353:  |   |
| 09-JUL-1999  | (first entry)                           |
| Human RAGE V-domain  | peptide SEQ ID NO:5.                    |
| RAGE, V-domain; receptor for advanced glycation endproduct;              |   |
| ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome; |   |
| senility; renal failure; hyperlipidaemic atherosclerosis; dementia;      |   |
| neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;       |   |
| multiple sclerosis; amyloidosis; autoimmune disease; inflammation;       |   |
| tumour; cancer; male impotence; wound healing; periodontal disease;      |   |
| neuropathy; retinopathy; nephropathy; neuronal degeneration.             |   |
| XX   |   |
| OS   | Homo sapiens.                           |
| XX   |   |
| PN   | W09918987-AI.                           |
| XX   |   |
| PD   | 22-APR-1999.                            |
| XX   |   |
| PF   | 09-OCT-1998; 98MO-US21346.              |
| XX   |   |
| PR   | 09-OCT-1997; 97US-0948131.              |
| XX   |   |
| PA   | (UYCO ) UNIV COLUMBIA NEW YORK.         |
| XX   |   |
| PI   | Lamster I, Schmidt AM, Stern D, Yan SD; |
| XX   |   |
| DR   | WPI; 1999-277439/23.                    |
| XX   |   |

Human soluble rece  
Human RAGE polypep  
Extracorporeal cir  
Mouse RAGE V-domai  
Rat RAGE V-domain  
Bovine RAGE V-doma  
N-terminal sequenc  
Plant retroelement  
M. smegmatis Inha.  
M. smegmatis Inha.  
M. smegmatis Inha  
M. smegmatis Inha  
VP4 protein of hum  
E. coli DP3A prote  
E. coli growth and  
Chlamydia pneumoni  
Stachybotrys chart  
Stachybotrys pheno  
Stachybotrys chart  
Stachybotrys chart  
Rat poly-immunoglo  
Chlamydia pneumoni  
Amino acid sequenc  
Cephalosporin anti  
Peptide #8843 enco  
Neisseria meningit  
Corynebacterium gl  
Rape leaf beta-ket  
Rape seed beta-ket  
Corynebacterium gl  
Human prostate tum  
Arabidopsis thalia

PT New peptides based on an advanced glycation end product receptor are  
 PT useful for treating Alzheimer's disease and Down's syndrome  
 XX  
 PS Claim 55; Page 85; 101pp; English.

CC The present invention describes novel isolated peptides (1) having an  
 CC amino acid sequence corresponding to an amino acid sequence of a  
 CC V-domain of a receptor for an advanced glycation end product (RAGE).  
 CC Also described are methods for: (1) inhibiting an amyloid-beta peptide  
 CC (ABP) interaction with a receptor for RAGE when the receptor is on the  
 CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)  
 CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting  
 CC extracellular assembly of an ABP into a fibril; (5) inhibiting  
 CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration  
 CC of a microglial cell into senile plaques; (7) inhibiting activation of a  
 CC microglial cell by an ABP; (8) treating a subject with a condition  
 CC associated with an interaction of an ABP with a receptor for RAGE on a  
 CC cell; (9) evaluating the ability of an agent to inhibit binding of an  
 CC ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)  
 CC inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting  
 CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction  
 CC with a receptor for RAGE when the receptor is on the surface of a cell;  
 CC and (13) treating a subject with a condition associated with an  
 CC interaction of an RAGE with a receptor for RAGE on a cell. The methods  
 CC can be used for treating conditions associated with an interaction of an  
 CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's  
 CC disease, senility, renal failure, hyperlipidaemic atherosclerosis,  
 CC neuronal cytotoxicity, Down's syndrome, dementia associated with head  
 CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,  
 CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,  
 CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy  
 CC or neuronal degeneration.

SQ Sequence 10 AA;

QY 1 AONTARIGE 10  
 |||||  
 Db 1 agnitarige 10

Query Match 100.0%; Score 48; DB 20; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0006;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2  
 AAY52135  
 ID AAY52135 standard; peptide; 10 AA.  
 XX  
 AC AAY52135;  
 XX  
 DT 28-JAN-2000 (first entry)  
 XX  
 DE Human Receptor to AGE (RAGE) amino acid sequence fragment #4.  
 XX  
 KW Soluble receptor for advanced glycation endproducts; RAGE; tumour;  
 KW invasion; metastasis; amphoterin; neuron; inhibit; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO954485-A1.  
 XX  
 PD 28-OCT-1999.  
 XX  
 PF 16-APR-1999; 99WO-US08427.  
 XX  
 PR 17-APR-1998; 98US-0062365.  
 XX  
 PA (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX  
 PI Schmidt AM, Stern D;  
 XX  
 DR WPI; 2000-013260/01.

XX  
 PT Inhibiting tumour invasion or spreading by administration of soluble  
 PT receptor for advanced glycation endproducts -  
 XX  
 PS Claim 30; Page 62; 88pp; English.

CC This is the amino acid sequence of a fragment of the human soluble  
 CC Receptor for Advanced Glycation Endproducts (RAGE). RAGE interacts with  
 CC a range of physiologically and pathophysiologically relevant ligands  
 CC when considering tumour invasion. In normal developing neurons RAGE  
 CC colocalises with amphoterin which is a matrix associated polypeptide.  
 CC The expression of both RAGE and amphoterin decreases after birth, but  
 CC both have increased expression in tumours. RAGE polypeptides  
 CC AAY52132-Y52135 are used in the invention in a method for inhibiting  
 CC tumour invasion and metastasis. The method involves inhibiting tumour  
 CC invasion and metastasis via administration of a therapeutically effective  
 CC amount of the pharmaceutical composition containing a RAGE polypeptide.  
 CC The invention also relates to a method for evaluating the ability of an  
 CC agent to inhibit tumour invasion in a local cellular environment. RAGE  
 CC can be administered to a patient in a pharmaceutically acceptable  
 CC carrier.

SQ Sequence 10 AA;

QY 1 AONTARIGE 10  
 |||||  
 Db 1 agnitarige 10

Query Match 100.0%; Score 48; DB 21; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0006;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3  
 AAM44208  
 ID AAM44208 standard; peptide; 15 AA.  
 XX  
 AC AAM44208;  
 XX  
 DT 14-MAY-1998 (first entry)  
 XX  
 DE Human soluble RAGE immunologically active fragment SEQ ID NO:12.  
 XX  
 KW Human; soluble receptor; advanced glycosylation end product; RAGE;  
 KW AGE; antibody; vascular permeability; immunologically active fragment;  
 KW diabetes mellitus.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9739125-A1.  
 XX  
 PD 23-OCT-1997.  
 XX  
 PF 11-APR-1997; 97WO-EP01834.  
 XX  
 PR 16-APR-1996; 96US-0633148.  
 XX  
 PA (SCHD ) SCHERING PATENTE AG.  
 XX  
 PI Hollander DA, Morser MJ, Nagashima M;  
 XX  
 DR WPI; 1997-558580/51.  
 XX  
 PF Anti-advanced glycosylation end product polypeptide antibody -  
 PT Prevents receptor binding and therefore reduces vascular  
 PT permeability, useful to treat diabetes mellitus  
 XX  
 PS Claim 2; Page 46; 90pp; English.

CC The present sequence represents an immunologically active fragment  
 CC of a soluble human receptor to an advanced glycosylation end  
 CC product (RAGE) polypeptide. The present invention describes



CC an isolated antibody (Ab), specifically immunoreactive with  
 CC RAGE. Advanced glycosylation end products (AGE) of proteins are  
 CC non-enzymatically glycosylated proteins, which accumulate in vascular  
 CC tissue in ageing, and at an accelerated rate in individuals with  
 CC diabetes. The Ab, which prevents the interaction between an AGE and its  
 CC receptor (RAGE), reduces vascular permeability. The Ab can be used to  
 CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive  
 CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis  
 CC associated amyloidosis or atherosclerosis. The Ab can also be used for  
 CC the isolation and purification of human RAGE polypeptide.

XX Sequence 15 AA;

SO Query Match 100.0%; Score 48; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.00095;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10  
 |||||  
 DB 1 agnitarige 10

RESULT 4  
 AAW33762

ID AAW33762 standard; peptide; 15 AA.

AC AAW33762;

DT 08-MAY-1998 (first entry)

DE Human RAGE polypeptide fragment 8.

XX Advanced glycosylation end-product receptor; RAGE; screening; AGE;  
 KM vascular permeability; diabetes mellitus; treatment; atherosclerosis;  
 KM Alzheimer's disease.

OS Homo sapiens.

PN WO9739121-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01832.

PR 16-APR-1996; 96US-0633147.

PA (SCHD ) SCHERING AG.

PI Morser MJ, Nagashima M;

DR WPI: 1997-526458/48.

PT New soluble advanced glycosylation end-product receptor polypeptide  
 PT - used for reducing vascular permeability, complications of diabetes  
 PT etc., also for purification and to screen for modulators  
 PS Claim 6; Page 55; 91pp; English.

CC This is a peptide fragment of a human advanced glycosylation end-product  
 CC receptor (RAGE) polypeptide. The RAGE polypeptides and its active  
 CC fragments or their mimetics can inhibit interaction between advanced  
 CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They  
 CC are used to treat diseases associated with AGE/RAGE interaction, such as  
 CC increased vascular permeability, diabetes mellitus (particularly  
 CC complications such as micro- or macro- vasculopathy or occlusive vascular  
 CC disorders such as neuropathy, nephropathy, atherosclerosis or  
 CC retinopathy) or haemodialysis-associated amyloidosis, also activation  
 CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or  
 CC age-related disorders such as oxidative stress. These RAGE polypeptides  
 CC are also used, when immobilised, to purify AGE from a protein mixture and  
 CC to screen for compounds that are agonists and antagonists of AGE/RAGE  
 CC interaction. They can also be used diagnostically to detect abnormal

CC levels of AGE. Antibodies against RAGE polypeptides are useful as  
 CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of  
 CC interaction between AGE and RAGE or other receptors and for purification  
 CC and quantification of RAGE polypeptides. The encoding nucleic acids are  
 CC used to express recombinant RAGE and as probes for isolating related  
 CC genes.

XX Sequence 15 AA;

SO Query Match 100.0%; Score 48; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.00095;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10  
 |||||  
 DB 1 agnitarige 10

RESULT 5  
 AAW4214

ID AAW4214 standard; peptide; 16 AA.

AC AAW4214;

DT 14-MAY-1998 (first entry)

DE Human soluble RAGE immunologically active fragment SEQ ID NO:18.

XX Human: soluble receptor; advanced glycosylation end product; RAGE;  
 KM AGE; antibody; vascular permeability; immunologically active fragment;  
 KM diabetes mellitus.

OS Homo sapiens.

PN WO9739125-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01834.

PR 16-APR-1996; 96US-0633148.

PA (SCHD ) SCHERING PATENTE AG.

PI Hollander DA, Morser MJ, Nagashima M;

DR WPI: 1997-558580/51.

PT Anti-advanced glycosylation end product polypeptide antibody -  
 PT prevents receptor binding and therefore reduces vascular  
 PT permeability, useful to treat diabetes mellitus  
 PS Claim 2; Page 49; 90pp; English.

CC The present sequence represents an immunologically active fragment  
 CC of a soluble human receptor to an advanced glycosylation end  
 CC product (RAGE) polypeptide. The present invention describes  
 CC an isolated antibody (Ab), specifically immunoreactive with  
 CC RAGE. Advanced glycosylation end products (AGE) of proteins are  
 CC non-enzymatically glycosylated proteins, which accumulate in vascular  
 CC tissue in ageing, and at an accelerated rate in individuals with  
 CC diabetes. The Ab, which prevents the interaction between an AGE and its  
 CC receptor (RAGE), reduces vascular permeability. The Ab can be used to  
 CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive  
 CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis  
 CC associated amyloidosis or atherosclerosis. The Ab can also be used for  
 CC the isolation and purification of human RAGE polypeptide.

XX Sequence 16 AA;

SO Query Match 100.0%; Score 48; DB 18; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.001;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10  
| | | | | | | |  
Db 1 agntarige 10

RESULT 6  
AAW33768

ID AAW33768 standard; peptide; 16 AA.

AC AAW33768;

DE 08-MAY-1998 (first entry)

DE Human RAGE polypeptide fragment 14.

KW Advanced glycosylation end-product receptor; RAGE; screening; AGE;  
KW vascular permeability; diabetes mellitus; treatment; atherosclerosis;  
KW Alzheimer's disease.

OS Homo sapiens.

PN WO9739121-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01832.

PR 16-APR-1996; 96US-0633147.

PA (SCHD ) SCHERING AG.

PI Morser MJ, Nagashima M;

DR WPI; 1997-526458/48.

PT New soluble advanced glycosylation end-product receptor polypeptide  
PT - used for reducing vascular permeability; complications of diabetes  
PT etc., also for purification and to screen for modulators

PS Disclosure; Page 9, 91pp; English.

CC This is a peptide fragment of a human advanced glycosylation end-product  
CC receptor (RAGE) polypeptide. The RAGE polypeptides and its active  
CC fragments or their mimetics can inhibit interaction between advanced  
CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They  
CC are used to treat diseases associated with AGE/RAGE interaction, such as  
CC increased vascular permeability, diabetes mellitus (particularly  
CC complications such as micro- or macro- vasculopathy or occlusive vascular  
CC retinopathy) or haemodialysis-associated amyloidosis, also activation  
CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or  
CC age-related disorders such as oxidative stress. These RAGE polypeptides  
CC are also used, when immobilised, to purify AGE from a protein mixture and  
CC to screen for compounds that are agonists and antagonists of AGE/RAGE  
CC interaction. They can also be used diagnostically to detect abnormal  
CC levels of AGE. Antibodies against RAGE polypeptides are useful as  
CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of  
CC interaction between AGE and RAGE or other receptors and for purification  
CC and quantification of RAGE polypeptides. The encoding nucleic acids are  
CC used to express recombinant RAGE and as probes for isolating related  
CC genes.

SO Sequence 16 AA;

Query Match 100.0%; Score 48; DB 18; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.001;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10

Db 1 agntarige 10  
| | | | | | | |

RESULT 7

ID AAY09349 standard; peptide; 30 AA.

AC AAY09349;

DT 09-JUL-1999 (first entry)

DE Human RAGE V-domain peptide SEQ ID NO:1.

KW RAGE; V-domain; receptor for advanced glycation endproduct;  
KW ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;  
KW senility; renal failure; hyperlipidaemic atherosclerosis; dementia;  
KW neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;  
KW multiple sclerosis; amyloidosis; autoimmune disease; inflammation;  
KW tumour; cancer; male impotence; wound healing; periodontal disease;  
KW neuropathy; retinopathy; nephropathy; neuronal degeneration.

OS Homo sapiens.

PN WO9918987-A1.

PD 22-APR-1999.

PF 09-OCT-1998; 98WO-US21346.

PR 09-OCT-1997; 97US-0948131.

PA (UYCO ) UNIV COLUMBIA NEW YORK.

PI Lamster I, Schmidt AM, Stern D, Yan SD;

DR WPI; 1999-277439/23.

PT New peptides based on an advanced glycation end product receptor are  
PT useful for treating Alzheimer's disease and Down's syndrome

PS Claim 2; Page 78; 101pp; English.

CC The present invention describes novel isolated peptides (1) having an  
CC amino acid sequence corresponding to an amino acid sequence of a  
CC V-domain of a receptor for an advanced glycation end product (RAGE).  
CC Also described are methods for: (1) inhibiting an amyloid-beta peptide  
CC (ABP) interaction with a receptor for RAGE when the receptor is on the  
CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)  
CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting  
CC extracellular assembly of an ABP into a fibril; (5) inhibiting  
CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration  
CC of a microglial cell into senile plaques; (7) inhibiting activation of a  
CC microglial cell by an ABP; (8) treating a subject with a condition  
CC associated with an interaction of an ABP with a receptor for RAGE on a  
CC cell; (9) evaluating the ability of an agent to inhibit binding of an  
CC ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)  
CC inhibiting activation of a NP-kappaB gene in a cell; (11) inhibiting  
CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction  
CC with a receptor for RAGE when the receptor is on the surface of a cell;  
CC and (13) treating a subject with a condition associated with an  
CC interaction of an RAGE with a receptor for RAGE on a cell. The methods  
CC can be used for treating conditions associated with an interaction of an  
CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's  
CC disease, senility, renal failure, hyperlipidaemic atherosclerosis,  
CC neuronal cytotoxicity, Down's syndrome, dementia associated with head  
CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,  
CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,  
CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy  
CC or neuronal degeneration.

SO Sequence 30 AA;

Query Match 100.0%; Score 48; DB 20; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 0.0021;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10  
 |||||  
 DB 1 agntarige 10

## RESULT 8

AAV52134  
 ID AAY52134 standard; protein; 30 AA.

AC AAY52134;

DT 28-JAN-2000 (first entry)

DE Human Receptor to AGE (RAGE) amino acid sequence fragment #3.

KW Soluble receptor for advanced glycation endproducts; RAGE; tumour;  
 invasion; metastasis; amphoterin; neuron; inhibit; therapy.

OS Homo sapiens.

PN WO954485-A1.

PD 28-OCT-1999.

PF 16-APR-1999; 99WO-US08427.

PR 17-APR-1998; 98US-0062365.

PA (UYCO ) UNIV COLUMBIA NEW YORK.

PI Schmidt AM, Stern D;

DR WPI; 2000-013260/01.

PT Inhibiting tumour invasion or spreading by administration of soluble  
 PT receptor for advanced glycation endproducts -

PS Claim 29; Page 62; 88pp; English.

CC This is the amino acid sequence of a fragment of the human soluble  
 CC Receptor for Advanced Glycation Endproducts (RAGE). RAGE interacts with  
 CC a range of physiologically and pathophysiologically relevant ligands  
 CC when considering tumour invasion. In normal developing neurons RAGE  
 CC localizes with amphoterin which is a matrix associated polypeptide.  
 CC The expression of both RAGE and amphoterin decreases after birth, but  
 CC both have increased expression in tumours. RAGE polypeptides  
 CC AAY52133-Y52135 are used in the invention in a method for inhibiting  
 CC tumour invasion and metastasis. The method involves inhibiting tumour  
 CC invasion and metastasis via administration of a therapeutically effective  
 CC amount of the pharmaceutical composition containing a RAGE polypeptide.  
 CC The invention also relates to a method for evaluating the ability of an  
 CC agent to inhibit tumour invasion in a local cellular environment. RAGE  
 CC can be administered to a patient in a pharmaceutically acceptable  
 CC carrier.

SQ Sequence 30 AA;

Query Match 100.0%; Score 48; DB 21; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.0021;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10  
 |||||  
 DB 1 agntarige 10

## RESULT 9

AAW44200  
 ID AAW44200 standard; protein; 318 AA.

AC AAW44200;

DT 14-MAY-1998 (first entry)

DE Human mature receptor to an advanced glycosylation end product.

KW Human; soluble receptor; advanced glycosylation end product; RAGE;  
 KW AGE; antibody; vascular permeability; diabetes mellitus.

OS Homo sapiens.

FT Key location/Qualifiers

FT Misc-difference 66 /note="encoded by CCR"

PN WO9739125-A1.

PD 23-OCT-1997.

PF 11-APR-1997; 97WO-EP01834.

PR 16-APR-1996; 96US-0633148.

PA (SCHD ) SCHERING PATENTE AG.

PI Hollander DA, Morser MJ, Nagashima M;

DR WPI; 1997-558580/51.

PR N-PDB; AAV12395.

PT Anti-advanced glycosylation end product polypeptide antibody -  
 PT prevents receptor binding and therefore reduces vascular  
 permeability, useful to treat diabetes mellitus

PS Claim 2; Page 42-43; 90pp; English.

CC The present sequence represents a mature human receptor to an advanced  
 CC glycosylation end product (RAGE) polypeptide. The present invention  
 CC describes an isolated antibody (Ab), specifically immunoreactive with  
 CC RAGE. Advanced glycosylation end products (AGE) of proteins are  
 CC non-enzymatically glycosylated proteins, which accumulate in vascular  
 CC tissue in ageing, and at an accelerated rate in individuals with  
 CC diabetes. The Ab, which prevents the interaction between an AGE and it's  
 CC receptor (RAGE), reduces vascular permeability. The Ab can be used to  
 CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive  
 CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis  
 CC associated amyloidosis or atherosclerosis. The Ab can also be used for  
 CC the isolation and purification of human RAGE polypeptide.

SQ Sequence 318 AA;

Query Match 100.0%; Score 48; DB 18; Length 318;

Best Local Similarity 100.0%; Pred. No. 0.03;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10  
 |||||  
 DB 1 agntarige 10

## RESULT 10

AAW33754  
 ID AAW33754 standard; protein; 318 AA.

AC AAW33754;

DT 08-MAY-1998 (first entry)

DE Human RAGE polypeptide (318 amino acid residues).

XX Advanced glycosylation end-product receptor; RAGE; screening; AGE;  
 KM vascular permeability; diabetes mellitus; treatment; atherosclerosis;  
 KW Alzheimer's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9739121-A1.  
 XX  
 PD 23-OCT-1997.  
 XX  
 PF 11-APR-1997; 97WO-EP01832.  
 XX  
 PR 16-APR-1996; 96US-0633147.  
 XX  
 PA (SCHD ) SCHERING AG.  
 XX  
 PI Morser MJ, Nagashima M;  
 XX  
 DR WPI: 1997-526458/48.  
 XX  
 DR N-PSDB: AAV06518.  
 XX  
 PT New soluble advanced glycosylation end-product receptor polypeptide  
 PT - used for reducing vascular permeability, complications of diabetes  
 PT etc., also for purification and to screen for modulators  
 XX  
 PS Claim 3; Fig 1B; 91pp; English.  
 XX  
 CC This is a human advanced glycosylation end-product receptor (RAGE)  
 CC polypeptide (318 amino acid residues). The RAGE polypeptides and its  
 CC active fragments or their mimetics, inhibit interaction between advanced  
 CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They  
 CC are used to treat diseases associated with AGE/RAGE interaction, such as  
 CC increased vascular permeability, diabetes mellitus (particularly  
 CC complications such as micro- or macro- vasculopathy or occlusive vascular  
 CC disorders such as neuropathy, nephropathy, retinopathy or  
 CC atherosclerosis) or haemodialysis-associated amyloidosis, also activation  
 CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or  
 CC age-related disorders such as oxidative stress. These RAGE polypeptides  
 CC are also used, when immobilised, to purify AGE from a protein mixture and  
 CC to screen for compounds that are agonists and antagonists of AGE/RAGE  
 CC interaction. They can also be used diagnostically to detect abnormal  
 CC levels of AGE. Antibodies against RAGE polypeptides are useful as  
 CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of  
 CC interaction between AGE and RAGE or other receptors and for purification  
 CC and quantification of RAGE polypeptides. The encoding nucleic acids are  
 CC used to express recombinant RAGE and as probes for isolating related  
 CC genes.  
 XX  
 SQ Sequence 318 AA:  
 XX  
 QY Query Match 100.0%; Score 48; DB 18; Length 318;  
 Best Local Similarity 100.0%; Pred. No. 0.03;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 DB 1 AONTARIGE 10  
 |||||||||  
 1 agnitarige 10  
 XX  
 RESULT 11  
 ID AAY52130 standard; protein; 332 AA.  
 XX  
 AC AAY52130;  
 XX  
 DT 28-JAN-2000 (first entry)  
 XX  
 DE Human Receptor to AGE (RAGE) amino acid sequence.  
 XX  
 KW Soluble receptor for advanced glycation endproducts; RAGE; tumour;  
 KW invasion; metastasis; amphoterin; neuron; inhibit; therapy.  
 XX

XX Homo sapiens.  
 OS  
 XX  
 PN WO9544485-A1.  
 XX  
 PD 28-OCT-1999.  
 XX  
 PF 16-APR-1999; 99WO-US08427.  
 XX  
 PR 17-APR-1998; 98US-0062365.  
 XX  
 PA (UYCO ) UNIV COLUMBIA NEW YORK.  
 XX  
 PI Schmidt AM, Stern D;  
 XX  
 DR WPI: 2000-013260/01.  
 XX  
 PT Inhibiting tumour invasion or spreading by administration of soluble  
 PT receptor for advanced glycation endproducts -  
 XX  
 PS Disclosure: Page 10-11; 88pp; English.  
 XX  
 CC This is the amino acid sequence of the human soluble Receptor for  
 CC Advanced Glycation Endproducts (RAGE). RAGE interacts with a range of  
 CC physiologically and pathophysiologically relevant ligands when  
 CC considering tumour invasion. In normal developing neurons RAGE  
 CC colocalizes with amphoterin which is a matrix associated polypeptide.  
 CC The expression of both RAGE and amphoterin decreases after birth, but  
 CC both have increased expression in tumours. RAGE polypeptides  
 CC AAY5132-Y52135 are used in the invention in a method for inhibiting  
 CC tumour invasion and metastasis. The method involves inhibiting tumour  
 CC invasion and metastasis via administration of a therapeutically effective  
 CC amount of the pharmaceutical composition containing a RAGE polypeptide.  
 CC The invention also relates to a method for evaluating the ability of an  
 CC agent to inhibit tumour invasion in a local cellular environment. RAGE  
 CC can be administered to a patient in a pharmaceutically acceptable  
 CC carrier.  
 XX  
 SQ Sequence 332 AA:  
 XX  
 QY Query Match 100.0%; Score 48; DB 21; Length 332;  
 Best Local Similarity 100.0%; Pred. No. 0.031;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 DB 1 AONTARIGE 10  
 |||||||||  
 1 agnitarige 10  
 XX  
 RESULT 12  
 ID AAM44199 standard; Protein; 340 AA.  
 XX  
 AC AAM44199;  
 XX  
 DT 14-MAY-1998 (first entry)  
 XX  
 DE Human soluble receptor to an advanced glycosylation end product.  
 XX  
 KW Human; soluble receptor; advanced glycosylation end product; RAGE;  
 KW AGE; antibody; vascular permeability; diabetes mellitus.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9739125-A1.  
 XX  
 PD 23-OCT-1997.  
 XX  
 PF 11-APR-1997; 97WO-EP01834.  
 XX  
 PR 16-APR-1996; 96US-0633148.  
 XX

PA (SCHD ) SCHERING PATENTE AG.  
 XX  
 PI Hollander DA, Morser MJ, Nagashima M;  
 XX WPI: 1997-558580/51.  
 DR N-PSDB: AAV12394.  
 XX  
 XX Anti-advanced glycosylation end product polypeptide antibody -  
 PT prevents receptor binding and therefore reduces vascular  
 PT permeability, useful to treat diabetes mellitus  
 XX  
 PS Claim 2; Page 40-41; 90pp; English.  
 XX  
 CC The present sequence represents a soluble human receptor to an advanced  
 CC glycosylation end product (RAGE) polypeptide. The present invention  
 CC describes an isolated antibody (Ab), specifically immunoreactive with  
 CC RAGE. Advanced glycosylation end products (AGE) of proteins are  
 CC non-enzymatically glycosylated proteins, which accumulate in vascular  
 CC tissue in ageing, and at an accelerated rate in individuals with  
 CC diabetes. The Ab, which prevents the interaction between an AGE and its  
 CC receptor (RAGE), reduces vascular permeability. The Ab can be used to  
 CC treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive  
 CC vascular disorders, neuropathy, nephropathy, retinopathy, haemodialysis  
 CC associated amyloidosis or atherosclerosis. The Ab can also be used for  
 CC the isolation and purification of human RAGE polypeptide.  
 CC  
 SQ Sequence 340 AA:

Query Match 100.0%; Score 48; DB 18; Length 340;  
 Best Local Similarity 100.0%; Pred. No. 0.032;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTTARIGE 10  
 |||||||||  
 DB 23 agnitarige 32

## RESULT 13

AAM33753  
 ID AAM33753 standard; Protein; 340 AA.

AC AAW33753;  
 XX

DT 08-MAY-1998 (first entry)  
 XX

DE Human RAGE polypeptide (340 amino acid residues).  
 XX

KW Advanced glycosylation end-product receptor; RAGE; screening; AGE;  
 KM vascular permeability; diabetes mellitus; treatment; atherosclerosis;  
 KW Alzheimer's disease.  
 XX

OS Homo sapiens.  
 XX

PN WO9739121-A1.  
 XX

PD 23-OCT-1997.  
 XX

PF 11-APR-1997; 97WO-EP01832.  
 XX

PR 16-APR-1996; 96US-0633147.  
 XX

PA (SCHD ) SCHERING AG.  
 XX

PI Morser MJ, Nagashima M;  
 XX

DR WPI: 1997-526458/48.  
 XX

DR N-PSDB: AAV06517.  
 XX

PT New soluble advanced glycosylation end-product receptor polypeptide  
 PT - used for reducing vascular permeability, complications of diabetes  
 PT etc., also for purification and to screen for modulators  
 XX

PS Claim 3; Fig 1A; 91pp; English.  
 XX

CC This is a human advanced glycosylation end-product receptor (RAGE)  
 CC polypeptide (340 amino acid residues). The RAGE polypeptides and its  
 CC active fragments or their mimetics, inhibit interaction between advanced  
 CC glycosylation end-products (AGE) and a receptor (specifically RAGE). They  
 CC are used to treat diseases associated with AGE/RAGE interaction, such as  
 CC increased vascular permeability, diabetes mellitus (particularly  
 CC complications such as micro- or macro-vasculopathy or occlusive vascular  
 CC disorders such as neuropathy, nephropathy, retinopathy or  
 CC atherosclerosis) or haemodialysis-associated amyloidosis, also activation  
 CC of microglial cells by beta-amyloid peptides in Alzheimer's disease or  
 CC age-related disorders such as oxidative stress. These RAGE polypeptides  
 CC are also used, when immobilised, to purify AGE from a protein mixture and  
 CC to screen for compounds that are agonists and antagonists of AGE/RAGE  
 CC interaction. They can also be used diagnostically to detect abnormal  
 CC levels of AGE. Antibodies against RAGE polypeptides are useful as  
 CC immunoassay reagents for measurement of RAGE levels, and as inhibitors of  
 CC interaction between AGE and RAGE or other receptors and for purification  
 CC and quantification of RAGE polypeptides. The encoding nucleic acids are  
 CC used to express recombinant RAGE and as probes for isolating related  
 CC genes.  
 CC  
 SQ Sequence 340 AA:

Query Match 100.0%; Score 48; DB 18; Length 340;  
 Best Local Similarity 100.0%; Pred. No. 0.032;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTTARIGE 10  
 |||||||||  
 DB 23 agnitarige 32

## RESULT 14

AAB81925  
 ID AAB81925 standard; protein; 404 AA.

AC AAB81925;  
 XX

DT 15-JUN-2001 (first entry)  
 XX

DE Extracorporeal circulation material receptor protein.  
 XX

KW Extracorporeal circulation; carbonyl stress product; receptor;  
 KM diabetes; vascular lesion; excretory dysfunction.  
 XX

OS Unidentified.  
 XX

PN WO200118060-A1.  
 XX

PD 15-MAR-2001.  
 XX

PF 08-SEP-2000; 2000WO-JP06172.  
 XX

PR 08-SEP-1999; 99JP-0254463.  
 XX

PA (TORA ) TORAY IND INC.  
 XX

PI Shimizu S, Kubota M, Akiyama H, Usui M;  
 XX

DR WPI: 2001-290314/30.  
 XX

PT Material for extracorporeal circulation, applicable in selective  
 PT elimination of diabetic complication factors such as carbonyl stress  
 PT products caused by abnormally promoted carbonyl stress from excretory  
 PT dysfunction in vascular lesions  
 XX

PS Claim 1; Page 31-32; 36pp; Japanese.  
 XX

CC The present invention describes a material for extracorporeal circulation  
 CC which is made from a water-insoluble carrier immobilized with a protein

CC having the sequence shown here. The materials of the invention, including  
 CC adsorbents, are for extracorporeal circulation, which are applicable in  
 CC the selective elimination of diabetic complication factors from a body  
 CC fluid, and are therefore useful in treating vascular lesions like  
 CC arteriosclerosis due to carbonyl stress products caused by abnormally  
 CC promoted carbonyl stress from excretory dysfunction.

SO Sequence 404 AA;

Query Match 100.0%; Score 48; DB 22; Length 404;  
 Best Local Similarity 100.0%; Pred. No. 0.039;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTTARIGE 10  
 Db 23 agnttarige 32

RESULT 15

AA09350  
 ID AAY09350 standard; peptide; 30 AA.

XX AAY09350;

XX 09-JUL-1999 (first entry)

DE Mouse RAGE V-domain peptide SEQ ID NO:2.

XX RAGE; V-domain; receptor for advanced glycation endproduct;  
 KW ligand binding site; amyloid-beta; Alzheimer's disease; Down's syndrome;  
 KW senility; renal failure; hyperlipidaemic atherosclerosis; dementia;  
 KW neuronal cytotoxicity; head trauma; amyotrophic lateral sclerosis;  
 KW multiple sclerosis; amyloidosis; autoimmune disease; inflammation;  
 KW tumour; cancer; male impotence; wound healing; periodontal disease;  
 KW neuropathy; retinopathy; nephropathy; neuronal degeneration.

XX Mus sp.

PN W0918987-A1.

XX 22-APR-1999.

XX 09-OCT-1998; 98WO-US21346.

XX 09-OCT-1997; 97US-0948131.

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX Lamster I, Schmidt AM, Stern D, Yan SD;

XX MPI; 1999-277439/23.

PT New peptides based on an advanced glycation end product receptor are  
 useful for treating Alzheimer's disease and Down's syndrome

PS Claim 3: Page 78; 101pp; English.

XX The present invention describes novel isolated peptides (1) having an  
 CC amino acid sequence corresponding to an amino acid sequence of a  
 CC V-domain of a receptor for an advanced glycation end product (RAGE).  
 CC Also described are methods for: (1) inhibiting an amyloid-beta peptide  
 CC (ABP) interaction with a receptor for RAGE when the receptor is on the  
 CC surface of a cell; (2) inhibiting degeneration of a neuronal cell; (3)  
 CC inhibiting formation of an ABP fibril on a cell; (4) inhibiting  
 CC extracellular assembly of an ABP into a fibril; (5) inhibiting  
 CC aggregation of ABP on the surface of a cell; (6) inhibiting infiltration  
 CC of a microglial cell into senile plaques; (7) inhibiting activation of a  
 CC microglial cell by an ABP; (8) treating a subject with a condition  
 CC associated with an interaction of an ABP with a receptor for RAGE on a  
 CC cell; (9) evaluating the ability of an agent to inhibit binding of an  
 CC ABP with a V-domain of a receptor for RAGE on the surface of a cell; (10)  
 CC inhibiting activation of a NF-kappaB gene in a cell; (11) inhibiting

CC periodontal disease in a subject; (12) inhibiting an RAGE's interaction  
 CC with a receptor for RAGE when the receptor is on the surface of a cell;  
 CC and (13) treating a subject with a condition associated with an  
 CC interaction of an RAGE with a receptor for RAGE on a cell. The methods  
 CC can be used for treating conditions associated with an interaction of an  
 CC ABP or an RAGE with a receptor for RAGE, e.g. diabetes, Alzheimer's  
 CC disease, senility, renal failure, hyperlipidaemic atherosclerosis,  
 CC neuronal cytotoxicity, Down's syndrome, dementia associated with head  
 CC trauma, amyotrophic lateral sclerosis, multiple sclerosis, amyloidosis,  
 CC an autoimmune disease, inflammation, a tumour, cancer, male impotence,  
 CC wound healing, periodontal disease, neuropathy, retinopathy, nephropathy  
 CC or neuronal degeneration.

SO Sequence 30 AA;

Query Match 91.7%; Score 44; DB 20; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 0.015;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ONITFARIGE 10  
 Db 2 qnltarige 10

Search completed: April 24, 2002, 09:17:37  
 Job time: 141 sec



**THIS PAGE BLANK (USPTO)**



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:18:16 ; Search time 32.34 Seconds  
(without alignments)  
6.958 Million cell updates/sec

Title: US-09-689-469-6  
Perfect score: 48  
Sequence: 1 AONTARIGE 10

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents.AA:\*  
1: /cgn2\_6/prodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/PCUTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description                         |
|------------|-------|-------------|--------|-------|-------------------------------------|
| 1          | 48    | 100.0       | 15     | 2     | US-08-633-148-12 Sequence 12, Appl  |
| 2          | 48    | 100.0       | 16     | 2     | US-08-633-148-18 Sequence 18, Appl  |
| 3          | 48    | 100.0       | 318    | 2     | US-08-633-148-4 Sequence 4, Appl    |
| 4          | 48    | 100.0       | 340    | 2     | US-08-633-148-2 Sequence 2, Appl    |
| 5          | 32    | 66.7        | 269    | 1     | US-08-241-766-6 Sequence 6, Appl    |
| 6          | 32    | 66.7        | 269    | 1     | US-08-241-766-7 Sequence 7, Appl    |
| 7          | 32    | 66.7        | 772    | 1     | US-08-802-141-4 Sequence 4, Appl    |
| 8          | 31    | 64.6        | 769    | 3     | US-08-434-000A-10 Sequence 10, Appl |
| 9          | 31    | 64.6        | 769    | 3     | US-09-312-157-10 Sequence 10, Appl  |
| 10         | 30    | 62.5        | 315    | 3     | US-08-793-035-9 Sequence 9, Appl    |
| 11         | 30    | 62.5        | 315    | 3     | US-08-793-035-10 Sequence 10, Appl  |
| 12         | 30    | 62.5        | 579    | 3     | US-08-704-711A-1 Sequence 1, Appl   |
| 13         | 30    | 62.5        | 582    | 3     | US-08-704-711A-2 Sequence 2, Appl   |
| 14         | 30    | 62.5        | 582    | 4     | US-08-448-489-1 Sequence 1, Appl    |
| 15         | 30    | 62.5        | 582    | 4     | US-09-211-704A-9 Sequence 9, Appl   |
| 16         | 29    | 60.4        | 198    | 1     | US-08-278-091-16 Sequence 16, Appl  |
| 17         | 29    | 60.4        | 198    | 1     | US-08-483-859-16 Sequence 16, Appl  |
| 18         | 29    | 60.4        | 198    | 1     | US-08-472-173-16 Sequence 16, Appl  |
| 19         | 29    | 60.4        | 198    | 2     | US-08-487-167-16 Sequence 16, Appl  |
| 20         | 29    | 60.4        | 198    | 2     | US-08-482-816-16 Sequence 16, Appl  |
| 21         | 29    | 60.4        | 198    | 2     | US-08-296-149-16 Sequence 16, Appl  |
| 22         | 29    | 60.4        | 198    | 2     | US-08-801-499-16 Sequence 16, Appl  |
| 23         | 29    | 60.4        | 198    | 2     | US-08-615-271-16 Sequence 16, Appl  |
| 24         | 29    | 60.4        | 198    | 3     | US-09-074-660-16 Sequence 16, Appl  |
| 25         | 29    | 60.4        | 198    | 3     | US-09-074-659-16 Sequence 16, Appl  |
| 26         | 29    | 60.4        | 198    | 3     | US-09-106-468-16 Sequence 16, Appl  |
| 27         | 29    | 60.4        | 198    | 4     | US-09-106-466A-16 Sequence 16, Appl |

|    |    |      |     |   |                                    |
|----|----|------|-----|---|------------------------------------|
| 28 | 29 | 60.4 | 198 | 4 | US-09-106-467-16 Sequence 16, Appl |
| 29 | 29 | 60.4 | 394 | 3 | US-08-673-814-6 Sequence 6, Appl   |
| 30 | 29 | 60.4 | 439 | 3 | US-08-993-359-24 Sequence 24, Appl |
| 31 | 29 | 60.4 | 439 | 3 | US-09-321-654-2 Sequence 2, Appl   |
| 32 | 29 | 60.4 | 439 | 3 | US-08-989-358A-2 Sequence 2, Appl  |
| 33 | 29 | 60.4 | 585 | 2 | US-08-867-941-21 Sequence 21, Appl |
| 34 | 29 | 60.4 | 585 | 2 | US-08-867-941-21 Sequence 21, Appl |
| 35 | 29 | 60.4 | 741 | 1 | US-08-277-231A-4 Sequence 4, Appl  |
| 36 | 29 | 60.4 | 741 | 2 | US-08-473-750-7 Sequence 7, Appl   |
| 37 | 29 | 60.4 | 741 | 2 | US-08-477-326-7 Sequence 7, Appl   |
| 38 | 29 | 60.4 | 753 | 2 | US-08-867-941-20 Sequence 20, Appl |
| 39 | 29 | 60.4 | 753 | 4 | US-09-074-658-20 Sequence 20, Appl |
| 40 | 29 | 60.4 | 757 | 3 | US-08-434-000A-6 Sequence 6, Appl  |
| 41 | 29 | 60.4 | 757 | 3 | US-09-312-157-6 Sequence 6, Appl   |
| 42 | 29 | 60.4 | 771 | 3 | US-08-434-000A-8 Sequence 8, Appl  |
| 43 | 29 | 60.4 | 771 | 4 | US-09-312-157-8 Sequence 8, Appl   |
| 44 | 29 | 60.4 | 985 | 2 | US-08-867-941-13 Sequence 13, Appl |
| 45 | 29 | 60.4 | 985 | 2 | US-08-867-941-17 Sequence 17, Appl |

#### ALIGNMENTS

RESULT 1  
US-08-633-148-12  
; Sequence 12, Application US/08633148  
; Patent No. 5864018  
; GENERAL INFORMATION:  
; APPLICANT: MORSE, MICHAEL J.  
; APPLICANT: NAGASHIMA, MARIKO  
; APPLICANT: HOLLANDER, DORIS A.  
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION  
; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP  
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: U.S.A.  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/633,148  
; FILING DATE: 16-APR-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MORPHY ESO, MATTHEW B.  
; REGISTRATION NUMBER: 39,787  
; REFERENCE/DOCKET NUMBER: 014618-005600US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-633-148-12

Query Match 100.0%; Score 48; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.0003;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AONTARIGE 10  
|||||||

Db 1 AONITARIGE 10

## RESULT 2

US-08-633-148-18

Sequence 18, Application US/08633148

Patent No. 5864018

## GENERAL INFORMATION:

APPLICANT: MORSER, MICHAEL J.

APPLICANT: NAGASHIMA, MARIKO

APPLICANT: HOLLANDER, DORIS A.

TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION

TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND &amp; TOWNSENT &amp; CREW LLP

STREET: TWO EMBARCADERO CENTER, 8TH FLOOR

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: U.S.A.

ZIP: 94111

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/633,148

FILING DATE: 16-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURPHY ESQ., MATTHEW B.

REGISTRATION NUMBER: 39,787

REFERENCE/DOCKET NUMBER: 014618-005600US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-633-148-18

Query Match 100.0%; Score 48; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00033;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 1 AONITARIGE 10

Db 1 AONITARIGE 10

RESULT 3  
US-08-633-148-4

Sequence 4, Application US/08633148

Patent No. 5864018

## GENERAL INFORMATION:

APPLICANT: MORSER, MICHAEL J.

APPLICANT: NAGASHIMA, MARIKO

APPLICANT: HOLLANDER, DORIS A.

TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION

TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND &amp; TOWNSENT &amp; CREW LLP

STREET: TWO EMBARCADERO CENTER, 8TH FLOOR

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: U.S.A.

ZIP: 94111

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/633,148

FILING DATE: 16-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURPHY ESQ., MATTHEW B.

REGISTRATION NUMBER: 39,787

REFERENCE/DOCKET NUMBER: 014618-005600US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 318 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-633-148-4

Query Match 100.0%; Score 48; DB 2; Length 318;  
Best Local Similarity 100.0%; Pred. No. 0.0097;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 1 AONITARIGE 10

Db 1 AONITARIGE 10

RESULT 4  
US-08-633-148-2

Sequence 2, Application US/08633148

Patent No. 5864018

## GENERAL INFORMATION:

APPLICANT: MORSER, MICHAEL J.

APPLICANT: NAGASHIMA, MARIKO

APPLICANT: HOLLANDER, DORIS A.

TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION

TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND &amp; TOWNSENT &amp; CREW LLP

STREET: TWO EMBARCADERO CENTER, 8TH FLOOR

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: U.S.A.

ZIP: 94111

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/633,148

FILING DATE: 16-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURPHY ESQ., MATTHEW B.

REGISTRATION NUMBER: 39,787

REFERENCE/DOCKET NUMBER: 014618-005600US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 340 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-633-148-2

Query Match 100.0%; Score 48; DB 2; Length 340;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AONTARIGE 10  
DB 23 AONTARIGE 32

RESULT 5  
US-08-241-766-6  
Sequence 6, Application US/08241766  
Patent No. 5686590  
GENERAL INFORMATION:  
APPLICANT: JACOBS, W. R.  
APPLICANT: COLLINS, D. M.  
APPLICANT: BANERJEE, A.  
APPLICANT: DELISLE, G. W.  
APPLICANT: WILSON, T. M.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING  
TITLE OF INVENTION: AND TREATING MYCOBACTERIAL INFECTIONS USING AN INHA AGENT  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/241.766  
FILING DATE: 12-MAY-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: MONROY, GLADYS H.  
REGISTRATION NUMBER: 32,430  
REFERENCE/DOCKET NUMBER: 25237-20003.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 269 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-241-766-6

Query Match 66.7%; Score 32; DB 1; Length 269;  
Best Local Similarity 70.0%; Pred. No. 22;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AONTARIGE 10  
DB 75 ADRITAEIGE 84

RESULT 6  
US-08-241-766-7

Sequence 7, Application US/08241766  
Patent No. 5686590  
GENERAL INFORMATION:  
APPLICANT: JACOBS, W. R.  
APPLICANT: COLLINS, D. M.  
APPLICANT: BANERJEE, A.  
APPLICANT: DELISLE, G. W.  
APPLICANT: WILSON, T. M.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING  
TITLE OF INVENTION: AND TREATING MYCOBACTERIAL INFECTIONS USING AN INHA AGENT  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/241.766  
FILING DATE: 12-MAY-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: MONROY, GLADYS H.  
REGISTRATION NUMBER: 32,430  
REFERENCE/DOCKET NUMBER: 25237-20003.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 269 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-241-766-7

Query Match 66.7%; Score 32; DB 1; Length 269;  
Best Local Similarity 70.0%; Pred. No. 22;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AONTARIGE 10  
DB 75 ADRITAEIGE 84

RESULT 7  
US-08-802-141-4  
Sequence 4, Application US/08802141  
Patent No. 5773009  
GENERAL INFORMATION:  
APPLICANT: GLASS, ROGER I.  
APPLICANT: GENTSCH, JOHN R.  
APPLICANT: BHAN, M. K.  
APPLICANT: DAS, BIMAL K.  
TITLE OF INVENTION: ROTAVIRUS STRAIN AND RELATED  
TITLE OF INVENTION: COMPOSITIONS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NEEDLE & ROSENBERG, P.C.  
STREET: 127 Peachtree Street, Suite 1200  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/802,141  
FILING DATE: 19-FEB-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/231,041  
FILING DATE: 15-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Spratt, Gwendolyn D.  
REGISTRATION NUMBER: 36,016  
REFERENCE/DOCKET NUMBER: 1414,609  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404/688-0770  
TELEFAX: 688-9880  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 772 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-802-141-4

Query Match  
Best Local Similarity 66.7%; Score 32; DB 1; Length 772;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 QNTARIGE 10  
:|:|:|  
Db 31 ENTVOIGE 39

RESULT 8  
US-08-434-000A-10  
Sequence 10, Application US/08434000A  
Patent No. 6046037  
GENERAL INFORMATION:  
APPLICANT: ANDREW C. HIATT, JULIAN  
APPLICANT: K.-C. MA, THOMAS LEHNER  
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION  
TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/434,000A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/367,395  
FILING DATE: 12/30/94  
ATTORNEY/AGENT INFORMATION:  
NAME: Guise, Jeffrey W.  
REGISTRATION NUMBER: 34,613  
REFERENCE/DOCKET NUMBER: 212/127

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 552-8400  
TELEFAX: (619) 552-0159  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 769 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
TOPOLOGY: DESCRIPTION: Rat Polymyoglobulin Receptor  
US-08-434-000A-10

Query Match  
Best Local Similarity 64.8%; Score 31; DB 3; Length 769;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QNTARIGE 10  
:|:|:|  
Db 470 QNTAVIGE 478

RESULT 9  
US-09-312-157-10  
Sequence 10, Application US/09312157  
Patent No. 6303341  
GENERAL INFORMATION:  
APPLICANT: ANDREW C. HIATT, JULIAN  
APPLICANT: K.-C. MA, THOMAS LEHNER  
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION  
TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/312,157  
FILING DATE: 14-May-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/434,000  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Guise, Jeffrey W.  
REGISTRATION NUMBER: 34,613  
REFERENCE/DOCKET NUMBER: 212/127  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 552-8400  
TELEFAX: (619) 552-0159  
TELEX: 67-351  
SEQUENCE LISTING  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 769 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
DESCRIPTION: Rat Polymyoglobulin Receptor  
US-09-312-157-10

Query Match 64.6%; Score 31; DB 4; Length 769;  
Best Local Similarity 77.8%; Pred. No. 1.2e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ONITARIGE 10  
111111  
DB 470 ONATAVIGE 478

RESULT 10  
US-08-793-035-9  
; Sequence 9, Application US/08793035  
; Patent No. 6011201

GENERAL INFORMATION:

APPLICANT: Slabas, Antoni R.

APPLICANT: White, Andrew

APPLICANT: Chase, Dianne

APPLICANT: Elborough, Keiran

APPLICANT: Pentem, Phillip A.

TITLE OF INVENTION: B-ketacyl ACP Reductase Genes From

TITLE OF INVENTION: Brassica Napus

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Arnold White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: US

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/793,035

FILING DATE: 28-JUL-1997

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9414622.2

FILING DATE: 20-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB95/01678

FILING DATE: 17-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: Kammerer, Patricia A.

REGISTRATION NUMBER: 29,775

REFERENCE/DOCKET NUMBER: MOBT:132

TELECOMMUNICATION INFORMATION:

TELEPHONE: 713.787.1400

TELEFAX: 713.787.1440

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 315 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-793-035-9

Query Match 62.5%; Score 30; DB 3; Length 315;  
Best Local Similarity 50.0%; Pred. No. 72;  
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 AONITARIGE 10  
1::11::11  
DB 256 ASDMTAKLGE 265

RESULT 11  
US-08-793-035-10

; Sequence 10, Application US/08793035

; Patent No. 6011201

GENERAL INFORMATION:

APPLICANT: Slabas, Antoni R.

APPLICANT: White, Andrew

APPLICANT: Chase, Dianne

APPLICANT: Elborough, Keiran

APPLICANT: Pentem, Phillip A.

TITLE OF INVENTION: B-ketacyl ACP Reductase Genes From

TITLE OF INVENTION: Brassica Napus

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Arnold White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: US

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/793,035

FILING DATE: 28-JUL-1997

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9414622.2

FILING DATE: 20-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB95/01678

FILING DATE: 17-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: Kammerer, Patricia A.

REGISTRATION NUMBER: 29,775

REFERENCE/DOCKET NUMBER: MOBT:132

TELECOMMUNICATION INFORMATION:

TELEPHONE: 713.787.1400

TELEFAX: 713.787.1440

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 315 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-793-035-10

Query Match 62.5%; Score 30; DB 3; Length 315;  
Best Local Similarity 50.0%; Pred. No. 72;  
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 AONITARIGE 10  
1::11::11  
DB 256 ASDMTAKLGE 265

RESULT 12

US-08-704-711A-1

; Sequence 1, Application US/08704711A

; Patent No. 6114159

GENERAL INFORMATION:

APPLICANT: WILK, Horst

APPLICANT: HINZMANN, Bernd

TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX

TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/704,711A  
FILING DATE: 20-NOV-1996  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/DE95/00357  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 4438838.1  
FILING DATE: 21-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 4409663.1  
FILING DATE: 17-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 26083/124  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 579 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-704-711A-1

Query Match 62.5%; Score 30; DB 3; Length 579;  
Best Local Similarity 55.6%; Pred. No. 1.4e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 QNTARIGE 10  
DB 126 QNTPKVGE 134

RESULT 13  
US-08-704-711A-2  
Sequence 2, Application US/08704711A  
Patent No. 6114159  
GENERAL INFORMATION:  
APPLICANT: WILK, Horst  
APPLICANT: HINZMANN, Bernd  
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX  
NUMBER OF SEQUENCES: 22  
TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/704,711A  
FILING DATE: 20-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/DE95/00357  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 4438838.1  
FILING DATE: 21-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 4409663.1  
FILING DATE: 17-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 26083/124  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 582 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-704-711A-2

Query Match 62.5%; Score 30; DB 3; Length 582;  
Best Local Similarity 55.6%; Pred. No. 1.4e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 QNTARIGE 10  
DB 129 QNTPKVGE 137

RESULT 14  
US-08-448-489-1  
Sequence 1, Application US/08448489  
Patent No. 6184022  
GENERAL INFORMATION:  
APPLICANT: SATO, Hiroshi  
APPLICANT: SHINAGAWA, Akira  
TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR  
FILE REFERENCE: 55-290P  
CURRENT APPLICATION NUMBER: US/08/448,489  
CURRENT FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 582  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-448-489-1

Query Match 62.5%; Score 30; DB 4; Length 582;  
Best Local Similarity 55.6%; Pred. No. 1.4e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 QNTARIGE 10  
DB 129 QNTPKVGE 137

RESULT 15  
US-09-211-704A-9  
Sequence 9, Application US/09211704A  
Patent No. 6271014  
GENERAL INFORMATION:  
APPLICANT: de Saint-Vis, Blandine Marie  
APPLICANT: Fossiez, Francois  
APPLICANT: Caux, Christophe  
APPLICANT: Lebèque, Serge J.E.

;; TITLE OF INVENTION: Mammalian Proteinases; Related Reagents  
;; TITLE OF INVENTION: and Methods  
;; NUMBER OF SEQUENCES: 10  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: DNAX Research Institute  
;; STREET: 901 California Avenue  
;; CITY: Palo Alto  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94304-1104  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/211,704A  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 09/005,263  
;; FILING DATE: 09-JAN-1998  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Ching, Edwin P.  
;; REGISTRATION NUMBER: 34,090  
;; REFERENCE/DOCKET NUMBER: SF0781K  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (650)852-9196  
;; TELEFAX: (650)496-1200  
;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 582 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: not relevant  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; US-09-211-704A-9

Query Match 62.5%; Score 30; DB 4; Length 582;  
Best Local Similarity 55.6%; Pred. No. 1.4e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 2 QNTARIGE 10  
|||::||  
DB 129 QNYTPKVG 137

Search completed: April 24, 2002, 09:18:16  
Job time: 175 sec

THIS PAGE BLANK (USPTO)



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:19:03 ; Search time 38.71 Seconds  
(without alignments)  
19.678 Million cell updates/sec

Title: US-09-689-469-6  
Perfect score: 48  
Sequence: 1 AONTARIGE 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 48    | 100.0       | 404    | 1 T61596 | advanced glycosyla |
| 2          | 44    | 91.7        | 402    | 2 T09062 | probable advanced  |
| 3          | 40    | 83.3        | 416    | 1 A42879 | advanced glycosyla |
| 4          | 36    | 75.0        | 879    | 2 E69792 | conserved hypotat  |
| 5          | 35    | 72.9        | 547    | 2 T29567 | hypothetical prote |
| 6          | 34    | 70.8        | 391    | 2 B83203 | arginate o-acetyl  |
| 7          | 34    | 70.8        | 808    | 2 E64492 | hypothetical prote |
| 8          | 34    | 70.8        | 1155   | 2 H71456 | probable pyrolysin |
| 9          | 34    | 70.8        | 1180   | 2 A35854 | integrin alpha-1 c |
| 10         | 33    | 68.8        | 223    | 2 H64065 | mutator muth - Hae |
| 11         | 33    | 68.8        | 387    | 2 G84190 | hypothetical prote |
| 12         | 33    | 68.8        | 437    | 2 T64114 | nfts protein homol |
| 13         | 33    | 68.8        | 486    | 2 E42902 | 2-hydroxymuconic s |
| 14         | 33    | 68.8        | 550    | 2 T06379 | SAR DNA-binding pr |
| 15         | 33    | 68.8        | 560    | 2 T06377 | SAR DNA-binding pr |
| 16         | 33    | 68.8        | 792    | 2 B82752 | penicillin binding |
| 17         | 33    | 68.8        | 4436   | 2 E71086 | hypothetical prote |
| 18         | 32    | 66.7        | 435    | 2 T01805 | hypothetical prote |
| 19         | 32    | 66.7        | 439    | 2 T01807 | hypothetical prote |
| 20         | 32    | 66.7        | 468    | 2 H69133 | argininosuccinate  |
| 21         | 32    | 66.7        | 508    | 2 T50180 | nucleolar protein  |
| 22         | 32    | 66.7        | 625    | 2 T16777 | hypothetical prote |
| 23         | 32    | 66.7        | 772    | 2 A46110 | outer capsid prote |
| 24         | 32    | 66.7        | 941    | 2 F71332 | probable chromosom |
| 25         | 32    | 66.7        | 1160   | 1 DJEC3A | DNA-directed DNA p |
| 26         | 32    | 66.7        | 1160   | 1 A45915 | DNA-directed DNA p |
| 27         | 32    | 66.7        | 1160   | 2 B85503 | DNA polymerase III |
| 28         | 32    | 66.7        | 1164   | 2 G82100 | DNA polymerase III |
| 29         | 32    | 66.7        | 1396   | 2 G70598 | hypothetical prote |

|    |    |      |     |          |                    |
|----|----|------|-----|----------|--------------------|
| 30 | 31 | 64.6 | 206 | 2 A64402 | probable phosphati |
| 31 | 31 | 64.6 | 215 | 2 JC5483 | ABC-type transport |
| 32 | 31 | 64.6 | 218 | 2 B83396 | probable COA trans |
| 33 | 31 | 64.6 | 240 | 2 E81261 | probable ABC trans |
| 34 | 31 | 64.6 | 250 | 2 C70869 | hypothetical prote |
| 35 | 31 | 64.6 | 262 | 2 T47002 | hypothetical prote |
| 36 | 31 | 64.6 | 268 | 2 D29826 | hypothetical prote |
| 37 | 31 | 64.6 | 286 | 1 C35124 | 2,6-dioxo-6-phenyl |
| 38 | 31 | 64.6 | 286 | 2 JN0816 | 2,6-dioxo-6-phenyl |
| 39 | 31 | 64.6 | 318 | 2 E70117 | membrane fusion pr |
| 40 | 31 | 64.6 | 354 | 2 B47065 | phosphate starvali |
| 41 | 31 | 64.6 | 354 | 2 B85647 | hypothetical prote |
| 42 | 31 | 64.6 | 380 | 2 T04343 | L-ascorbate oxidas |
| 43 | 31 | 64.6 | 418 | 2 D75283 | hypothetical prote |
| 44 | 31 | 64.6 | 494 | 2 D86493 | polymorphic outer  |
| 45 | 31 | 64.6 | 507 | 2 T20966 | hypothetical prote |

## ALIGNMENTS

RESULT 1  
161596  
advanced glycosylation end-products receptor precursor - human  
N:Alternate names: advanced glycosylation end product-binding protein, 35K, glycoprot  
C:Species: Homo sapiens (man)  
C:Date: 24-May-1996 #sequence\_revision 07-Feb-1997 #text\_change 16-Jul-1999  
C:Accession: 161596; B42879; S27968  
R:Snigaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, G.  
Genomics 23, 408-419, 1994  
A:Title: Three genes in the human MHC class III region near the junction with the cla  
nterpart of mouse mammary tumor gene Int-3.  
A:Reference number: A55562; MUID:95137587  
A:Accession: 161596  
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/  
A:Molecule type: DNA  
A:Residues: 1-404 <RES>  
A:Cross-references: GB:D82769; NID:9561657; PTDN:BA005958.1; PTD:9561659  
R:Neepert, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.;  
J. Biol. Chem. 267, 14998-15004, 1992  
A:Title: Cloning and expression of a cell surface receptor for advanced glycosylation  
A:Reference number: A42879; MUID:92340547  
A:Accession: B42879  
A:Molecule type: mRNA  
A:Residues: 'G', 2-99, 'R', 101-404 <NEE>  
A:Cross-references: EMBL:M91211; NID:9190845; PTDN:AAA03574.1; PTD:9190846  
A:Experimental source: lung  
A:Note: sequence extracted from NCBI backbone (NCBI:109438)  
C:Comment: Advanced glycosylation end products are heterogeneous nonenzymatically gly  
cellular function, thus contributing to tissue lesions in diabetes.  
C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide  
ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.  
C:Genetics:  
A:Gene: GDB:AGER  
A:Cross-references: GDB:306354; OMIM:600214  
A:Map position: 6p21.3-6p21.3  
A:Introns: 18/1; 53/3; 119/1; 140/3; 170/1; 231/1; 274/3; 322/1; 331/1; 373/2  
C:Function:  
A:Description: neuronal receptor for amphoterin, a DNA-binding protein involved in ne  
C:Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein  
C:Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-404/Product: advanced glycosylation end products receptor #status predicted <MAT  
F:23-344/Domain: extracellular #status predicted <EXT>  
F:31-101/Domain: immunoglobulin homology <IM1>  
F:137-210/Domain: immunoglobulin homology <IM2>  
F:252-303/Domain: immunoglobulin homology <IM3>  
F:345-363/Domain: transmembrane #status predicted <TM>  
F:363-404/Domain: intracellular #status predicted <INT>  
F:25-81/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:38-99, 144-208, 259-301/Disulfide bonds: #status predicted

```

Query Match      100.0%; Score 48; DB 1; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ANONTARIGE 10
    |||||
Db 23 ANONTARIGE 32

RESULT 2
T09062
Probleme advanced glycosylation end-products receptor precursor - mouse
N:Alternate names: RAGE
C:Species: Mus musculus (house mouse)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000
C:Accession: T09062
R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; St
submitted to the EMBL Data Library, October 1997
A:Description: Sequence of the mouse major histocompatibility locus class III region.
A:Reference number: Z16543
A:Accession: T09062
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-402 <ROW>
A:Cross-references: EMBL:AF030001; NID:g2564945; PID:g2564950
C:Genetics:
A:Gene: RAGE
A:Map position: 17
A:Introns: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1; 272/3; 320/1; 329/1; 371/2
C:Superfamily: advanced glycosylation end-products receptor; immunoglobulin homology
C:Keywords: receptor; transmembrane protein
F:31:100/Domain: immunoglobulin homology <IMM>

Query Match      91.7%; Score 44; DB 2; Length 402;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ONITARIGE 10
    |||||
Db 24 ONITARIGE 32

RESULT 3
A42879
Advanced glycosylation end-products receptor precursor - bovine
N:Alternate names: advanced glycosylation end product-binding protein, 35k; glycoprotein
C:Species: Bos primigenius taurus (cattle)
C>Date: 04-Mar-1993 #sequence_revision 07-Feb-1997 #text_change 16-Jul-1999
C:Accession: A42879; A42878; S27949
R:Nepper, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; St
J. Biol. Chem. 267, 14998-15004, 1992
A>Title: Cloning and expression of a cell surface receptor for advanced glycosylation en
A:Reference number: A42879; MUID:92340547
A:Molecule type: mRNA
A:Accession: A42879
A:Residues: 1-416 <NEER>
A:Cross-references: GB:M01212; NID:g163650; PIDN:AA03575.1; PID:g163651
A:Experimental source: lung
A>Note: sequence extracted from NCBI backbone (NCBI:109436)
A>Note: parts of this sequence, including the amino end of the mature protein, were dete
R:Schmidt, A.M.; Viana, M.; Gerlach, M.; Brett, J.; Ryan, J.; Kuo, J.; Esposto, C.; He
J. Biol. Chem. 267, 14987-14997, 1992
A>Title: Isolation and characterization of two binding proteins for advanced glycosylati
A:Reference number: A42878; MUID:92340546
A:Accession: A42878
A:Molecule type: protein
A:Residues: 23-24, 'X', '26-37', 'X', '39-49', 'XX', '52-54' <SCH>
A:Experimental source: endothelial cells
A>Note: sequence extracted from NCBI backbone (NCBI:109434)
C:Comment: Advanced glycosylation end-products are heterogeneous nonenzymatically glycos
cellular function, thus contributing to tissue lesions in diabetes.
C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide on

```

```

ates in the neurotoxic pathway that produces dementia in Alzheimer's disease.
C:Function:
A:Description: neuronal receptor for anaphroterin, a DNA-binding protein involved in ne
C:Superfamily: advanced glycosylation end-products receptor; immunoglobulin homology
C:Keywords: Alzheimer's disease; glycoprotein; receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-416/Product: advanced glycosylation end-products receptor RAGE #status predicted
F:23-354/Domain: extracellular #status predicted <EXT>
F:31-100/Domain: immunoglobulin homology <IM1>
F:136-209/Domain: immunoglobulin homology <IM2>
F:1262-313/Domain: immunoglobulin homology <IM3>
F:355-372/Domain: transmembrane #status predicted <TM>
F:373-416/Domain: intracellular #status predicted <INT>
F:25,80/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:38-98,143-207,269-311/Disulfide bonds: #status predicted

Query Match      83.3%; Score 40; DB 1; Length 416;
Best Local Similarity 88.9%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 ONITARIGE 10
    |||||
Db 24 ONITARIGE 32

RESULT 4
E69792
Conserved hypothetical protein yeaA - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: E69792
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C:Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A:Enrich, S.D.; Emerson, P.T.; Eutlan, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizli, A.; Gal
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y, M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portele
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scani
A:Authors: Schleich, S.; Schroeder, R.; Scofield, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yamoto, K.; Yata, K.; Yoshida
A:Authors: Yoshikawa, H.F.; Zumestein, E.; Yoshikawa, H.; Danchin, A.
A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A:Reference number: A69580; MUID:98044033
A:Accession: E69792
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-879 <KUN>
A:Cross-references: GB:Z29107; GB:AL009126; NID:g2632866; PIDN:CAB12496.1; PID:g26329
A:Experimental source: strain 168
C:Genetics:
A:Gene: yeaA

Query Match      75.0%; Score 36; DB 2; Length 879;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 ONITARIGE 10
    |||
Db 45 ONITARIGE 53

RESULT 5
T29567
Hypothetical protein C44C1.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T29567

```

R:Bradshaw, H.; Stellyes, L.  
submitted to the EMBL Data Library, November 1995  
A:Description: The sequence of C. elegans cosmid C44C1.  
A:Reference number: 220642  
A:Accession: J29567  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-547 <BRA>  
A:Cross-references: EMBL:U01030; PIDN:AA82364.1; CESP:C44C1.4  
C:Genetics:  
A:Gene: CESP:C44C1.4  
A:Introns: 31/3; 98/1; 119/3; 178/2; 343/3; 373/3; 404/3; 440/2; 481/2; 531/2  
C:Superfamily: vacuolar protein sorting protein VPS45

Query Match 72.9%; Score 35; DB 2; Length 547;  
Best Local Similarity 70.0%; Pred. No. 19;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 AONTARIGE 10  
|:|||||:  
DB 265 ARNITANFGE 274

RESULT 6  
B83203  
alignate o-acetyltransferase AlgJ PA3549 [imported] - Pseudomonas aeruginosa (strain PAO  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: B83203  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br  
aman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapid, K.; Lam,  
L.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A>Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho  
A:Reference number: A82950; MUID:20437337  
A:Accession: B83203  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-391 <STO>  
A:Cross-references: GB:AE004775; GB:AE004091; NID:g9949692; PIDN:AA606937.1; GSPDB:GN001  
A:Experimental source: strain PAO1  
C:Genetics:  
A:Gene: algJ; PA3549

Query Match 70.8%; Score 34; DB 2; Length 391;  
Best Local Similarity 60.0%; Pred. No. 21;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 AONTARIGE 10  
|:|||||:  
DB 222 AONTATRIGE 231

RESULT 7  
B64492  
hypothetical protein MJ1542 - Methanococcus jannaschii  
C:Species: Methanococcus jannaschii  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 22-Oct-1999  
C:Accession: E64492  
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,  
R.; Reich, C.L.; Overbeek, R.; Kirkness, E.F.; Weissbrock, K.G.; Merrick, J.M.; Glodek, A.;  
Iron, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.  
Science 273, 1058-1073, 1996  
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C  
A>Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii  
A:Reference number: A64300; MUID:96337999  
A:Accession: E64492  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-808 <BOU>  
A:Cross-references: GB:U67595; GB:L77117; NID:g1592170; PIDN:AAB95570.1; PID:g1500434; T

C:Genetics:  
A:Map position: REV1521171-1518745

Query Match 70.8%; Score 34; DB 2; Length 808;  
Best Local Similarity 66.7%; Pred. No. 47;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 ONITARIGE 10  
:|||||:  
DB 229 ENITTRIGD 237

RESULT 8  
H71456  
probable pyrolysin (EC 3.4.-.-) homolog PH0310 [similarity] - Pyrococcus horikoshii  
C:Species: Pyrococcus horikoshii  
C:Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 21-Jul-2000  
C:Accession: H71456  
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Se  
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushtida, N.; Ogu  
DNA Res. 5, 55-76, 1998  
A>Title: Complete sequence and gene organization of the genome of a hyper-thermophilic  
A:Reference number: A71000; MUID:98344137  
A:Accession: H71456  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1155 <KAN>  
A:Cross-references: GB:AP000001; NID:g3236128; PIDN:BA429383.1; PID:g3256700  
A:Experimental source: strain OT3  
A:Note: this accession replaces an interim accession for a sequence replaced by Genba  
C:Genetics:  
A:Gene: PH0310  
C:Keywords: hydrolase

Query Match 70.8%; Score 34; DB 2; Length 1155;  
Best Local Similarity 62.5%; Pred. No. 70;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 NITARIGE 10  
|:|||||:  
DB 817 NITAKVGE 824

RESULT 9  
A35854  
Integrin alpha-1 chain precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 23-Oct-1990 #sequence\_revision 13-Sep-1991 #text\_change 20-Sep-1999  
C:Accession: A35854; S11243  
R:Ignatius, M.J.; Large, T.H.; Houde, M.; Tawil, J.W.; Barton, A.; Esch, F.; Carbonet  
J. Cell Biol. 111, 709-720, 1990  
A>Title: Molecular cloning of the rat integrin alpha-1-subunit: a receptor for laminin  
A:Reference number: A35854; MUID:90338125  
A:Accession: A35854  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1180 <IGN>  
A:Cross-references: GB:X52140; NID:g56493; PIDN:CAA36384.1; PID:g56494  
C:Superfamily: unassigned collagens; von Willebrand factor type A repeat homology  
C:Keywords: cell adhesion; cytoskeleton; transmembrane protein  
F:170-345/Domain: von Willebrand factor type A repeat homology <WMA>

Query Match 70.8%; Score 34; DB 2; Length 1180;  
Best Local Similarity 75.0%; Pred. No. 72;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 ONITARIGE 9  
|:|||||:  
DB 881 ONITCRVG 888

```

RESULT 10
mutator muth - Haemophilus influenzae (strain Rd KW20)
H64065
N:Alternate names: DNA mismatch protein
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 26-Aug-1999
C:Accession: H64065
R:Flerschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630
A:Accession: H64065
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-223 <TIGR>
A:Cross-references: GB:U32723; GB:I42023; NID:g1573363; PIDN:AAC22062.1; PID:g1573374; T
C:Genetics:
A:Gene: muth
C:Superfamily: mutator muth

Query Match 68.8%; Score 33; DB 2; Length 223;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ITARIGE 10
DB 165 ITARIGE 171

RESULT 11
G84190
hypothetical protein Vng0310c [Imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: G84190
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leihnauser, B.; Keller, K.; Cruz, R.; Danison, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo, Jung, K.H.; Alam, M.; Eitelas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Epphardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483
A:Accession: G84190
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-387 <STO>
A:Cross-references: GB:AEO04437; NID:g10579939; PIDN:AGI8891.1; GSPDB:GN00138
C:Genetics:
A:Gene: VNG0310C
C:Superfamily: conserved hypothetical protein MJ1249

Query Match 68.8%; Score 33; DB 2; Length 387;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 ONTARIGE 10
DB 147 ONTARIGE 155

RESULT 12
I64114
nifs protein homolog H11295 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 21-Jul-2000
C:Accession: I64114; T09423
R:Flerschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.

```

```

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630
A:Accession: I64114
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-437 <TIGR>
A:Cross-references: GB:U32809; GB:I42023; NID:g3212217; PIDN:AAC22941.1; PID:g1574753
R:White, O.; Clayton, R.A.; Kerlavage, A.R.; Flerschmann, R.D.; Peterson, J.; Hickey, submitted to the EMBL Data Library, May 1998
A:Reference number: Z16667
A:Accession: T09423
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-437 <WHI>
A:Cross-references: EMBL:U32809; NID:g3212217; PID:g1574753
C:Genetics:
A:Gene: H11295
C:Superfamily: nifs protein

Query Match 68.8%; Score 33; DB 2; Length 437;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 ONTARIGE 10
DB 385 ONTARIGE 393

RESULT 13
E42902
2-hydroxyxynuconic semialdehyde dehydrogenase (EC 1.2.1.-) - Pseudomonas putida plasmid
C:Species: Pseudomonas putida
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 11-May-2000
C:Accession: E42902; S18244; S23488
R:Harayama, S.; Reik, M.; Bairoch, A.; Neidle, E.L.; Ornston, L.N.
unpublished results 1991, cited by Genbank
A:Reference number: A57135
A:Accession: E42902
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-486 <HAR>
A:Cross-references: GB:M64747; NID:g151718; PIDN:AAA26053.1; PID:g151725
R:Harayama, S.; Reik, M.; Bairoch, A.; Neidle, E.L.; Ornston, L.N.
J. Bacteriol. 173, 7540-7548, 1991
A:Title: Potential DNA slippage structures acquired during evolutionary divergence of zolate dioxygenases.
A:Reference number: A41659; MUID:92041666
A:Contents: annotation
A:Note: Genbank cited this reference and reported DNA sequence with its translation n in the reference paper
R:Horn, J.M.; Harayama, S.; Timmis, K.N.
Mol. Microbiol. 5, 2459-2474, 1991
A:Title: DNA sequence determination of the TOL plasmid (pWMO) xylGR genes of Pseudom
A:Reference number: S18244; MUID:92167811
A:Accession: S18244
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-486 <HAR>
R:Neidle, E.L.; Hartnett, C.; Ornston, L.N.; Bairoch, A.; Reik, M.; Harayama, S.
Eur. J. Biochem. 204, 113-120, 1992
A:Title: Cis-diol dehydrogenases encoded by the TOL pWMO plasmid xylL gene and the Ac
A:Reference number: S23477; MUID:92155191
A:Accession: S23488
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-486 <NEI>
A:Cross-references: EMBL:M64747
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1992

```

C:Genetics:  
 A:Gene: xylG  
 A:Genome: plasmid TOL PWM0  
 C:Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology  
 C:Keywords: oxidoreductase  
 F:42-308/Domain: aldehyde dehydrogenase homology <ALD>

Search completed: April 24, 2002, 09:19:04  
 Job time: 203 sec

Query Match 68.8%; Score 33; DB 2; Length 486;  
 Best Local Similarity 70.0%; Pred. No. 44;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AONITARIGE 10  
 | |||| |  
 Db 74 ADGIFARFGE 83

RESULT 14  
 T06379  
 SAR DNA-binding protein 2 - garden pea  
 C:Species: Pisum sativum (garden pea)  
 C:Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 02-Jun-2000  
 C:Accession: T06379  
 R:Hatton, D.; Gray, J.C.  
 submitted to the EMBL Data Library, April 1998  
 A:Description: cDNA encoding a pea SAR DNA-binding protein that shows homology to nucle  
 A:Reference number: 215637  
 A:Accession: T06379  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-550 <HAT>  
 A:Cross-References: EMBL:AF061963; NID:g3132697; PIDN:AMC16331.1; PID:g3132698  
 C:Genetics:  
 A:Gene: SARBP-2  
 C:Superfamily: garden pea SAR DNA-binding protein

Query Match 68.8%; Score 33; DB 2; Length 550;  
 Best Local Similarity 60.0%; Pred. No. 50;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 AONITARIGE 10  
 | |||| |  
 Db 281 APNLTAMVGE 290

RESULT 15  
 T06377  
 SAR DNA-binding protein-1 - garden pea  
 C:Species: Pisum sativum (garden pea)  
 C:Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 02-Jun-2000  
 C:Accession: T06377  
 R:Hatton, D.; Gray, J.C.  
 submitted to the EMBL Data Library, April 1998  
 A:Description: cDNA encoding a pea SAR DNA-binding protein that shows homology to nucle  
 A:Reference number: 215637  
 A:Accession: T06377  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-560 <HAT>  
 A:Cross-References: EMBL:AF061962; NID:g3132695; PIDN:AMC16330.1; PID:g3132696  
 C:Genetics:  
 A:Gene: SARBP-1  
 C:Superfamily: garden pea SAR DNA-binding protein

Query Match 68.8%; Score 33; DB 2; Length 560;  
 Best Local Similarity 60.0%; Pred. No. 51;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 AONITARIGE 10  
 | |||| |  
 Db 281 APNLTAMVGE 290



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:20:40 ; Search time 21.42 Seconds  
(without alignments)  
17.117 Million cell updates/sec

Title: US-09-689-469-6  
Perfect score: 48  
Sequence: 1 AONTARIGE 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 segs, 3664827 residues  
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID            | Description         |
|------------|-------|-------------|--------|---------------|---------------------|
| 1          | 48    | 100.0       | 404    | 1 RAGE_HUMAN  | Q15109 homo sapien  |
| 2          | 44    | 91.7        | 402    | 1 RAGE_RAT    | Q63495 rattus norv  |
| 3          | 44    | 91.7        | 403    | 1 RAGE_MOUSE  | O62151 mus musculu  |
| 4          | 40    | 83.3        | 416    | 1 RAGE_BOVIN  | Q28173 bos taurus   |
| 5          | 34    | 70.8        | 1180   | 1 ITPL_RAT    | P18614 rattus norv  |
| 6          | 33    | 68.8        | 223    | 1 MUTH_HAEN   | P44688 haemophilus  |
| 7          | 33    | 68.8        | 270    | 1 NTFH_CLOCB  | Q52700 clostridium  |
| 8          | 33    | 68.8        | 437    | 1 CSD_HAEN    | Q57476 haemophilus  |
| 9          | 33    | 68.8        | 474    | 1 VDCC_STRD7  | O95697 streptomyce  |
| 10         | 33    | 68.8        | 486    | 1 XYLG_PSEPU  | P23105 pseudomonas  |
| 11         | 32    | 66.7        | 268    | 1 INHA_MYCAV  | O07400 mycobacteri  |
| 12         | 32    | 66.7        | 269    | 1 INHA_MYCSM  | P42829 mycobacteri  |
| 13         | 32    | 66.7        | 435    | 1 V413_ARAYH  | O04656 arabidopsis  |
| 14         | 32    | 66.7        | 439    | 1 V412_ARAYH  | O04658 arabidopsis  |
| 15         | 32    | 66.7        | 468    | 1 ARLY_METHN  | O26369 methanobact  |
| 16         | 32    | 66.7        | 772    | 1 VP4_ROTHT   | O09113 human rotav  |
| 17         | 32    | 66.7        | 1159   | 1 DP3A_VIBCH  | P52022 vibrio chol  |
| 18         | 32    | 66.7        | 1160   | 1 DP3A_ECOLI  | P10443 escherichia  |
| 19         | 32    | 66.7        | 1160   | 1 DP3A_SALTY  | P14567 salmonella   |
| 20         | 31    | 64.6        | 201    | 1 VID3_AGR6   | P09816 agrobacteri  |
| 21         | 31    | 64.6        | 206    | 1 Y817_METJA  | O58227 methanococc  |
| 22         | 31    | 64.6        | 286    | 1 BPMD_BURCE  | P47229 burkholderi  |
| 23         | 31    | 64.6        | 354    | 1 PHOH_ECOLI  | P31544 escherichia  |
| 24         | 31    | 64.6        | 767    | 1 CC10_SCHPO  | P01129 schistosach  |
| 25         | 31    | 64.6        | 769    | 1 PIGR_RAT    | P15083 rattus norv  |
| 26         | 31    | 64.6        | 1159   | 1 DP3A_PASMU  | O9CPK3 pasteurella  |
| 27         | 30    | 62.5        | 89     | 1 M7_LILHE    | O40190 lillium henr |
| 28         | 30    | 62.5        | 90     | 1 L1M1_LILLO  | O43533 lillium long |
| 29         | 30    | 62.5        | 90     | 1 L1M2_LILLO  | O43534 lillium long |
| 30         | 30    | 62.5        | 115    | 1 YX03_CAEEL  | Q11110 caenorhabdi  |
| 31         | 30    | 62.5        | 137    | 1 KDG_L_PSEDE | P29944 pseudomonas  |
| 32         | 30    | 62.5        | 274    | 1 IF34_YEAST  | O04067 saccharomyc  |
| 33         | 30    | 62.5        | 275    | 1 BLOI_PSEAE  | O07293 pseudomonas  |

|    |    |      |      |               |                    |
|----|----|------|------|---------------|--------------------|
| 34 | 30 | 62.5 | 285  | 1 YDHJ_ECOLI  | P76185 escherichia |
| 35 | 30 | 62.5 | 401  | 1 ENO_THEAC   | O9h1t1 thermoplasm |
| 36 | 30 | 62.5 | 580  | 1 MM14_PIG    | O9x490 sus scrofa  |
| 37 | 30 | 62.5 | 582  | 1 MM14_HUMAN  | P50281 homo sapien |
| 38 | 30 | 62.5 | 582  | 1 MM14_MOUSE  | P53690 mus musculu |
| 39 | 30 | 62.5 | 582  | 1 MM14_RABIT  | O95220 oryctolagus |
| 40 | 30 | 62.5 | 582  | 1 MM14_RAT    | Q10739 rattus norv |
| 41 | 30 | 62.5 | 772  | 1 VP4_ROTBT   | P35746 bovine rota |
| 42 | 30 | 62.5 | 850  | 1 DEXT_STRMU  | O54443 streptococc |
| 43 | 30 | 62.5 | 4644 | 1 DYHC_MOUSE  | O9jhu4 mus musculu |
| 44 | 30 | 62.5 | 4644 | 1 DYHC_RAT    | P38650 rattus norv |
| 45 | 29 | 60.4 | 83   | 1 RL23_HAALHA | Q06842 halobacteri |

## ALIGNMENTS

| RESULT | ID   | Sequence | Standard                | PRT | AA  |
|--------|--|----------|-------------------------|-----|-----|
| 1      | RAGE_HUMAN   | Q15109   | Q15279; Q9Y3R3; Q9H2X7; | 404 | AA. |
| AC     | 01-NOV-1997 (Rel. 35, Created)   |          |                         |     |     |
| DT     | 01-NOV-1997 (Rel. 35, Last sequence update)  |          |                         |     |     |
| DT     | 20-AUG-2001 (Rel. 40, Last annotation update)  |          |                         |     |     |
| DE     | ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS). |          |                         |     |     |
| GN     | AGER OR RAGE.  |          |                         |     |     |
| OS     | Homo sapiens (Human).  |          |                         |     |     |
| OC     | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |          |                         |     |     |
| OC     | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.   |          |                         |     |     |
| OX     | NCBI_TaxID=9606;   |          |                         |     |     |
| RN     | [1]  |          |                         |     |     |
| RP     | SEQUENCE FROM N.A. (ISOFORM 1).  |          |                         |     |     |
| RC     | TISSUE=Lung;   |          |                         |     |     |
| RX     | MEDLINE=92340547; PubMed=1378843;  |          |                         |     |     |
| RA     | Neuper M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,  |          |                         |     |     |
| RA     | Elliston K., Stern D., Shaw A.;  |          |                         |     |     |
| RT     | "Cloning and expression of a cell surface receptor for advanced  |          |                         |     |     |
| RT     | glycosylation end products of proteins.";  |          |                         |     |     |
| RL     | J. Biol. Chem. 267:14998-15004(1992).  |          |                         |     |     |
| RN     | [2]  |          |                         |     |     |
| RP     | SEQUENCE FROM N.A. (ISOFORM 1).  |          |                         |     |     |
| RX     | MEDLINE=95137587; PubMed=7835890;  |          |                         |     |     |
| RA     | Sugaya K., Fukagawa T., Matsumoto K., Mita K., Takahashi E., Ando A.,  |          |                         |     |     |
| RA     | Inoko H., Ikemura T.;  |          |                         |     |     |
| RT     | "Three genes in the human MHC class III region near the junction with  |          |                         |     |     |
| RT     | the class II: gene for receptor of advanced glycosylation end  |          |                         |     |     |
| RT     | products, PBX2 homeobox gene and a notch homolog, human counterpart  |          |                         |     |     |
| RT     | of mouse mammary tumor gene int-3.";   |          |                         |     |     |
| RL     | Genomics 23:408-419(1994).   |          |                         |     |     |
| RN     | [3]  |          |                         |     |     |
| RP     | SEQUENCE FROM N.A. (ISOFORM 1).  |          |                         |     |     |
| RA     | Rowen L., Dankers C., Baskin D., Faust J., Loretz C., Ahearn M.E.,   |          |                         |     |     |
| RA     | Banta A., Spies T., Hood L.;   |          |                         |     |     |
| RT     | Submitted (Feb-1997) to the EMBL/GenBank/DBJ databases.  |          |                         |     |     |
| RN     | [4]  |          |                         |     |     |
| RP     | SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-100.   |          |                         |     |     |
| RA     | Abedin M.J., Yonekura H., Migita H., Karasawa J., Yamamoto Y.,   |          |                         |     |     |
| RA     | Yamamoto H.;   |          |                         |     |     |
| RT     | "Molecular heterogeneity of the receptor for advanced glycation  |          |                         |     |     |
| RT     | endproducts.";   |          |                         |     |     |
| RL     | Submitted (Jan-2000) to the EMBL/GenBank/DBJ databases.  |          |                         |     |     |
| RN     | [5]  |          |                         |     |     |
| RP     | SEQUENCE FROM N.A. (ISOFORM 2).  |          |                         |     |     |
| RA     | Malherbe P., Richards J., Galliard H., Thompson A., Diener C.,   |          |                         |     |     |
| RA     | Schuler A., Huber G.;  |          |                         |     |     |
| RT     | "CDNA cloning of a novel secreted isoform of the human Receptor for  |          |                         |     |     |
| RT     | advanced glycation end products (RAGE) and characterization of cells   |          |                         |     |     |
| RT     | co-expressing cell-surface scavenger receptors and Swedish mutant  |          |                         |     |     |
| RT     | amyloid precursor protein.";   |          |                         |     |     |
| RL     | Submitted (May-1999) to the EMBL/GenBank/DBJ databases.  |          |                         |     |     |
| RN     | [6]  |          |                         |     |     |
| RP     | SEQUENCE OF 1-12 FROM N.A.   |          |                         |     |     |

RA Hudson B.I., Puters T.S.;  
 RT "Novel polymorphisms in the receptor for advanced glycation  
 RL end-products (RAGE) gene";  
 CC Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATED END  
 CC PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS  
 CC WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED  
 CC RATE IN DIABETES.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1) AND  
 CC SECRETED (ISOFORM 2).  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2/RAGESEC;  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.  
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS  
 CC 2 C2-LIKE AND ONE V-LIKE DOMAINS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: M91211; AAA03574.1; -  
 CC EMBL: D28769; BAA05958.1; -  
 CC EMBL: U89336; AAB47491.1; -  
 CC EMBL: AB036432; BAA89369.1; -  
 CC EMBL: AJ133823; CAB43108.1; -  
 CC EMBL: AF208289; AAG35728.1; -  
 CC MIM: 600214; -  
 CC InterPro: IPR003006; Iq\_MHC.  
 CC InterPro: IPR003598; Iq\_C2.  
 CC InterPro: IPR003600; Iq\_Like.  
 CC Pfam: PF00047; Iq\_2.  
 CC SMART: SM00408; Igc2; 1.  
 CC SMART: SM00410; Iq\_Like; 1.  
 CC PROSITE: PS00290; Iq\_MHC; 1.  
 CC Immunoglobulin domain; Glycoprotein; Transmembrane; Signal;  
 CC Alternative splicing; Polymorphism.  
 CC FT SIGNAL 1 22  
 CC FT CHAIN 23 404  
 CC FT DOMAIN 23 342  
 CC FT TRANSMEM 343 363  
 CC FT DOMAIN 364 404  
 CC FT DOMAIN 31 106  
 CC FT DOMAIN 137 214  
 CC FT DOMAIN 252 308  
 CC FT DISULFID 38 99  
 CC FT DISULFID 144 208  
 CC FT DISULFID 259 301  
 CC FT CARBOHYD 25 25  
 CC FT CARBOHYD 81 81  
 CC FT CARBOHYD 380 384  
 CC FT VASAPLIC 54 67  
 CC FT VASAPLIC 275 404  
 CC FT VASAPLIC 275 404  
 CC FT VARIANT 100 100  
 CC FT CONFLICT 1 1  
 CC FT SEQUENCE 404 AA: 42802 MW: 0D584C436C30CE7 CRC64;  
 CC  
 CC Query Match 100.0%; Score 48; DB 1; Length 404;  
 CC Best Local Similarity 100.0%; Pred. No. 0.013;  
 CC Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC 1 AONTARIGE 10

DB 23 AONTARIGE 32  
 II|IIIIIIII|  
 RESULT 2  
 ID RAGE\_RAT STANDARD; PRT; 402 AA.  
 AC 063495;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE ADVANCED GLYCOSYLATED END PRODUCT-SPECIFIC RECEPTOR PRECURSOR  
 DE (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).  
 GN AGER OR RAGE.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxId=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Lung;  
 RX MEDLINE=97368045; PubMed=9224812;  
 RA Renard C., Chappey O., Wautier M.P., Nagashima M., Lunn E.,  
 RA Worsler J., Zhao L., Schmidt A.M., Schermann J.M., Wautier J.L.;  
 RA "Recombinant advanced glycation end product receptor pharmacokinetics  
 RA in normal and diabetic rats.";  
 RL Mol. Pharmacol. 52:54-62(1997).  
 CC -1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END  
 CC PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS  
 CC WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED  
 CC RATE IN DIABETES.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.  
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS  
 CC 2 C2-LIKE AND ONE V-LIKE DOMAINS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: L33413; AAA42027.1; -  
 CC InterPro: IPR003006; Iq\_MHC.  
 CC InterPro: IPR003598; Iq\_C2.  
 CC InterPro: IPR003600; Iq\_Like.  
 CC Pfam: PF00047; Iq\_3.  
 CC SMART: SM00408; Igc2; 1.  
 CC SMART: SM00410; Iq\_Like; 1.  
 CC PROSITE: PS00290; Iq\_MHC; 1.  
 CC Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.  
 CC FT SIGNAL 1 22  
 CC FT CHAIN 23 402  
 CC FT DOMAIN 23 341  
 CC FT TRANSMEM 342 362  
 CC FT DOMAIN 363 402  
 CC FT DOMAIN 31 105  
 CC FT DOMAIN 136 212  
 CC FT DOMAIN 250 306  
 CC FT DISULFID 38 98  
 CC FT DISULFID 143 206  
 CC FT DISULFID 257 299  
 CC FT CARBOHYD 25 25  
 CC FT CARBOHYD 80 80  
 CC FT CARBOHYD 80 80  
 CC FT SEQUENCE 402 AA: 42663 MW: 594481BC3A51E94E CRC64;  
 CC  
 CC Query Match 91.7%; Score 44; DB 1; Length 402;  
 CC Best Local Similarity 100.0%; Pred. No. 0.088;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 2 QNTARIGE 10  
 |||||  
 DB 24 QNTARIGE 32

RESULT 3  
 RAGE\_MOUSE STANDARD: PRT: 403 AA.

ID RAGE\_MOUSE STANDARD: PRT: 403 AA.

AC 062151:

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR

DE (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).

GN AGER OR RAGE.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BAUB/C; TISSUE=Lung;

RA MEDLINE=97368045; PubMed=9224812;

RA Renard C., Chappey O., Wautier M.P., Nagashima M., Lunde E.,

RA Morser J., Zhao L., Schmidt A.M., Scherrenmann J.M., Mautier J.L.;

RT "Recombinant advanced glycation end product receptor pharmacokinetics

in normal and diabetic rats."

RL Mol. Pharmacol. 52:54-62(1997).

-1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END

PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS

WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED

RATE IN DIABETES.

-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.

-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS

2 C2-LIKE AND ONE V-LIKE DOMAINS.

-----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation  
 at the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 -----

CC EMBL: L33412; AAA40040.1; -

DR MGD; MGI:893592; Ager.

DR InterPro: IPR003006; IG\_MHC.

DR InterPro: IPR003598; IG\_C2.

DR InterPro: IPR003600; IG\_Like.

DR Pfam: PF00047; Ig\_3

DR SMART; SM00408; IgC2; 1.

DR SMART; SM00410; IG\_Like; 1.

DR PROSITE; PS00290; IG\_MHC; 1.

KW Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 22

FT CHAIN 23 403

FT DOMAIN 23 403

FT TRANSMEM 342 362

FT DOMAIN 363 403

FT DOMAIN 31 105

FT DOMAIN 136 213

FT DOMAIN 251 307

FT DISULFID 38 98

FT DISULFID 143 207

FT DISULFID 258 300

FT CARBOHYD 25 25

FT CARBOHYD 80 80

FT SEQUENCE 403 AA: 42668 MW: 1279796FD1579357 CRC64;

Query Match 91.7%; Score 44; DB 1; Length 403;  
 Best Local Similarity 100.0%; Pred. No. 0.089;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QNTARIGE 10  
 |||||  
 DB 24 QNTARIGE 32

RESULT 4  
 RAGE\_BOVIN STANDARD: PRT: 416 AA.

ID RAGE\_BOVIN STANDARD: PRT: 416 AA.

AC Q28173;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR

DE (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS).

GN AGER OR RAGE.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;

OC Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE=Lung;

RA MEDLINE=92340547; PubMed=1378843;

RA Neepser M., Schmidt A.M., Brett J., Yan S.D., Wang F., Pan Y.C.,

RA Elliston K., Stern D., Shaw A.;

RT "Cloning and expression of a cell surface receptor for advanced

glycosylation end products of proteins."

RL J. Biol. Chem. 267:14998-15004(1992).

-1- FUNCTION: MEDIATES INTERACTIONS OF ADVANCED GLYCOSYLATION END

PRODUCTS (AGE). THESE ARE NONENZYMATICALLY GLYCOSYLATED PROTEINS

WHICH ACCUMULATE IN VASCULAR TISSUE IN AGING AND AT AN ACCELERATED

RATE IN DIABETES.

-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-1- TISSUE SPECIFICITY: ENDOTHELIAL CELLS.

-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS

2 C2-LIKE AND ONE V-LIKE DOMAINS.

-----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation  
 at the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 -----

CC EMBL: M91212; AA03575.1; -

DR InterPro: IPR003006; IG\_MHC.

DR InterPro: IPR003598; IG\_C2.

DR InterPro: IPR003600; IG\_Like.

DR Pfam: PF00047; Ig\_2.

DR SMART; SM00408; IgC2; 1.

DR SMART; SM00410; IG\_Like; 1.

DR PROSITE; PS00290; IG\_MHC; 1.

KW Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 22

FT CHAIN 23 416

FT DOMAIN 23 352

FT TRANSMEM 353 373

FT DOMAIN 374 416

FT DOMAIN 31 105

FT DOMAIN 136 213

FT DOMAIN 262 318

FT DISULFID 38 98

FT DISULFID 143 207

FT DISULFID 269 311

FT CARBOHYD 25 25

FT CARBOHYD 80 80

FT SEQUENCE 403 AA: 42668 MW: 1279796FD1579357 CRC64;



DE DNA MISMATCH REPAIR PROTEIN MUTH.  
GN MUTH OR H10403.  
OS Haemophilus influenzae.  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
CC Haemophilus.  
OX NCBI\_TaxID=727;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=RD / KW20 / ATCC 51907;  
RX MEDLINE=95350630; Pubmed=7542800;  
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
RA Kienley A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,  
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,  
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
RA Venter J.C.;  
RT "Whole-genome random sequencing and assembly of Haemophilus  
influenzae Rd.";  
RL Science 269:496-512(1995).  
CC -I- FUNCTION: SEQUENCE-SPECIFIC ENDONUCLEASE THAT CLEAVES UNMETHYLATED  
CC GATC SEQUENCES. IT IS INVOLVED IN DNA MISMATCH REPAIR (BY  
CC SIMILARITY).  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
-----  
DR EMBL: U32723; AAC22062.1; -  
DR HSSP: P06722; 2A2O.  
DR TIGR: H10403; -  
DR DNA repair: Hydrolase; Endonuclease; Complete proteome.  
KW SEQUENCE 223 AA; 24906 MW; 339A4EF9DA0E822A CRC64;  
SO  
  
Query Match 68.8%; Score 33; DB 1; Length 223;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 4 ITARIGE 10  
DB 165 ITARIGE 171  
  
RESULT 7  
NIFH\_CLOCB STANDARD: PRT; 270 AA.  
AC 059270;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE NITROGENASE IRON PROTEIN (EC 1.18.6.1) (NITROGENASE COMPONENT II)  
DE (NITROGENASE REDUCTASE).  
GN NIFH.  
OS Clostridium cellulosum.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;  
CC Clostridium.  
OX NCBI\_TaxID=29355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 18532;  
RA Chen T., Leschine S.B.;  
RT Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.  
CC -I- FUNCTION: THE KEY ENZYMAIC REACTIONS IN NITROGEN FIXATION ARE  
CC CATALYZED BY THE NITROGENASE COMPLEX, WHICH HAS 2 COMPONENTS: THE  
CC IRON PROTEIN AND THE MOLYBDENUM-IRON PROTEIN.  
CC -I- CATALYTIC ACTIVITY: 3 REDUCED FERREDOXIN + 6 H(+) + N ATP =

CC 3 OXIDIZED FERREDOXIN + 2 NH(3) + N ADP + N ORTHOPHOSPHATE.  
CC -I- COFACTOR: BINDS ONE 4FE-4S CLUSTER PER DIMER.  
CC -I- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -I- SIMILARITY: BELONGS TO THE NIFH/CHL FAMILY.  
CC -I- CAUTION: LACKS THE FIRST CONSERVED IRON-SULFUR BINDING CYSTEINE.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
-----  
DR EMBL: U59414; AAB63257.1; -  
DR HSSP: P00459; INIP.  
DR InterPro: IPR000392; NitrogenaseII.  
DR Pfam: PF00142; fer4\_NIFH; 1.  
DR PRINTS: PR00091; NITROGENASEII.  
DR PROSITE: PS00746; NIFH\_FRXC\_1; FALSE\_NEG.  
DR PROSITE: PS00692; NIFH\_FRXC\_2; 1.  
KW Oxidoreductase; Nitrogen fixation; Iron-sulfur; 4Fe-4S; ATP-binding.  
FT NP\_BIND 8 15  
FT METAL 128 128  
FT SEQUENCE 270 AA; 29112 MW; 783335DBFB0ADE88 CRC64;  
SO  
  
Query Match 68.8%; Score 33; DB 1; Length 270;  
Best Local Similarity 66.7%; Pred. No. 12;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
OY 2 ONTARIGE 10  
DB 19 ONTARIGE 27  
  
RESULT 8  
CSD\_HAEIN STANDARD: PRT; 437 AA.  
AC 057476; 005054;  
DT 20-AUG-2001 (Rel. 40, Created)  
DT 20-AUG-2001 (Rel. 40, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE PROBABLE CYSTEINE DESULFURASE (EC 4.4.1.-).  
GN CSD OR H11295.  
OS Haemophilus influenzae.  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
CC Haemophilus.  
OX NCBI\_TaxID=727;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=RD / KW20;  
RX MEDLINE=95350630; Pubmed=7542800;  
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
RA Kienley A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,  
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,  
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
RA Venter J.C.;  
RT "Whole-genome random sequencing and assembly of Haemophilus  
influenzae Rd.";  
RL Science 269:496-512(1995).  
CC -I- FUNCTION: CATALYZES THE REMOVAL OF ELEMENTAL SULFUR AND SELENIUM  
CC ATOMS FROM L-CYSTEINE, L-CYSTEINE, L-ALANINE (BY SIMILARITY).  
CC SELENOCYSTINE TO PRODUCE L-CYSTEINE (BY SIMILARITY).  
CC -I- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
CC -I- SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
CC AMIOTRANSFERASES. CSD SUBFAMILY.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))).  
 CC -----  
 CC EMBL; U32809; AAC22941.1; -  
 CC TIGR; H11295; -  
 CC InterPro: IPR000192; AminoTransf\_class\_V.  
 CC Pfam: PF00266; aminotran\_5; 1.  
 CC PROSITE; PS00595; AA\_TRANSFERR\_CLASS\_5; FALSE\_NEG.  
 CC KEGG; PYRIDOXAL\_P; Complete proteome.  
 CC BINDING; 258 258 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 CC SEQUENCE 437 AA; 49048 MW; 1126FEC23DE8BB9B CRC64;  
 OY 2 ONTARIGE 10  
 DB 385 ONTARIGE 393  
 Query Match 68.8%; Score 33; DB 1; Length 437;  
 Best Local Similarity 66.7%; Pred. No. 20;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 RESULT 9  
 ID VDCG\_STRD7 STANDARD; PRT; 474 AA.  
 AC 09X697;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE VDCG PROTEIN.  
 GN VDCG.  
 OS Streptomyces sp. (strain D7).  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptomycetales; Streptomycetaceae; Streptomycetes.  
 OX NCBI\_TaxID=92742;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Chow K.T., Pope M.K., Davies J.E.;  
 RT "Characterization of a vanillic acid non-oxidative decarboxylation  
 RT gene cluster from Streptomyces.";  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- INDUCTION: SYNTHESIZED IN RESPONSE TO VANILLATE.  
 CC -1- SIMILARITY: BELONGS TO THE UBD FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))).  
 CC -----  
 CC EMBL; AF134589; AAD28782.1; -  
 CC DR EMBL; AF134589; AAD28782.1; -  
 CC DR InterPro: IPR002830; UPF0096.  
 CC Pfam: PF01977; UPF0096; 1.  
 CC SEQUENCE 474 AA; 52120 MW; 1DAE84542E75C75C CRC64;  
 OY 1 AONTARIGE 10  
 DB 35 AONTARIGE 44  
 Query Match 68.8%; Score 33; DB 1; Length 474;  
 Best Local Similarity 70.0%; Pred. No. 22;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 RESULT 10  
 XYL6\_PSEPD

ID XYL6\_PSEPD STANDARD; PRT; 486 AA.  
 AC P23105;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE 2-HYDROXYMUCONIC SEMIALDEHYDE DEHYDROGENASE (EC 1.2.1.-) (HMSD).  
 GN XYL6.  
 OS Pseudomonas putida.  
 OG Plasmid TOL PMMO.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 OC Pseudomonas.  
 OX NCBI\_TaxID=303;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-92167811; PubMed=1791759;  
 RA Horn J.M., Harayama S., Timmis K.N.;  
 RT "DNA sequence determination of the TOL plasmid (pmmo) xylGJ genes of  
 RT Pseudomonas putida: implications for the evolution of aromatic  
 RT catabolism.";  
 RL Mol. Microbiol. 5:2459-2474(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PAO;  
 RX MEDLINE-92317087; PubMed=1339433;  
 RX Steele M.I., Lorenz D., Hatter K., Park A., Sokatch J.R.;  
 RT "Characterization of the mmsAB operon of Pseudomonas aeruginosa PAO  
 RT encoding methylmalonate-semialdehyde dehydrogenase and 3-  
 RT hydroxyisobutyrate dehydrogenase.";  
 RL J. Biol. Chem. 267:13585-13592(1992).  
 RN [3]  
 RP SEQUENCE OF 1-15.  
 RX MEDLINE-95173094; PubMed=7868591;  
 RA Inoue J., Shaw J.P., Reik M., Harayama S.;  
 RT "Overlapping substrate specificities of benzaldehyde dehydrogenase  
 RT (the xylC gene product) and 2-hydroxymuconic semialdehyde  
 RT dehydrogenase (the xylG gene product) encoded by TOL plasmid pmmo of  
 RT Pseudomonas putida.";  
 RL J. Bacteriol. 177:1196-1201(1995).  
 CC -1- FUNCTION: 2-HYDROXYMUCONIC ACID SEMIALDEHYDE CAN BE CONVERTED TO  
 CC 2-HYDROXYMUCONIC ACID SEMIALDEHYDE EITHER DIRECTLY BY THE ACTION OF 2-  
 CC 2-HYDROXYMUCONIC SEMIALDEHYDE DEHYDROGENASE (HMSH) OR BY THE ACTION OF  
 CC THREE SEQUENTIAL ENZYMES, THE FIRST OF WHICH IS HMSD. CAN OXIDIZE  
 CC NOT ONLY 2-HYDROXYMUCONIC SEMIALDEHYDE AND ITS ANALOGS BUT ALSO  
 CC BENZALDEHYDE AND ITS ANALOGS. OPTIMAL PH OF CATALYSIS FOR THE  
 CC OXIDATION OF 2-HYDROXYMUCONIC SEMIALDEHYDE AND BENZALDEHYDE ARE  
 CC RESPECTIVELY 8.3 AND 9.6.  
 CC -1- PATHWAY: META-CLEAVAGE PATHWAY FOR THE DEGRADATION OF PHENOLS,  
 CC CRESOLS AND CATRECHOL. PHENOL METABOLISM.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))).  
 CC -----  
 CC EMBL; M64747; AAA26053.1; -  
 CC DR EMBL; M64747; AAA26053.1; -  
 CC DR PIR; S18244; S18244.  
 CC DR PIR; E42902; E42902.  
 CC DR PIR; S23488; S23488.  
 CC HSSP: P20000; 1A4Z.  
 CC InterPro: IPR002086; Aldehyde\_dehydr.  
 CC Pfam: PF00171; aldehyd\_1.  
 CC PROSITE; PS00070; ALDEHYDE\_DEHYDR\_CYS; 1.  
 CC DR PROSITE; PS00687; ALDEHYDE\_DEHYDR\_GLU; 1.  
 CC KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD; Plasmid.  
 CC ACT\_SITE 254 254 BY SIMILARITY.  
 CC FT ACT\_SITE 288 288 BY SIMILARITY.  
 CC FT CONFLICT 11 12 EL -> AF (IN REF. 3).  
 CC SEQUENCE 486 AA; 51761 MW; 854303F121B2FFBD CRC64;

Query Match 68.8%; Score 33; DB 1; Length 486;  
 Best Local Similarity 70.0%; Pred. No. 23;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AONTARIGE 10  
 DB 74 ADITARIGE 83

RESULT 11  
 INHA\_MYCAV STANDARD: PRT; 268 AA.

AC 007400:  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) (NADH-DEPENDENT ENOYL-ACP REDUCTASE).  
 GN INHA.  
 OS Mycobacterium avium.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1764;  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GI10:  
 RA MEDLINE=98195739; PubMed=9534249;  
 RA Labo M., Gubserli L., de Rossi E., Speciale P., Riccardi G.;  
 RT "Determination of a 15437 bp nucleotide sequence around the inhA gene  
 of Mycobacterium avium and similarity analysis of the products of  
 putative ORFs."  
 RL Microbiology 144:807-814(1998).  
 CC -1- CATALYTIC ACTIVITY: ACYL-[ACYL-CARRIER PROTEIN] + NAD(+) =  
 TRANS-2,3-DEHYDROACYL-[ACYL-CARRIER PROTEIN] + NADH.  
 CC -1- PATHWAY: SECOND REDUCTIVE STEP IN FATTY ACID BIOSYNTHESIS. THIS  
 CC ISOZYME IS INVOLVED IN MYCOLIC ACID BIOSYNTHESIS.  
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).  
 CC -1- SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN  
 CC DEHYDROGENASES/REDUCTASES (SDR) FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AF002133; AAC46204.1;..  
 DR Oxidoreductase; NAD: Fatty acid biosynthesis.  
 KW NP\_BIND 135 164 NAD (POTENTIAL).  
 FT SEQUENCE 268 AA; 28529 MW; F73501BD2B0F9990 CRC64;  
 SQ

Query Match 66.7%; Score 32; DB 1; Length 268;  
 Best Local Similarity 60.0%; Pred. No. 20;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 AONTARIGE 10  
 DB 75 AORVTGEIGE 84

RESULT 12  
 INHA\_MYCSM STANDARD: PRT; 269 AA.

AC P42829:  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9) (NADH-

DEPENDENT ENOYL-ACP REDUCTASE).  
 GN INHA.  
 OS Mycobacterium smegmatis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1772;  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 700084 / MC(2)155;  
 RA MEDLINE=94112548; PubMed=8284673;  
 RA Banerjee A., Dubnau E., Quemard A., Balasubramanian V., Um K.S.,  
 RA Wilson T., Collins D., de Lisle G., Jacobs W.R. Jr.;  
 RT "inhA, a gene encoding a target for isoniazid and ethionamide in  
 Mycobacterium tuberculosis."  
 RL Science 263:227-230(1994).  
 CC -1- CATALYTIC ACTIVITY: ACYL-[ACYL-CARRIER PROTEIN] + NAD(+) =  
 TRANS-2,3-DEHYDROACYL-[ACYL-CARRIER PROTEIN] + NADH.  
 CC -1- PATHWAY: SECOND REDUCTIVE STEP IN FATTY ACID BIOSYNTHESIS. THIS  
 CC ISOZYME IS INVOLVED IN MYCOLIC ACID BIOSYNTHESIS.  
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).  
 CC -1- MISCELLANEOUS: INVOLVED IN THE RESISTANCE AGAINST THE  
 CC ANTITUBERCULOSIS DRUGS ISONIAZID AND ETHIONAMIDE.  
 CC -1- SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN  
 CC DEHYDROGENASES/REDUCTASES (SDR) FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: U02530; AAC43211.1;..  
 DR HSSP: P46533; 1ENZ.  
 KW Oxidoreductase; NAD: Fatty acid biosynthesis; Antibiotic resistance.  
 FT NP\_BIND 136 165 NAD (POTENTIAL).  
 FT VARIANT 94 94 S -> A (IN INH-RESISTANT STRAIN MC  
 FT SQUARED 651).  
 SQ SEQUENCE 269 AA; 28527 MW; AD3BD962DB78FC6 CRC64;  
 DB 75 ADITARIGE 84

Query Match 66.7%; Score 32; DB 1; Length 269;  
 Best Local Similarity 70.0%; Pred. No. 20;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AONTARIGE 10  
 DB 75 ADITARIGE 84

RESULT 13  
 Y413\_ARATH STANDARD: PRT; 435 AA.

AC O04656:  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE HYPOTHETICAL 48.8 KDA PROTEIN M021B04.13.  
 GN A\_TW021B04.13.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RA Dante M., Mansley P., Gibson A.;  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE NOP5/NOP56 FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AF007271; AAB61074.1; -  
 DR InterPro: IPR002687; Nop.  
 DR Pfam: PF01798; Nop; 1.  
 DR ProDom: PD004104; Nop; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 435 AA; 48818 MW; BE502C8C244AF085 CRC64;

Query Match  
 Best Local Similarity 66.7%; Score 32; DB 1; Length 435;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 AONTARIGE 10  
 DB 238 APTLTALVGE 247

RESULT 14  
 Y412.ARATH STANDARD; PRT; 439 AA.  
 AC 004658;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DE 01-NOV-1997 (Rel. 35, Last annotation update)  
 GN HYPOTHETICAL 47.9 KDA PROTEIN M021B04.12.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RP STRAIN=CV. COLUMBIA;  
 RA Dante M., Wamsley P., Gibson A.;  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE NOP5/NOP56 FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AF007271; AAB61073.1; -  
 DR InterPro: IPR002687; Nop.  
 DR Pfam: PF01798; Nop; 1.  
 DR ProDom: PD004104; Nop; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 439 AA; 47932 MW; BE0E2214F9BCA4FDB CRC64;

Query Match  
 Best Local Similarity 66.7%; Score 32; DB 1; Length 439;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 AONTARIGE 10  
 DB 281 APTLTALVGE 290

RESULT 15  
 ARLY\_METTH STANDARD; PRT; 468 AA.  
 ID ARLY\_METTH

AC 026369;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DE 20-ANG-2001 (Rel. 40, Last annotation update)  
 GN ARGININOSUCCINATE LYASE (EC 4.3.2.1) (ARGINOSUCCINASE) (ASAL).  
 GN ANGH OR MTH269.  
 OS Methanobacterium thermoautotrophicum.  
 OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;  
 OC Methanobacter.  
 OX NCBI\_TaxID=145262;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RP STRAIN=DELTA H;  
 RX MEDLINE=98037514; PubMed=93711463;  
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,  
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,  
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pochler B., Qiu D.,  
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,  
 RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,  
 RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,  
 RA Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;  
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum  
 RT deltaH: functional analysis and comparative genomics.";  
 RL J. Bacteriol. 179:7135-7155(1997).  
 CC -1- CATALYTIC ACTIVITY: L-ARGININOSUCCINATE = FUMARATE + L-ARGININE.  
 CC -1- PATHWAY: THE LAST STEP IN ARGININE BIOSYNTHESIS.  
 CC -1- SIMILARITY: BELONGS TO THE LYASE I FAMILY. ARGININOSUCCINATE LYASE  
 CC SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AE000812; AAB84775.1; -  
 DR InterPro: IPR000362; Fumarate\_Lyase.  
 DR Pfam: PF00206; Lyase\_1; 1  
 DR PRINTS: PR00145; DCRISTALLIN.  
 DR PRINTS: PR00149; FUMARATE\_LYASE.  
 DR PROSITE: PS00163; FUMARATE\_LYASES; FALSE\_NEG.  
 KW Arginine biosynthesis; Lyase; Complete proteome.  
 SQ SEQUENCE 468 AA; 52439 MW; 2DD1F7A65FB5DP57 CRC64;

Query Match  
 Best Local Similarity 66.7%; Score 32; DB 1; Length 468;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 ITARIGE 10  
 DB 90 VTARIGE 96

Search completed: April 24, 2002, 09:20:41  
 Job time: 255 sec



**THIS PAGE BLANK (USPTO)**



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 09:20:13 ; Search time 62.94 Seconds  
(without alignments)  
23.240 Million cell updates/sec

Title: US-09-689-469-6  
Perfect score: 48  
Sequence: 1 AONITRARGE 10

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SPREMBL\_17:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID     | Description         |
|------------|-------|-------------|--------|-----------|---------------------|
| 1          | 48    | 100.0       | 342    | 4 O9Y3R3  | O9Y3R3 homo sapien  |
| 2          | 44    | 91.7        | 402    | 11 O35444 | O35444 mus musculu  |
| 3          | 37    | 77.1        | 246    | 2 P71291  | P71291 escherichia  |
| 4          | 36    | 75.0        | 879    | 2 O30579  | O30579 bacillus su  |
| 5          | 36    | 75.0        | 879    | 2 O31504  | O31504 bacillus su  |
| 6          | 35    | 72.9        | 84     | 12 O40496 | O40496 human immu   |
| 7          | 35    | 72.9        | 547    | 5 O18609  | O18609 caenorhabdi  |
| 8          | 35    | 72.9        | 851    | 12 O73304 | O73304 human immu   |
| 9          | 34    | 70.8        | 76     | 12 O9WAE2 | O9WAE2 human immu   |
| 10         | 34    | 70.8        | 90     | 12 O76444 | O76444 human immu   |
| 11         | 34    | 70.8        | 90     | 12 O9YWS9 | O9YWS9 human immu   |
| 12         | 34    | 70.8        | 391    | 2 O51393  | O51393 pseudomonas  |
| 13         | 34    | 70.8        | 401    | 2 O9ZIC1  | O9ZIC1 pseudomonas  |
| 14         | 34    | 70.8        | 459    | 12 O91900 | O91900 human immu   |
| 15         | 34    | 70.8        | 715    | 2 O30965  | O30965 rhizobium l  |
| 16         | 34    | 70.8        | 808    | 1 O58937  | O58937 methanococ   |
| 17         | 34    | 70.8        | 1155   | 1 O58048  | O58048 pyrococcus   |
| 18         | 33    | 68.8        | 32     | 6 O9TRQ1  | O9TRQ1 bos taurus   |
| 19         | 33    | 68.8        | 42     | 10 O9LE26 | O9LE26 psittacus nu |

|    |    |      |      |           |                     |
|----|----|------|------|-----------|---------------------|
| 20 | 33 | 68.8 | 135  | 2 O56486  | O56486 unidentified |
| 21 | 33 | 68.8 | 135  | 2 O56487  | O56487 unidentified |
| 22 | 33 | 68.8 | 135  | 2 O56489  | O56489 unidentified |
| 23 | 33 | 68.8 | 141  | 2 O66292  | O66292 unidentified |
| 24 | 33 | 68.8 | 141  | 2 O66293  | O66293 unidentified |
| 25 | 33 | 68.8 | 141  | 2 O66324  | O66324 unidentified |
| 26 | 33 | 68.8 | 141  | 2 O66349  | O66349 unidentified |
| 27 | 33 | 68.8 | 141  | 2 O66358  | O66358 unidentified |
| 28 | 33 | 68.8 | 141  | 2 O66361  | O66361 unidentified |
| 29 | 33 | 68.8 | 141  | 2 O66499  | O66499 unidentified |
| 30 | 33 | 68.8 | 269  | 2 O9CBM1  | O9CBM1 mycobacteri  |
| 31 | 33 | 68.8 | 387  | 1 O9HSB6  | O9HSB6 halobacteri  |
| 32 | 33 | 68.8 | 550  | 10 O65335 | O65335 pismu sativ  |
| 33 | 33 | 68.8 | 555  | 2 O9A310  | O9A310 caulobacter  |
| 34 | 33 | 68.8 | 560  | 10 O65334 | O65334 pismu sativ  |
| 35 | 33 | 68.8 | 792  | 2 O9PEZ4  | O9PEZ4 xyella fas   |
| 36 | 33 | 68.8 | 848  | 5 O25198  | O25198 hydra atten  |
| 37 | 33 | 68.8 | 4436 | 1 O58659  | O58659 pyrococcus   |
| 38 | 32 | 66.7 | 42   | 10 O9LE27 | O9LE27 lycopodium   |
| 39 | 32 | 66.7 | 42   | 10 O9LDB7 | O9LDB7 marchantia   |
| 40 | 32 | 66.7 | 149  | 2 O9F6U7  | O9F6U7 bacteroides  |
| 41 | 32 | 66.7 | 223  | 2 O9S6L2  | O9S6L2 corynebacte  |
| 42 | 32 | 66.7 | 247  | 2 O9AQM1  | O9AQM1 pseudomonas  |
| 43 | 32 | 66.7 | 268  | 2 O9Z473  | O9Z473 corynebacte  |
| 44 | 32 | 66.7 | 269  | 2 O9X6U5  | O9X6U5 brevbacter   |
| 45 | 32 | 66.7 | 269  | 2 O9LAH3  | O9LAH3 corynebacte  |

# ALIGNMENTS

RESULT 1  
O9Y3R3 PRELIMINARY; PRT: 342 AA.

AC O9Y3R3: 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE RECEPTOR FOR ADVANCED GLYCATION END PRODUCTS PRECURSOR.  
GN RAGESEC.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Malherbe P., Richards J., Gallard H., Thompson A., Diener C.,  
RA Schuler A., Huber G.;  
RT "CDNA cloning of a novel secreted isoform of the human Receptor for  
RT co-expressing glycation end products (RAGE) and characterization of cells  
RT amyloid precursor protein.";  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
CC DOMAIN.  
DR EMBL: A113822; CABA3108.1; -  
DR InterPro: IPR003598; IG\_C2.  
DR InterPro: IPR003600; IG\_Like.  
DR InterPro: IPR003006; IG\_MHC.  
DR Pfam: PF00047; Ig\_2.  
DR SMART: SM00408; IGC2; 1.  
DR SMART: SM00410; IG\_Like; 1.  
KW Signal; Receptor.  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 342 RECEPTOR FOR ADVANCED GLYCATION END  
FT PRODUCT.  
SQ SEQUENCE 342 AA; 36193 MW; 35DDF6A13E3B38 CRC64;

Query Match 100.0%; Score 48; DB 4; Length 342;  
Best Local Similarity 100.0%; Pred. No. 0.058;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ANONTARIGE 10  
 DB 23 ANONTARIGE 32

RESULT 2  
 ID 035444 PRELIMINARY: PRT: 402 AA.  
 AC 035444:  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE PAGE.  
 GN PAGE.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Rowen L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,  
 RA Lorentz C., Schmidt S., Tipton S., Traicoff R., Zachrone K., Hood L.:  
 RL Submitted (Oct-1997) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 CC EMBL: AF030001; AAB82007.1; -  
 DR InterPro: IPR003598; Iq\_c2.  
 DR InterPro: IPR003600; Iq\_like.  
 DR InterPro: IPR003006; Iq\_MHC.  
 DR Pfam: PF00047; Iq\_3.  
 DR SMART: SM00408; IqC2; 1.  
 DR SMART: SM00410; Iq\_Like; 1.  
 DR PROSITE: PS00290; Iq\_MHC; UNKNOWN\_1.  
 SQ SEQUENCE 402 AA; 42653 MW; DBFDC50A6C8CB902 CRC64;

Query Match 91.7%; Score 44; DB 11; Length 402;  
 Best Local Similarity 100.0%; Pred. No. 0.49;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ONTARIGE 10  
 DB 24 ONTARIGE 32

RESULT 3  
 ID P71291 PRELIMINARY: PRT: 246 AA.  
 AC P71291:  
 DT 01-FEB-1997 (TREMBLrel. 02, Created)  
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
 DT 01-FEB-1997 (TREMBLrel. 02, Last annotation update)  
 DE SIMILAR TO E. COLI YJHH.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OC NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung E.,  
 RA Davis R., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,  
 RA Laskhari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,  
 RA Davis R.W.:  
 RL Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U70214; AAB08689.1; -  
 SQ SEQUENCE 246 AA; 26806 MW; 93FBCA6B432BE37D CRC64;

Query Match 77.1%; Score 37; DB 2; Length 246;  
 Best Local Similarity 70.0%; Pred. No. 8.5;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 78 ADMARIGE 87

RESULT 4  
 ID 030579 PRELIMINARY: PRT: 879 AA.  
 AC 030579:  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE YEBA.  
 GN YEBA.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Staphylococcus group; Bacillus.  
 OC NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168 TRPC2;  
 RA Borries R., Schroeter R.:  
 RL Submitted (Jul-1997) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF012532; AAB66474.1; -  
 DR InterPro: IPR002052; N6\_Mtase.  
 DR PROSITE: PS00092; N6\_Mtase; UNKNOWN\_1.  
 SQ SEQUENCE 879 AA; 101108 MW; B5E35926796B49AA CRC64;

Query Match 75.0%; Score 36; DB 2; Length 879;  
 Best Local Similarity 66.7%; Pred. No. 57;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 ONTARIGE 10  
 DB 45 ONTARIGE 53

RESULT 5  
 ID 031504 PRELIMINARY: PRT: 879 AA.  
 AC 031504:  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE YEBA PROTEIN.  
 GN YEBA.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Staphylococcus group; Bacillus.  
 OC NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=98044033; PubMed=9384377;  
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
 RA Azevedo V., Bertero M.G., Bessieres P., Boltin A., Borchert S.,  
 RA Borries R., Bourrier L., Brans A., Braun M., Brigelli S.C., Bron S.,  
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,  
 RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,  
 RA Dentan F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,  
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,  
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
 RA Ghm S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,  
 RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,  
 RA Hilbert H., Holtsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,  
 RA Joris B., Karamata D., Kasahara Y., Kjaer-Blanchard M., Klein C.,  
 RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,  
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
 RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,  
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,  
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,  
 RA Paro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,  
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,  
 RA Sato T., Scanlan E., Schlech S., Schroeder R., Scoffone F.,  
 RA Seriguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,  
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,  
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni K.,  
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,  
 RA Viari A., Wambutt R., Wedler E., Wedler H., Wetzenecker T.,  
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,  
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,  
 RT "The complete genome sequence of the gram-positive bacterium Bacillus  
 RT subtilis.";  
 RL Nature 390:249-256(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-168;  
 RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.,  
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Z99107; CAB12496.1; -;  
 DR InterPro: IPR002052; N6\_Mtase.  
 DR PROSITE: PS00092; N6\_MTASE; UNKNOWN\_1.  
 KW Complete proteome.  
 SQ SEQUENCE 879 AA; 101157 MW; 555B1607264285A5 CRC64;

Query Match 75.0%; Score 36; DB 2; Length 879;  
 Best Local Similarity 66.7%; Pred. No. 57;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 ONTARIGE 10  
 DB 45 ONLTRKRGV 53

RESULT 6  
 AC 040496 PRELIMINARY; PRT; 84 AA.  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentiviruses.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-95M145;  
 RA Peeters M., Koumare B., Mulanga C., Brengues C., Mountrou B.,  
 RA Bougoudogo F., Ravel S., Bibollet-Ruche F.,  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Y14356; CAA74727.1; -;  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 KW Envelope protein.  
 FT NON\_TER 1  
 FT NON\_TER 84  
 SQ SEQUENCE 84 AA; 9256 MW; 6D5031F860B23C75 CRC64;

Query Match 72.9%; Score 35; DB 12; Length 84;  
 Best Local Similarity 55.6%; Pred. No. 6.8;  
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 2 ONTARIGE 10  
 DB 65 ONVTAKLQ 73

RESULT 7  
 ID 018609 PRELIMINARY; PRT; 547 AA.  
 AC 018609;

DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE SIMILAR TO YEAST VACUOLAR SORTING PROTEIN SLP1.  
 GN C44C1.4.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Alnscough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showken R.,  
 RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,  
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RT elegans.";  
 RL Nature 368:32-38(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Bradshaw H., Stellyes L.,  
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Waterston R.,  
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U41050; AAA82364.1; -;  
 DR InterPro: IPR001619; Sec1.  
 DR Pfam: PF00995; Sec1; 1.  
 SQ SEQUENCE 547 AA; 62119 MW; 4F8B7B99607789E1 CRC64;

Query Match 72.9%; Score 35; DB 5; Length 547;  
 Best Local Similarity 70.0%; Pred. No. 55;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 AONTARIGE 10  
 DB 265 ARNTANFGE 274

RESULT 8  
 ID 073304 PRELIMINARY; PRT; 851 AA.  
 AC 073304;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE ENVELOPE GLYCOPROTEIN.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentiviruses.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96263682; PubMed=8924250;  
 RA Douglas N.W., Knight A.I., Hayhurst A., Barrett W.Y., Kevany M.J.,  
 RA Daniels R.S.,  
 RT "An efficient method for the rescue and analysis of functional HIV-1  
 RT env genes: evidence for recombination in the vicinity of the tat/rev  
 RT splice site.";  
 RL AIDS 10:39-46(1996).  
 DR EMBL: U36879; AAC55538.1; -;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.  
 KW Envelope protein.  
 SQ SEQUENCE 851 AA; 96525 MW; F985DB4E881F718 CRC64;

Query Match 72.9%; Score 35; DB 12; Length 851;  
 Best Local Similarity 87.5%; Pred. No. 90;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 NITARIGE 10  
 ||:|:|:  
 Db 157 NITRIGE 164

RESULT 9  
 O9WBE2 PRELIMINARY; PRT; 76 AA.

AC O9WBE2; 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, last sequence update)  
 DE 01-JUN-2001 (TREMBlrel. 17, last annotation update)  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RUI153;  
 RA Bobkov A.F., Kazenova E.V., Selimova L.M., Ladnaya N.N.,  
 RA Kravchenko A.V., Foley B., Morrison I., Pokrovsky V.V.,  
 RA Chelngsong-Popov R., Weber J.N.;  
 RT "Hiv-1 gagD/envG recombinants in Russia."  
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF051468; AAD02595.1;  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 FT NON\_TER 1 76  
 FT SEQUENCE 76 AA; 8205 MW; 3B731642912E1954 CRC64;

Query Match 70.8%; Score 34; DB 12; Length 76;  
 Best Local Similarity 55.6%; Pred. No. 9.9;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 ONTARIGE 10  
 ||:|:|:  
 Db 47 QNVTTRIGE 55

RESULT 10  
 O76444 PRELIMINARY; PRT; 90 AA.

AC O76444; 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)  
 DE 01-JUN-2001 (TREMBlrel. 17, last annotation update)  
 GN ENVELOPE GLYCOPROTEIN 120 VS REGION (FRAGMENT).  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RUS12;  
 RA MEDLINE=93367213; PubMed=7639968;  
 RA Lukashov V.V., Cornelissen M.T., Goudsmit J., Papushvili M.N.,  
 RA Rytlik P.G., Khalitov R.M., Karanov E.V., De Wolf F.;  
 RT "Simultaneous introduction of distinct HIV-1 subtypes into different  
 RT risk groups in Russia, Belarusia and Lithuania."  
 RL AIDS 9:435-439(1995).  
 DR EMBL: U38413; AAA91757.1; -.

DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 KW Envelope protein.  
 FT NON\_TER 1 90  
 FT SEQUENCE 90 AA; 10076 MW; 5AD80C9ADB28E330 CRC64;

Query Match 70.8%; Score 34; DB 12; Length 90;  
 Best Local Similarity 55.6%; Pred. No. 12;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 QNTARIGE 10  
 ||:|:|:  
 Db 73 QNVTTRIGE 81

RESULT 11  
 O9YWS9 PRELIMINARY; PRT; 90 AA.

AC O9YWS9; 01-MAY-1999 (TREMBlrel. 10, Created)  
 DT 01-MAY-1999 (TREMBlrel. 10, last sequence update)  
 DE 01-JUN-2001 (TREMBlrel. 17, last annotation update)  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RUI153;  
 RA Bobkov A.F., Kazenova E.V., Selimova L.M., Ladnaya N.N.,  
 RA Kravchenko A.V., Foley B., Morrison I., Pokrovsky V.V.,  
 RA Chelngsong-Popov R., Weber J.N.;  
 RT "Hiv-1 gagD/envG recombinants in Russia."  
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF051469; AAD02596.1;  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 FT NON\_TER 1 90  
 FT SEQUENCE 90 AA; 9755 MW; 6F04439DFE45B5EB CRC64;

Query Match 70.8%; Score 34; DB 12; Length 90;  
 Best Local Similarity 55.6%; Pred. No. 12;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 QNTARIGE 10  
 ||:|:|:  
 Db 61 QNVTTRIGE 69

RESULT 12  
 O51393 PRELIMINARY; PRT; 391 AA.

AC O51393; 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)  
 DE 01-MAR-2001 (TREMBlrel. 16, last annotation update)  
 GN ALGJ (ALGINATE O-ACETYLTRANSFERASE ALGJ).  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 OX Pseudomonas.  
 OX NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FRD1;  
 RA Franklin M.J., Ohman D.E.;  
 RL J. Bacteriol. 178:0-0(0).  
 RN [2]

RP SEQUENCE FROM N.A.  
RC STRAIN-PA01.  
RX MEDLINE=20437337; PubMed=10984043;  
RA Stover C.K., Plam K.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
RA Hickey M.J., Brinkman F.S.L., Hutnagle W.O., Kowalik D.J., Lagrou M.,  
RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,  
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;  
RT \*Complete genome sequence of *Pseudomonas aeruginosa* PA01, an  
RT opportunistic pathogen.;"  
RL Nature 406:959-964(2000).  
DR EMBL; U50202; AAB09782.1; -.  
DR EMBL; AE004775; AAC06937.1; -.  
KW Transference; Complete proteome.  
SQ SEQUENCE 391 AA; 43106 MW; AE04882394D5503 CRC64;

|                       |       |              |      |              |
|-----------------------|-------|--------------|------|--------------|
| Query Match           | 70.8% | Score 34     | DB 2 | Length 391   |
| Best Local Similarity | 60.0% | Pred No      | 62   |              |
| Matches               | 6     | Conservative | 1    | Mismatches 3 |
|                       |       |              |      | Indels 0     |
|                       |       |              |      | Gaps 0       |
| QY                    | 1     | AONTARIGE    | 10   |              |
|                       |       |              |      |              |
|                       |       |              |      |              |
| Db                    | 222   | AONTVRAGE    | 231  |              |

| RESULT | 13   |        |                           |
|--------|--|--------|---------------------------|
| 09Z1C1 | ID   | 09Z1C1 | PRELIMINARY; PRT; 401 AA. |
| AC     | 09Z1C1;  |        |                           |
| DT     | 01-MAY-1999 (TREMBLrel. 10, Created)   |        |                           |
| DT     | 01-MAY-1999 (TREMBLrel. 10, last sequence update)                                  |        |                           |
| DT     | 01-JUN-2001 (TREMBLrel. 17, last annotation update)                                |        |                           |
| DE     | EXODEOXYRIBONUCLEASE VII LARGE SUBUNIT (FRAGMENT).                                 |        |                           |
| GN     | XSEA.  |        |                           |
| OS     | Pseudomonas fluorescens.   |        |                           |
| OC     | Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;                     |        |                           |
| OC     | Pseudomonas.   |        |                           |
| OX     | NCBI_TaxID=294;  |        |                           |
| RN     | [1]  |        |                           |
| RP     | SEQUENCE FROM N.A.   |        |                           |
| RC     | STRATN-MF0;  |        |                           |
| RA     | Regeard C., Merieau A., Leriche F., Guespin-Michel J.;                             |        |                           |
| RT     | *Genetic studies of thermoregulated genes in the psychrotrophic                    |        |                           |
| RT     | vii <sup>+</sup> bacterium Pseudomonas fluorescens: unexpected role of exonuclease |        |                           |
| RL     | Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.                            |        |                           |
| DR     | EMBL; AF033853; AAC73362.1; -  |        |                           |
| DR     | InterPro; IPR003753; Exonuc_VII_L.   |        |                           |
| DR     | Pfam; PF02601; Exonuc_VII_L.1.   |        |                           |
| FT     | NON_TER  |        |                           |
| SO     | SEQUENCE   |        |                           |
|        | 401 AA; 44453 MW; 882B6EEA69BBD31 CRC64;   |        |                           |

|                       |       |              |      |              |
|-----------------------|-------|--------------|------|--------------|
| Query Match           | 70.8% | Score 34     | DB 2 | Length 401   |
| Best local similarity | 66.7% | Pred No      | 63   |              |
| Matches               | 6     | Conservative | 2    | Mismatches 1 |
|                       |       |              |      | Indels 0     |
|                       |       |              |      | Gaps 0       |
| QY                    | 2     | QNTARIGE     | 10   |              |
|                       | 1     | : : : : : 11 |      |              |
| Db                    | 372   | ORLTARLE     | 380  |              |

| RESULT 14                            |   |
|--------------------------------------|---|
| 091900                               | PRELIMINARY; PRT; 459 AA.               |
| ID 091900.                           |   |
| AC 091900.                           |   |
| DT 01-NOV-1998                       | (TREMBlrel. 08, Created)                |
| DT 01-NOV-1998                       | (TREMBlrel. 08, Last sequence update)   |
| DT 01-JUN-2001                       | (TREMBlrel. 17, Last annotation update) |
| DE ENVELOPE GLYCOPROTEIN (FRAGMENT). |   |
| GN ENV.                              |   |

OS Human immunodeficiency virus type 1  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CNG30.5;  
RA Moriyama H.;  
RT "HIV-1 in Congo."  
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases  
DR EMBL; AF056186; AAC6199.1; -  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
KW Envelope protein.  
FT NON\_TER 459  
SQ SEQUENCE 459 AA; 51218 MW; 123C315B3A19500C CRC64;

|                       |       |              |       |            |
|-----------------------|-------|--------------|-------|------------|
| Query Match           | 70.8% | Score 34     | DB 12 | Length 459 |
| Best Local Similarity | 55.6% | Pred. No. 74 |       |            |
| Matches               | 5     | Conservative | 4     | Mismatches |
|                       |       |              | 0     | Indels     |
|                       |       |              |       | Gaps 0     |
| OY                    | 2     | UNITARIGE    | 10    |            |
|                       |       | : :          |       |            |
| DB                    | 337   | ONVSASLGE    | 345   |            |

| RESULT | 15   |              |              |
|--------|--|--------------|--------------|
| 030965 |  | PRELIMINARY; | PRT; 715 AA. |
| ID     | 030965   |              |              |
| AC     | 030965;  |              |              |
| DT     | 01-JAN-1998 (TrEMBLrel. 05, Created)                             |              |              |
| DT     | 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)                |              |              |
| DT     | 01-JUN-2001 (TrEMBLrel. 17, last annotation update)              |              |              |
| DE     | PURATIVE METHYL ACCEPTING CHEMOTAXIS PROTEIN.                    |              |              |
| GN     | MCP-1.   |              |              |
| OS     | Rhizobium leguminosarum.   |              |              |
| OC     | Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group. |              |              |
| OC     | Rhizobiaceae; Rhizobium.   |              |              |
| OX     | NCBI_TaxID=384;  |              |              |
| RN     | [1]  |              |              |
| RP     | SEQUENCE FROM N.A.   |              |              |
| RA     | Yost C.K., Rochepau P., Hynes M.F.;                              |              |              |
| RL     | Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.          |              |              |
| DR     | EMBL: AF022807; AAC6418.1; -                                     |              |              |
| DR     | HSSP: P02942; 10U7   |              |              |
| DR     | InterPro: IPR000122; Chemotaxis_transducer.                      |              |              |
| DR     | InterPro: IPR000658; DUF5.                                       |              |              |
| DR     | InterPro: IPR003660; HAMF.                                       |              |              |
| DR     | Pfam: PF000672; DUF5; 1.   |              |              |
| DR     | Pfam: PF00015; MCPsignal; 1.                                     |              |              |
| DR     | SMART: SM00304; HAMF; 1.   |              |              |
| DR     | SMART: SM00283; MA; 1.   |              |              |
| DR     | SEQUENCE 715 AA; 76671 MW; CBD74CA16DA0DF81 CRC64;               |              |              |

|                       |        |                    |       |               |
|-----------------------|--------|--------------------|-------|---------------|
| Query Match           | 70.8%; | Score 34;          | DB 2; | Length 715;   |
| Best Local Similarity | 66.7%; | Pred. No. 1,2e+02; |       |               |
| Matches               | 6;     | Conservative       | 2;    | Mismatches 1; |
|                       |        |                    |       | Indels 0;     |
|                       |        |                    |       | Gaps 0;       |
| Qy                    | 2      | ONTIARIGE          | 10    |               |
|                       |        | 1111111            |       |               |
| Db                    | 235    | ONTYARLGD          | 243   |               |

Search completed: April 24, 2002, 09:20:14  
Job time: 243 sec

